Copyright

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Minimum DB
Maximum DB
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MODEL-frame+_p2n.model -DEV=xlh

-Q-/cgn2_1/USPTO_spool/US09914168/runat_28042003_151614_6787/app_query.fasta_1.1095
-O=/cgn2_1/USPTO_spool/US09914168/runat_28042003_151614_6787/app_query.fasta_1.1095
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=40 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MILEN=0 -MAXLEN=2000000000
-USER=-US09914168_eCGN_1_1_2655_erunat_28042003_151614_6787 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THERADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Ygapop 10.0 , 1
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

## Result No. 259 259 259 259 259 259 259 255.5 255.5 245.5 243.5 244.5 243.5 245.5 245.5 245.5 245.5 245.5 245.5 486.5 486.5 486.5 436.5 433.6 433.6 Score Query Match 201050 2379 10029 2394 2394 2394 2394 2394 2394 13538 11000 340806 6340806 6444 1239 181233 110242 1731 1731 11870 10839 20310 10074 944 333800 6617 11158 1374 10302 108302 10831 216050 24892 249050 14390 1737 11833 243184 10819 Length DB AE003957 AL64604 AL6460493 AE010493 AE010493 AE010493 AE010493 AE010493 AE002489 AX155449 AX202489 AX202491 AE0122491 AE012245 AE012345 AE012345 AE012345 AX033468 U32752 AP002568 AE000493 AE005654 AE012531 AE012071 AY010120 AX034847 AX067459 AX034849 AE0078576 AE006218 AE013668 AJ414157 AE008906 AL627283 AE004323 SME591792 AX139467 AE008175 Ħ AX033470 AXO78576 Sequence AE001368 Yersinia AB013688 Yersinia AJ414157 Yersinia AJ414157 Yersinia AJ414157 Yersinia AB008906 Salmonell AL627283 Salmonell AL627283 Salmonell AE004323 Vibrio ch AX033468 Sequence U32752 Haemophilus AP002568 Escherich AE00564 Escherichia AX033470 Sequence AE012511 Xanthomon AE012071 Xanthomon AE012077 Xylella f AX473246 Sequence AL646064 Ralstonia AX155443 Sequence AX202493 Sequence AX202493 Sequence AX202493 Sequence AX202493 Sequence AX202497 Sequence AX155447 Sequence AX155447 Sequence AX15547 Sequence AX15547 Sequence AX15548 Sequence AX15548 Sequence AX1549 Sequence AX1549 Sequence AX15547 Sequence AX1548 Sequence AX15548 Sequence AX15548 Sequence AX15549 Sequence AX15548 Sequence AX15548 Sequence AX15549 Sequence AX15548 Sequence AX15549 Sequence AX15547 Sequence AX15677 Neisseria Continuation (2 of AL162752 Neisseria Continuation (3 of AL162752 Neisseria Continuation (3 of AL162752 Neisseria AX043922 Sequence AX15461795 Bartonia AX043927 Sequence AX15461795 Bartonia AX043927 Sequence AX139467 Sequence AX139467 Sequence AX139467 Sequence AX139467 Sequence AX139467 Sequence AX034847 Sequence AX067459 Sequence AX034849 Sequence AE004682 Pseudomon Description

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Immunogenic compounds
Patent: WO 0052042-A 1 08-SEP-2000;
Patent: WO 0052040 SMITHKLINE BEECHAM
RUELLE JEAN LOUIS (BE) : SMITHKLINE BEECHAM
LOCATION/QUALIFIERS
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Moraxella catarrhalis
Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
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	ThrProAlaAspValTyrClnSerLysLysValProLeuTyrValPheValAlaSerAsp	561	Оу
JLys           CAAG	AspGluSerGluAsnGluValIleAspLeuProGluArgThrAlaLeuAlaAsnArg	541 1621	Db Qy
$\sigma - \sigma$	gSerIleLeuGlyArgIleSerAspAlaValSerAlaValAla 		Db ,
Asn     AAT	HisLeuTyrAspMetProAspAspArgValLeuAlaIleAsnHisAspAspGlyVal 	501 1501	Qу
Arg	GluPheSerAlaSerAsnLeuIleGlnAspLysLeuAsnLeuValAlaAlaLysAla.	481 1441	Qy Db
TC I le	GluProVall1eGluThrValGluLeuThrAspGlyIleLeuMetAspIleSerProI	461 1381	Qу
CTT	SerPheGluGinSerSerSerSerArgThrGluProAlaGlnValAspGluSerThrI	441 1321	Оу
/al	AsnMetValAsnThrGluIleValPheProGluArgGluGlnIleGlnAsnAspGlnV 	421 1261	Оy
TT — pe	AlaTyrAsnLeuGlnAlaValArgAlaLeuSerAsnAspLeuIleAlaThrArgTyrP 	401 1201	Оy
AG I	AspLysLeuProValLysArgGluLeuLeuGluGlnLeuLeuThrValAsnMetGlyG 	381 1141	Оу
CA To	PheAspGluValValPhePheThrIleAspProLysThrAsnGlnLeuThrThrAspF 	361 1081	Qy Db
9 – £	IleLeuProAspAsnThrAlaAspValSerLeuIleTyrAspThrGlyThrGlnTyrA 	341 1021	Qy Db
7a1	AsnAlaSerAlaGluHisGlyTyrPheAspGlyArgTrpLeuAspArgSerValAspV 	321 961	Фр
ă=ü	LeuLeulleGlyAspValPheHisHisGlyLysTyrGluThrLysLysAsnLeulleG 	301 901	Qy Db
GA – r	GluValArgGlyGluGlyAlaAspAspLysAlaPheThrThrValAlaAspGluValP 	281 841	Дb
7a1	luValAsp           AGGTGGAT	261 781	Оу
GA-Y	AlaAlaArgAlaValGlyTyrTyrAspIleAspLeuSerIleIleArgAsnSerIleG 	241 721	Qy Db
Val	GlnGluSerAlametAspLeuAsnGlySerIleProArgLeuArgGlnThrAlaLeuV 	221 661	Qу
ACC		601	Db .

	PAT 24-JAN-2001	NA linear	-	9 89047 bp	AX067459	JLT 2 57459 JS	RESU AX06 LOCU
	Phe 919      TTT 2757	nePheIleGlyThrPro                   TTTTATTGGCACACCA	Hisph        CATTT	llyValLysGluGluGlyAsnProIleLysLeuHisPhePheIleGlyThrProPhe 	GlyValLys6           GGTGTCAAAG	901 2701	g 99
	alAlaThr 900          TGGCAACT 2700	.nValArgValAspVal              AGTTCGTGTTGATGTG	G1yG1        GGTCA	AlaGlyValGlyValArgTrpAlaSerProValGlyGlnValArgValAspVal 	AlaGlyValG	881 2641	pb oy
	IleGly 880        ATTGGT 2640	eThrAsnAspThrLys             TACTAATGATACCAAA	G1yPh        GGCTT	ValPheGlyAspIleGlyAsnalaTyrAspLysGlyPheThrAsnAspThrLysIleGl 	ValPheGlyA          GTTTTTGGTG	861 2581	Дb
	LeuAla 860         TTGGCG 2580	neMetLysAspLeuArg	GluPh        GAATT	\leualaValGlyThrAlaGluTyrAsnTyrGluPheMetLysAspLeuArgLeuAl 	ValLeuAlav            GTATTGGCGG	8 <b>41</b> 2521	Оу
	GlyGln 840        GTCAA 2520	/sG1yTyrLeuThrG1y           GGGTTATCTGACAGGC	AspLy         GATA!	GlyTyralaHisAspSerLeuSerProIleSerAspLysGlyTyrLeuThrGlyGlyGln 	GlyTyrAlaH            GGATATGCAC	821 2461	Db
	IleArg 820        ATTCGT 2460	aGlyGlyAspGlnSer             TGGTGGCGACCAAAGT	PheAl	AsnPheAsnHisValProTyrArgLeuArgPhePheAlaGlyGlyAspGlnSerIleArg 	AsnPheAsnH            AATTTTAATC	801	ОУ
	SerAsp 800         TCGGAT 2400	lnAlaGlyTyrIleTrp 	IleG1	GlySerAsnArgAlaHisGlnMetThrGlyGlyIleGlnAlaGlyTyrIleTrpSerAs 	GlySerAsnA                GGCAGCAATC	781 2341	Оy
	AlaTyr 780        CTTAT 2340	/rSerPheGlyAspAsn            	ValTy        GTGT#	AsnMetAlaIleAlaArgAlaGlyIleSerGlyValTyrSerPheGlyAspAsnAlaTyr 	AsnMetAlaI                 AATATGGCTA	761 2281	Db Oy
	AspAla 760         GATGCT 2280	erSerGlyLeuValSer            	Glyse         GGCTC	ArgGlyTyrArgGlnArgTyrSerLeuGluValGlySerSerGlyLeuValSerAspAla 	ArgGlyTyra           CGTGGCTATC	741 2221	Db Qy
	ProMet 740         CCGATG 2220	laAspAsnLeuValAsn  -  -  - - - - - - - - - - -	ValAl 	AlaLeuLeuAlaGlyValAlaValHisLysThrValAlaAspAsnLeuValAsnProMet 	AlaLeuLeuA            GCGTTATTGG	721 2161	Оy
	GlnGlu 720         CAAGAG 2160	alAsnGlyLysProSer 	PheVa        TTTG1	ProProGluThrTrpGlnAspLeuProValAspPheValAsnGlyLysProSerGlnGlu 	ProProGluT	701 2101	ОУ
·	Glnala 700         CAAGCA 2100	auAspLysLeuLysThr 	ArgLe	GlyGlyTrpAsnArgThrTyrSerLeuArgTyrArgLeuAspLysLeuLysThrGlnAla 	GlyGlyTrpA            GGTGGCTGGA	681 2041	g 99
	GlnAsn 680         CAAAAT 2040	eSerArgSerIleIle   +             TAGCCGCAGTATTATO	GAGAT	GlyPheAspLeuSerThrArgThrLeuGluHisGluIleSerArgSerIleIleGlnAsn 	GlyPheAspI           GGTTTTGATT	661 1981	Оy
	Thrasn 660        ACCAAT 1980	LuValPheGlyHisSer	GlnGl        CAAGA	AsnAspGlnLeuArgAlaThrLeuGlyTyrGlnGlnGluValPheGlyHisSerThrAsn 	AsnAspGlnI             AATGATCAGO	641 1921	Дb
	ProLeu 640         CCTCTA 1920	nrLysProLeuSerHis             CAAACCGCTTAGCCAC	AlaTh	LeuSerGluAspLysLysGlyValLysLeuTyrAlaThrLysProLeuSerHisProLeu 	LeuSerGluA             CTGTCTGAGG	621 1861	Db Oy
	LeuArg 620        CTAAGA 1860	/rGlnAlaGlyAlaGlu 	G1yTy        GCT#	ThrLysPheGluHisAsnLeuIleAsnArgAspGlyTyrGlnAlaGlyAlaGluLeuAr 	ThrLysPhed	601 1801	D 9
	LeuVal 600         CTAGTC 1800	erAspThrGlyThrArg              GGACACAGGTACCCGC	Glyse        GGATC	LysProArgAspGlyGlnIleGlyLeuGlyTrpGlySerAspThrGlyThrArgLeuVal 	LysProArgA            AAACCACGAG	581 1741	Оy
	AGTGAT 1740	PATATGTCTTTGTGGCG	cccc	ACCCCTGCTGATGTCTATCAAAGTAAAAAAGTGCCGCTATATGTCTTTGTGGCGAGTGAT	ACCCCTGCTG	1681	DЬ

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                                                                                                                 GluTyrGlnGlyGluGlnProAsnSerGluValValValProProThrLeuGluProGlu
                                                                                                                                                           GluGluLeuPheAlaGlnGluSerThrGluMetGlyIleAsnProAsnAspTyrIlePro
                                                                                                                                                                                          CAATCACCCCCTTTGGGTTTGGATATGTCGGTCATCGAAGAAACCACACCGCTAAGCTTG
                                                                                                                                                                                                     GlnSerProProLeuGlyLeuAspMetSerValIleGluGluThrThrProLeuSerLeu
SerSerHisGlnLysThrGluProTyrAlaAsnIleLysAlaAlaLeuGluAspIleThr 220
                                                              AAACCAGGTTTGATCAAGCGTCTTTATGCACGCCTATTTAATGATGGTGTCAATAAGGTG
                                                                                                      GAATATCAAGGCGAGCAACCTAATAGTGAGGTGGTTGTACCACCGACATTAGAACCTGAA
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Moraxella catarrhalis
Bacteria; Proteobacteria;
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linear PAT 1	т е 9	pValAlaTh          TGTGGCAAC	hrasnaspThrLysIleGly             TaaTGATACCAAAATTGGT	LLYSASPLEUATGLEUAL 	.IleSerAspLysGlyTyrLeuThrGlyGlyGln 	pGlnSerIleAr             CCAAAGTATTCG	lnAlaGlyTyrIleTrpSerAs; 	rPheGlyAspAsnAlaTy 	lSerAspAl         ATCGGATGC	LysThrvalAlaAspAsnLeuValAsnProMe 	snGlyLysProSerGlnGlu 	spLysLeuLysThrGlnal                TAAGCTTAAAACCCAAGC	SerIleIleGlnAs             GTATTATCCAAAA	GlnGluValPheGlyHisSerThrAsn 	ProLeuSerHigProLe            CGCTTAGCCACCCTCT	lnAlaGlyAlaGluLeuAr 	spThrGlyThrArgLeuVa 	ATATGTCTTTGTGGCGAGTGAT
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SITARGEGLDLALQESGDMPLQAEATTLGLPAPEGKEWKLAVQVGGELQQALTIKK
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TYKYSDDAVIGGSCPARRENDIDVEVGQDKLAFSGFGLSAELAGHLHIGDNLD
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GAGVASGLLPLAWIDWLMLLIAALLLLTIGNRVRQGLAELAASRRGSDGQA"
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30.1"
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DIGIGBENRKRWLKTCKCSFLPEEREWLATLKNWGLVDSFRALNPEVNDRFSWFDYRS
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LGVHPEYQGRQIGEQLLAAVORWCAEDSASOGLVLDTGNARYLDFYQRHGYREIGEVT
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                                                                                        /transl_table=11
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translation="MNYPVDHLTALKVFRAVAANGGFAAAARQMNLSPAAVSKNVAEL"

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170 aArgLeuPheAsnAspGlyValAsn------

-LysValProArgLeuLysAlaLy 186

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CCTGTC - AGGCGCTTGGCGTCATAAAAACCCGAATGTCAGGAGGTGGTCGGCGGCGTCCGC
                                            yLeuIleLysArgLeu----
                                                                                            TGGCGAGACGCCGGC-GGCGACCTGAGCGTTCCCCCGGACGCGCGA----GAAAAGCCATG
                                                                                                                                                                                        CTACCGCGAGATCGGCGAGGTGACGCTGGGAGCGTGCGCGAGCACGTCCTGCATCC
                                                                                                                                                                                                                                                                                    GCAGGGGCTGGTCCTGGATACCGGCAATGCGCGCTACCTGGACTTCTACCAGCGGCACGG 6466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCTGCGCATGCTGTTCAGCGTCGGCCTGGCCGCGACCCGGCGCTA---
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                                                                                                                                      -GlyGluGlnProAsnSerGluValValValProProThrLeuGluProGluLysProGl 163
                                                                                                                                                                                                                                                                                                                                 uMetGlyIle-----
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PLTLALTCLTPAIPAFLORY PELRELLIADGRODLIAEGIDLALRGSDRVADSGLVA
RPLLVLEHVLCAAPAVLSOHGOPLREELLIADGROETESLSGHADRWTFRKDRECIAV
IAGRYRVSSSLAVRDALLAGFGLSLIPRLYVQAELAEGRLVELLADWKADETAIHAVY
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9660. .11054
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VQIAPRPQMPAEYRKLAEQARRLTVNFRFQEGSALLDNKALLDVQRLLDYLRQNRKLQ
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/gene="PA2548"
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Mismatches:
Indels:
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524	)4 pMetProAspAspArgValLeuAlaIleAsnHisAspAspGlyValAsnArgSerIleLe	50	9
5492	)2 C	549	Db
504	84 aSerAsnLeuIleGlnAspLysLeuAsnLeuValAlaAlaLysAlaArgHisLeuTyrAs	48	8
5493	3GP	553	망
484	4 eGluThrValGluLeuThrAspGlyIleLeuMetAspIleSerProIleGluPheS	46	ογ
5534	34	553	Db
464	14 nSerSerSerArgThrGluProAlaGlnValAspGluSerThrLeuGluProValIl	4 4	9
5534	34	5534	Db
444	$24\ nThrGlufleValPheProGluArgGluGlnIleGlnAsnAspGlnValSerPheGluGlnClnClnClnClnClnClnClnClnClnClnClnClnCl$	42	ογ
5534	CGAACTGATCGCCGAACTCAACCAGAACCTGCAATCCAGCGG	5582	DЪ
424	uGlnAlaValArgAlaLeuSerAsnAspLeuIleAlaThrArgTyrPh	404	Ş
5583	1 -ATCGAGG	564	рb
404	oValLysArgGluLeuLeuGluGlnLeuLeuThrValAsnMetGlyGluAlaTyrAs	384	Š
5642		5663	рь
384	34 lValPhePheThrIleAspProLysThrAsnGlnLeuThrThrAspProAspLysLeuPr	364	γ
5664	CGGCATCGCCGACATCGACCTGGTCTACGACAGCGCCAGCGCTACACCTTCGGCAAGG	5723	В
364	pAsnThrAlaAspValSerLeuIleTyrAspThrGlyThrGlnTyrArgPheAsp	344	9
5724	3 GCGCTACGGCTTCTTCCAGGGCCGCTTCAGCACCCAGCGCCTGAGCATCGATCCGCGCGC	5783	망
344	aGluHisGlyTyrPheAspGlyArgTrpLeuAspArgSerVal	324	Q
5784	CCCGAAGCTGAACCAGGGTGTCTACGAGGATGCCAAC	584	망
324	yAspValPheHisHisGlyLysTyrGluThrLysLysAsnLeuIleGluAsnAlaSe	304	ş
5844	CGAGGCCGCCAGCCTGGAGAGCTTCCGCTTGCCGTCGGGCAAGCAGCTGAAACCGG	5900	g B
304	yGluGlyAlaAspAspLysAlaPheThrThrValAlaAspGluValProLe	284	ş
5901	GCTCAAGGTAGTGCCCG	5960	밁
284	59LeuGlyGluProValTyrIleAspTyrArgAlaValGluValArgGl	26	δ.
5961	)7	600	Вþ
268	5 eArgAsnSerIle	25	οy
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255	9 uValAlaAlaArgAla	23	Qγ
6051	0 TGTGGGTAGCCTCGGCGAGCGGGACGAAGCGGCGTT	611	DЪ
239	9 eThrGlnGluSerAlaMetAspLeuAsnGlySerIleProArgLeu	21	Qy
6111		617	В
219	rHisGlnLysThrGluProTyrAla	202	Q
6171	0 ATTGTTCCGGTTCCCGCTGGCCGGCTGCTGTGCCTGAGTACGGCCGCCTTCGCGG	623	р
202	86 sPheTyrGlnSerSerGlnSerGlyGluThrSerAlaIleGlySerSe	18	Ş
6231		629	В

858 gLeuAlaValPheGlyAspIleGlyAsnAlaTyrAspLySGlyPheThrAsnAspThrLy 8		
838 yGlyGlnValLeuAlaValGlyThrAlaGluTyrAsnTyrGluPheMetLysAspLeuAr 858	ОУ 8 рь 47	
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4871 CACCAACGACTACAAGTCGGATCCCGCCCTCGCTGCGCTTCTTCGCTGGCGGCGGCAGAG	.4	
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778 nAlaTyrGlySerAsnArgAlaHisGlnMetThrGlyGlyIleGlnAlaGlyTyrIleTr 798		
7 738 FASSMETALASIMETALATITEALAATGALAGIYLLESETOLYVAITYTSETTHEGIYASPAS 778 :	Db 49	
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	Qy 7	
5090 GAGCAGCTTCCTGATGCCGGGGATCGGCTACTCGCTGCTGGAGACCGACAACAAGGTCGA 5031	Db 50	
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5252	Db 52	
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5312 ACGGCAGAACGTCGGCGCCTGGTACGAGATTCCCCTCGATCCGCCGCTCACCGACAAGCT	ر. ري	
624 pLysLysGlyValLysLeuTyrAlaThrLysProLeuSerHisProLeuAsnAspGlnLe		
/ 604 uHisasnLeuileAsnArgAspGlyTyrGlnAlaGlyAlaGluLeuArgLeuSerGluAs 624	оу 6 53	
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5491	Db 54	

US-09-914-168-2 (1-919) x AX078576 (1-1374)  Oy 290 LysAlaPheThrThrValAlaAspGluValProLeuLeuIleGlyAspValPheHisHis 309	Alignment Scores: 1.82e-29 Length: 1374 .  Score: 604.50 Matches: 165  Percent Similarity: 40.41% Conservative: 90  Best Local Similarity: 26.15% Mismatches: 195  Query Match: 12.79% Indels: 181  DB: 6 Gaps: 12	Pseudomonas putida kt2440  AL Patent: WO 0107624 A 90 01-FEB-2001; THE INSTITUTE FOR GENOMIC RESEARCH (US); QIAGEI Gesellschaft fuer Biotechnologische Forschung mi Deutsches Krebsforschungszentrum (DKFZ) (DE); lengt Hannover (DE)  S Location/Qualifiers 11374  UNT 264 a 428 c 429 g 251 t 2 other		RESULT 5 AX078576 AX078576  LOCUS AX078576  AX078576  ACCESSION AX078576  VERSION AX078576.1 GI:13158218	Qy 878 sileglyAlaGlyValGlyValArgTrpAlaSerProValGlyGlnValArgValAspVa 898
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Submitted (24-OCT-2000) Department of Veterinary Pathobiology, University of Minnesota, 1971 Commonwealth Ave., St. Paul, MN
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VIMORLSQLANTIDELTVLDVNFDAVNNNEKLTDSLDDMKENAEKSATSFLNHFIRIT 
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                                        AspLysProArgAspGlyGlnIleGlyLeuGlyTrpGlySerAspThrGlyThrArgLeu 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuGluProValIleGluThrValGluLeuThrAspGlyIleLeuMetAspIleSerPro
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                                                                                                                                                                                                                                                                                                                                                                                   ArgHisLeuTyrAspMetProAspAspArgValLeuAlaIleAsnHisAspAspGlyVal 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IleGluPheSerAlaSerAsnLeuIleGlnAspLysLeuAsnLeuValAlaAlaLysAla 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GluAlaTyrAsnLeuGlnAlaValArgAlaLeuSerAsnAspLeuIleAlaThrArgTyr 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---GAAAATGCGCAAATACGCGAAGATTATTTGCGTAACATGATTAATTTTAATAAAGGT
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                                                                                                                                       LysThrProAlaAspValTyrGlnSerLysLysValProLeuTyrValPheValAlaSer 579
                                                                                                                                                                                                                      ProAspGluSerGluAsnGluValIleAspLeuProGluArgThrAlaLeuAlaAsnArg 559
                                                                                                                                                                                                                                                                                                     AsnArgSerIleLeuGlyArgIleSerAspAlaValSerAlaValAlaArgAlaIleLeu 539
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734 AspAsnLeuValAsnProMetArgGlyTyrArgGlnArgTyrSerLeuGluValGlySer
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                                                                                                TATATTGGA
                                                                                                                          PhelleGly
                                                                                                                                                                ValArgValAspValAlaThrGlyValLysGluGluGlyAsnProIleLysLeuHisPhe
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                                                                                                                                                                                                ACAAAAGAATTACGCTATGGCGCAGGAATGGGGGTACGTTGGGCCTCACCCGTAGGGGCA
                                                                                                                                                                                                               TATCCTGACTGGTTAGCCACTTTCGCGGATACGGGACTGGCTGCTAACCAGTTTACA 217
                                                                                                                                                                                                                                                                                     MetLysAspLeuArgLeuAlaValPheGlyAspIleGlyAsnAlaTyrAspLysGlyPhe
                                                                                                                                                                                                                                                                                                                                   GlyTyrLcuThrGlyGlyGlnValLeuAlaValGlyThrAlaGluTyrAsnTyrGluPhe 853
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Yersinia
AE013668
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                                                                                                                                                                                                                                                                                                                                                                            GGGGGAGATCGCÁGTATTCGTGGTTÁTGGCTATAAAAAAAATTGCGCCÁAAAAAAACAATGCA 337
                                                                                                                                                                                                                                                                                                                                                                                                   GlyGlyAspGlnSerTleArgGlyTyrAlaHisAspSerLeuSerProIleSerAspLys ::::::||| ::::::
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACATGGTGGCTGTČTĞATGTGGATTTCCTCAAAATGCAAGGGTCGAGTTTATGGĞTČAGA 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SerGlyLeuValSerAspAlaAsnMetAlaIleAlaArgAlaGlyIleSerGlyValTyr 773
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AATGTAAAAGACAAAACATTGCTTGTGTTCCCAACTGCCTCTGTCAGACGAACCCGTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LysproSerGlnGluAlaLeuLeuAla-----GlyValAlaValHisLysThrValAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ThrAsnGlyPheAspLeuSer-----ThrArgThrLeuGluHisGluIleSerArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SerIleIleGlnAsnGlyGlyTrpAsnArgThrTyrSerLeuArgTyrArgLeuAspLys 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACAGAATCCTTTGCCTCTTCCTTATCTGCAATTCGCTATTGGAATCATGAA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCGCTCAACTATTATTACGAGTACTCGGCGGGTTTAGAAAATGAA----AATAAAAATGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProLeuAsnAspGlnLeuArgAlaThrLeuGlyTyrGlnGlnGluValPheGlyHisSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TATGTTTCTGCGCCAAAACAGACCTTAGAAGCCACCTACAAAATGCCTTTATTGAAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ArgLeuSerGluAspLysLysGlyValLys---LeuTyrAlaThrLysProLeuSerHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAATTAGGTTGGACAAAGCCTTGGATTAACAATCGTGGTCACAGTTTCCGTACCAATTTA 901
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   Pestis KIM section 68 c AE009952
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           of 415
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        of the
                     linear
complete genome
              BCT 26-JUL-2002
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FEATURES
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KEYWORDS
SOURCE
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AUTHORS
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JOURNAL
PUBMED
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Submitted (21-FEB-2002) Genetics,
Henry Mall, Madison, WI 53706, US/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Deng, W., Burland, V., Plunkett, G. III, Boutin, A., Mayhew, G.F., Liss, P., Perna, N.T., Rose, D.J., Mau, B., Zhou, S., Schwartz, D.C., Fetherston, J.D., Lindler, L.E., Brubaker, R.R., Plana, G.V., Straley, S.C., McDonough, K.A., Nilles, M.L., Matson, J.S., Blattner, F.R. and Perry, R.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Deng, W., Burland, V., Plunkett, G. III, Boutin, A., Mayhew, G. Liss, P., Perna, N.T., Rose, D.J., Mau, B., Zhou, S., Schwartz, Fetherston, J.D., Lindler, L.E., Brubaker, R.R., Plana & Straley, S.C., McDonough, K.A., Nilles, M.L., Matson, J.S., Stather, F.R. and Perry, R.D. Genome Sequence of Yersinia pestis KIM
J. Bacteriol. 184 (16), 4601-4611 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria;
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                                                                                                                                                                                  /note="residues 26 to 211 of 212 are 59.13 pct identical to residues 1 to 184 of 184 from E. coli K12: B4216; residues 26 to 212 of 212 are 60.42 pct identical to 185 of 185 from GenPept: >emb[CAD06684.1] subsp. enterica serovar Typhi]"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"affects pool of 3'-phosphosulfate in pathway of sulfite synthesis; residues 2 to 247 of 247 are 78.45 pct B4214; residues 1 to 246 of 246 from E. coli K12: residues 1 to 246 of 246 from E. coli K12: residues 1 to 246 of 246 from GenPept: >9b|AAL23224.1| of 246 of 246 from GenPept: >9b|AAL23224.1| of phosphoadenosine-5'-phosphosulfate in pathway of sulfite synthesis [Salmonella typhimurium LT2]"
                                                                                                                                                                                                                                                                                                                                                                                                               /gene="y0655"
                                                                                                                                                                                                                                                                                                                                                                                                                    AQVHDWQGKTLSYTPRESFLNPGERVSLF"
complement(993...1631)
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/transl_table=11
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Sulfur metabolism"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="y0654"
247. .990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /Organism="Yersinia pestis
/Strain="KIM"
/db_xref="taxon:187410"
247. .990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'gene="cysQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene='
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Schwartz, D.C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(2212. .3543)

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/function="putative transport"
/note="residues 1 to 437 of 443 are 82.15 pct identical to residues 1 to 437 of 447 from E. coli K12: B4218;
residues 1 to 443 of 443 are 81.39 pct identical to residues 1 to 446 of 447 from GenPept: >9blAAL2327.1|
(AE008906) putative hemolysin-related protein [Salmonella typhimurium LT2]"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="residues 1 to 210 of 212 are 73.33 pct identical residues 1 to 210 of 212 from E. coli K12: B4219; residues 1 to 210 of 212 are 72.21 pct identical to residues 1 to 211 of 212 are 72.51 pct :>gb|AAL23228.1| (AE008906) peptide methionine sulfoxide reductase [Salmonella typhimurium LT2]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="residues 1 to 66 of 70 are 77.27 pct identical to residues 14 to 79 of 81 from E. coli KI2: B4217; residues 1 to 66 of 70 are 75.75 pct identical to residues 23 to 88 of 90 from GenPept: >gb|AAL23226.1| (AE008906) putative cytoplasmic protein [Salmonella typhimurium LT2]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(3821. .4459)
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/function="enzyme; proteins - translation and
                                                                                                                                                                                                                             PAVISYQQLLQIFWENHDPAQGMRQGGDVGTQYRSAIYVLTPEQEEQAHKSRERFQQA
MEKAGDQRVITSEITVALPFYYAEDDHQQYLHKNPHGYCGLGGIGVCLPPNV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="msrA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="putative membrane protein"
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                                                                                                                                                                                                                                                                                                                        /product="peptide methionine sulfoxide reductase"
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                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modification"
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1892. .2104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="y0656"
                                          to 577 to 578 to 577
                       putative outer membrane protein
                                        to 578 of 578 are 71.20 pct identical of 577 from E. coli K12: B4220; of 578 are 71.32 pct identical to of 577 from GenPept: >gb|AAL23229.1|
                          [Salmonella
                                                                                                                  6
В
                                   Ωy
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                                                                                                                                Qy
                                                                                                                                                                                  Db
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                                                                                                                                                                                                                                                                           US-09-914-168-2 (1-919) x AE013668 (1-10831)
                                                                                                                                                                                                                                                                                                                                              Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                   Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
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4845 AACGTCAGGGCACGTTTGTCCACAATTGGCACTGATGAAGTTACCGCAGAT-----GGC

4898 229

211 AsnIleLysAlaAlaLeuGluAspIle---ThrGlnGluSerAlaMetAspLeuAsnGly

2.56e-21 494.00 38.04% 23.36% 10.45%

Mismatches: Indels:

11

Conservative:

Gaps:

Length: Matches:

249

GATCCCACCATTACGTTTGAATTACAAAACCGCCCGGCACCCGCACGTTCAGTGTTAATT 5018 Asp-----IleAspLeuSerIleIleArgAsnSerIleGlyGluValAspValIleIle CGTTTTCGTTCACGGGTCGATGAAGCTATTCGGCAGGGGCTGCGCGCATTAGGTTATTAC SerIle---ProArgLeuArgGlnThrAlaLeuValAlaAlaArgAlaValGlyTyrTyr 248

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CDS
                                                                                                                                                                                                                                                               LAKAGLPLSLTLQSKQLRWPLTGEPQYQMNNLRWRLNGQATDYALSIRSDIKGTDLPP
AVFTLEGKGNVEQFNLTRLRLALQGHTDLTGVVDWRQAISWNSVLTLSGINAKQWP
EWPAKLEGKIVTRGSIHGGSWQQVPELVLDGNVKQNRVTARGSLTGNAAGQWHIPGI
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KQHQLRLNMQGDPVSGQLSLEGSFDKQQQRWRGTLNNTRFDTPVGENRLSRAWTLDYQ
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ADWLYKLVNNGQFSQQVQVADPEGRRNLSGNVAISNLSLAMINPILSDCEKAAGILNA
NLRLAGNAKSPLVYGRLALDKVDIDGSWMPFDITEGRLAMNFDLGGLANGGCAN
NLRLAGNAKSPLVYGRLALDKVDIDGSWMPFDITEGRLAMNFDLGGLANGVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TASGQSTTASGRSATASGQSATTGGQLATVPAEPATPLGESLKALFAKPLLPALPDFR LPLDLQIEEISGQQLRLTGDNEVLISSLLLQASTQDQRITLDTLEIKSPQGGLSAQGQ ATLANKWPLDLVVNSALNIDSLKGEKVKLTVGGALREELKVTLNLSGPVSAQLETETS
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/note="residues 5 to 1305 of 1305 are 57.45 pct identical to residues 5 to 1259 of 1259 from E. coli Kl2: B4221"
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FGLKARLQGDLRMMQDQRGLGLNGQINIPSGSFRAYGQDLIVNKGILLFSGPPDQPLL
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6467. .10384
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FRRTDLDTNSDTTTLMVARFWDLSSGWQRAINLRWSLDHFTQGRAYTDTTMLLYVBGVS
INRTRORGGAMPVWGDSGRYSIDVSDTTWGSDVDFGIFQAQNVWIRTLGEKNRFVARG
NVGWIETNNFDRVPDSLRFFAGGDRSIRGYKFRNISPRDSDGKLTGASKLATGSLEYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation-"MLRYPILCFVCLLLATPIAYAANVRLQVEGLSGDLERNVRARLS
TIGTDEVTADGRFRSRVDEAIRQGLRALGYYDPTITFELQNRPAPARSVLIAKVVPGE
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KYGYGIFDSLATLTLRYRLMPRLYLEAVSGIDQALDLLYQFEF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HWKQRSLALMPTKINGLLIALPKTVSAGVPDAVKPAVETAMAAKEAVAQLSAAPGRSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GVQFYIGLGPEL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DANMIKSQLGVAAQLHEAFWDIDFDSGQRYRFGKVIFQGSQIREDYLQNLVPFHEGEF
YTSDELAELNRRLAATNWFNSVVVSPDFQDAKESKILPLDAVVTPRTENTVELGGGYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="hypothetical
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5657	AAGCCTTGGATGAACTCCTTCGGGCATAGCTTAACCACCACTACCGCGCTTTCGGCACCT	5598	Db
624	leAsnArgAspGly	605	Оу
5597	GTTATG	5541	DЬ
604	GlyGlnIleGlyLeuGlyTrpGlySerAspThrGlyThrArgLeuValThrLysPheGlu	585	Оy
5540		5540	Db
584	ValTyrGlnSerLysLysValProLeuTyrValPheValAlaSerAspLysProArgAsp	565	Qy
5540	AATACCGTC	5532	Db
564	AsnGluVa IleAspLeuProGluArgThrAlaLeuAlaAsnArgLysThrProAlaAsp	545	Оу
5531		5508	рь
544	GlyArgIleSerAspAlaValSerAlaValAlaArgAlaIleLeuProAspGluSerGlu	525	Оy
5507		5507	Db
524	${\tt MetProAspAspArgValLeuAlaIleAsnHisAspAspGlyValAsnArgSerIleLeu}$	505	Qy
5507		5507	рь
504	Ser Asn Leu Ile Gln Asp Lys Leu Asn Leu Val Ala Ala Lys Ala Arg His Leu Tyr Asparan Leu Val Ala Ala Lys Ala Arg His Leu Tyr Asparan Leu Val Ala Ala Lys Ala Arg His Leu Tyr Asparan Leu Val Ala Ala Lys Ala Arg His Leu Tyr Asparan Leu Val Ala Ala Lys Ala Arg His Leu Tyr Asparan Leu Val Ala Ala Lys Ala Arg His Leu Tyr Asparan Leu Val Ala Ala Lys Ala Arg His Leu Tyr Asparan Leu Val Ala Ala Ala Lys Ala Arg His Leu Tyr Asparan Leu Val Ala Ala Ala Lys Ala Arg His Leu Tyr Asparan Leu Val Ala Ala Ala Ala Ala Ala Ala Ala Ala A	485	Оy
5507	ATTTTACCGCTTGAT	5493	рь
484	GluThrValGluLeuThrAspGlyIleLeuMetAspIleSerProIleGluPheSerAla	465	Qy
5492		5478	DЬ
464	Ser Ser Ser Arg Thr Glu Pro Ala Glu Val Asp Glu Ser Thr Leu Glu Pro Val Ile	445	Qy
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444	ArgGluGlnIleGlnAsnAspGlnValSerPheG	425	Qy
5453	CCGCCGCTTGGCAGCCACC	5397	DЪ
424	gAlaLeuSerAsnAspLeuIleAlaThrArgTyrPheAsr	405	Qy
5396	ATCCGAGAGGATTATCTGCAGAATTTAGTGCCGTTCCATGAGGGGGAATTCTATACCTCT	5337	Db
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5336	ATTTTCCAAGGCTCACAA	5319	DЬ
384	$\tt ValPhePheThrIleAspProLysThrAsnGlnLeuThrThrAspProAspLysLeuPro$	365	οy
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364	snT	345	Qy
5258	GCCGTGGCTATTTCGACGCCAATATGATCAAAAGCCAGCTCGGTGTTGCCGCTCAATTA	5199	Db
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5198	TCGGTCCTCAACCATGGTGATTTTGATAATTTCACCAGTTCTCTTACTGGTTTAGCGTTA	5139	DЬ
324	AspValPheHisHisGlyLysTyrGluThrLysLysAsnLeuIleGluAsnAlaSerAla	305	Qy
5138	GTGCGAAAACGGATCCTGATTATCAGGCACTCGTTCGCCGTGATACCCCCGAAAATTGGC	5079	рь
304	GluGlyAlaAspAspLysAlaPheThrThrValAlaAspGluValProLeuLeuIleGly	285	Qy
5078		5019	B
284	HisAspLeuGlvGluProValTvrIleAspTvrArgAlaValGluValArgGl	267	Οy

REFEREI AUTHO	RESULT 8 AJ414157/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	Db 6,	Oy :	Db 6:	Qy 1	Db 6:	Qy	- თ		מ	0у	ОУ 6:	Db 61	Qy .	6	Ωγ .	u	Qy .	رب رب		Db 49	U	1	Db 57	Qy	Db 5'	Qy	Db 5	Qy
ENCE	T 8 157/c ITION SION ON RDS E ANISM	411	902	351	882	291	862	31	42	7	822	802	063	782	012	762	952	742	9	724	853	۸ ر	00	760	664	718	644	658	625
s 1 to 216050) s 1 to 216050) ,J., Wren, B.W., Thomson, N.R	AJ414157  216050 bp DNA linear BCT 06-JUN Yersinia pestis strain CO92 complete genome; segment 17/20. AJ414157 AL590842 AJ414157.1 GI:15981328  . Yersinia pestis. Yersinia pestis. Parteria. Brotophacteria. Gamma subdivision: Externactions	ATAGGCGATAACGAGACACATGGCGTGCAATTTTACATCGGT 6452	alLys	GGTGTCGGGGTACGTTGGGCATCACCCGTTGGACCGATCAAACTGGATATCGCGGCACCA 6410	lyValGlyValArgTrpAlaSerProValGlyGlnValArgValAspValA	TTCGTCGATTCGGGCGAGGCGGTGAATAATTTCAGCAAGAGTGACTTAAAAACAGGGGCA 6350	heGlyAspIleGlyAsnAlaTyrAspLysGlyPheThrAsnAspThrLysIleGlyAl	GGCTCTCTTGAATATCAATATAACTTCACGGGTAGATGGTGGGGGGCCCGTT 62	avalGlvThrAlaGluTvrAsnTvrGluPhoMetIvsAspLeuArgLeuAlaVal 861	TARATTCCCTARTRTTCACCCCCTCATACTCACCCAAAATTAACCCCCCTTCCAAC	yrAlaHisAspSerLeuSerProI	PheAsnHisValProTyrArgLeuArgPhePheAlaGlyGlyAspGlnSerIleArgGly 821    :::        TTTGACCGTGTTCCACCGTCGCTGCGTTTCTTCGCCGGGGGCGACCGCAGTATCCGTGGC 6170	AATCGTTTTGTGGCGCGTGGCAATGTGGGGTGGATCGAAACCAATAAT 6110	Asp	:::    :::	aGlyIleSerGly		lyTyrArgGlnArgTyrSerLeuGluValGlySerSerGlyLeuValSerAspAlaA	GTATCCGGGGGTGAGTATTAATCGTACCCGCCAACGTGGTGGGGGGATGCCGGTCTGG 59	ValalaaspaspionValaspPrometaro 741	THEFT DELEASE PROVIDED AND THE STATE OF THE	AAAGGGCGATTAACCTGCGTTGGAGCCTCGAT58	snArgThrTyrSerLeuArgTyrArgLeuAspLysLeuLysThrGlnAlaProProGlu 703	GTTTTTGGGATCTCTCCAGCGGCTG	snGly	TACCTGATACAAGGGGGCTTTAGACGTACCGACTTAAACGAC 5759	nGluValPheGlyHisSer	: ::: GACACTGGATTTCAGC	LysLysGlyValLysLeuTyrAlaThrLysProLeuSerHisProLeuAsnAspGln 643

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PUBMED
REFERENCE
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Submitted (04-QCT-2001) Submitted on behalf of the Yersinia
sequencing team, Sanger Centre, Wellcome Trust Genome Campus,
Hinxton, Cambridge CB10 1SA E-mail: parkhill@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prentice,M.B., Sebaihia,M., James,K.D., Churcher,C., Mungall,K.L., Baker,S., Basham,D., Bentley,S.D., Brooks,K., Cerdeno-Tarraga,A.M. Chillingworth,T., Cronnin,A., Davies,R.M., Davis,P., Dougan,G., Feltwell,T., Hamlin,N., Holtoyd,S., Jagels,K., Leather,S., Karlyshev,A.V., Moule,S., Oyston,P.C.F., Quail,M., Rutherford,K., Simmondes,M., Skelton,J., Stevens,K., Whitehead,S. and Barrell,B.G. Genome sequence of Yersinia pestis, the causative agent of plague Nature 413 (6855), 523-527 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Details of Y. pestis sequencing at the Sanger Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Parkhill, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Notes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the World Wide Web.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.sanger.ac.uk/Projects/Y_pestis/).
                                                                                                                                                                                                                                                                 /note-"Similar to Escherichia coli aspartate
1-decarboxylase precursor PanD SW:PAND_ECOLI (P31664) (126
aa) fasta scores: E(): 0, 78.6% id in 126 aa, and to
Pseudomonas aeruginosa aspartate 1-decarboxylase precursor
Pa4731 TR:AAGO8117 (EMBL:AE004887) (126 aa) fasta scores:
E(): 1.5e-27, 58.2% id in 122 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-"Similar to Escherichia coli pantoate--beta-alanine Ligase PanC SW:PANC_ECOLI (P31663) (283 aa) fasta scores: E(): 0, 72.0% id in 282 aa, and to Vibrio cholerae pantoate--beta-alanine ligase Vc0591 TR:09KUD1 (EMBL:AE004144) (293 aa) fasta scores: E(): 0, 59.0% id in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KMVADMGYDINIVGVPTVRAKDGLALSSRNGYLTEEERQIAPQLSKIMWALAEKMALG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NQLVDLRH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LEKQTYVDVPALSTILEGASRPGHFRGVSTIVSKLFNLIQPDVACFGEKDYQQLALIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="biovar: Orientalis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="C092"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Yersinia pestis"
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                    misc_teature
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transmembrane

helices

predicted

membrane proteins signature. complement(3592. .3657)
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transmembrane

helices

predicted

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transmembrane

helices predicted

probable transmembrane helices predicted

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein in hpt-panD intergenic region YadH SW:YADH_ECOLI (P3680) (256 aa) fasta scores: E(): 0, 80+18*id in 256 aa, and to Vibrio cholerae putative permease Vc0590 TR:Q9KUD2 (EMBL:AE004144) (256 aa) fasta scores: E(): 0, 66.0% id in 256 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(3400 .4170)
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/note="Similar to Escherichia coli hypothetical 28.5 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(3400..4170)
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YadE SW:YADE_ECOLI (P31666) (409 aa) fasta scores: E(): 0,
65.4% id in 382 aa"
                                                                                                                                                                                                                                                                                                                                                                              complement(3409. .4164)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Pfam match to entry PF02261 Asp_decarbox, Aspartate
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LGITDVSLAYTIGVLVVFIAVFYAWAWYLIERGTGLRT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein"
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AKNAGFHLAVTTMQGKVKPGDNPYTLKRLYILRTDSIPTMAERIANQPGPVAVKPAPA
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/protein_id="CAC92634.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(1880.
                                                                                                                                                                                                                                                                                                        /note="Pfam match to entry PF01061 ABC2_membrane,
type transporter, score -22.30, E-value 5.8e-05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="putative ABC transporter, integral membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /transl_table=11
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Db 136674 GGTGCGAAAACGGATCCTGATTATCAGGCACTCGTTCGCCGTGATACCCCGAAAATTGGC 136615
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Best Local Similarity:
Query Match:
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                                                                                          Db 136734 GCAAAAGTGGTTCCTGGCGAGCCGGTATTGATTGCCGGTGTCGATATCGTACTGCAAGGC
                                                                                                                                                                                    Db 136794 GATCCCACCATTACGTTTGAATTACAAAACCGCCCGGCACCCGCACGTTCAGTGTTAATT
                                                                                                                                                                                                                                                                                                                                                                   Db 136908 AACGTCAGGGCACGTTTGTCCACAATTGGCACTGATGAAGTTACCGCAGAT-----GGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-914-168-2 (1-919) x AJ414157 (1-216050)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                            136854 CGTTTTCGTTCACGGGTCGATGAAGCTATTCGGCAGGGGGCTGCGCGCATTAGGTTATTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
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                                          285 GluGlyAlaAspAspLysAlaPheThrThrValAlaAspGluValProLeuLeuIleGly 304
                                                                                                                                                                                                                                 249
                                                                                                                                                                                                                                                                                                               230 SerIle---ProArgLeuArgGlnThrAlaLeuValAlaAlaArgAlaValGlyTyrTyr 248
                                                                                                               211 AsnīleLysAlaAlaLeuGluAspIle---ThrGlnGluSerAlaMetAspLeuAsnGly
                                                                                                                                                                                                                              Asp------IleAspLeuSerIle1leArgAsnSerIleGlyGluValAspValIleIle 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="YPO3407"
/note="yadf"
5329. 5991
/gene="YPO3407"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         \translation="myyaletyoltkyymgovoalroidlheerddyyallororgk
Stiigiisslvnktsgkyovegydidddivnakkolgcynopefnynfetyloivyto
Agyygvtyrrdalarbekylsoldlwskrderalklsggmkrrlmiaralmheerllil
Deptagvdielrrsmmgflkelnaogttiiltthyleeramlcrnigiiongelvent
TMKQLLSKLESETFIFOLGAKSPLPKLEGYGYNTTTSTEVDVKREOGINSLFSOLN
VOGVOYOSMRKANKLEELYTYLVAGHEGEKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-"Similar to Escherichia coli hypothetical ABC transporter ATP-binding protein YadG SW:YADG_ECOLI (P36879) (308 aa) fasta scores: E(): 0, 81.8% id in 308 aa, and to Vibrio cholerae ABC transporter ATP-binding protein Vc0589 TR:Q9KUD3 (EMBL:AE004144) (305 aa) fasta scores: E(): 0, 71.4% id in 304 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /geneu "YPO3406"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-"Pfam match to entry PF00005 ABC_tran, transporter, score 198.80, E-value 8.5e-56"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="YPO3406"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for YPO3405 by TMHMM2.0" complement(4045. .4110) /genew "YPO3405"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(4458. .5003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product-"putative ABC transporter, ATP-binding protein"
/protein_id-"CAC92636.1"
/db_xreff"GI:15981333"
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494.00
38.04%
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10.45%
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Matches:
Conservative:
Mismatches:
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ωć	CCTGATACAAGGGGGCTTTAGACGTACCGACTTAAACGAC	w	B 7
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643 136036	LysLysGlyValLysLeuTyrAlaThrLysProLeuSerHisProLeuAsnAspGln:::::	625 136095	DP QA
136096	7	136155	Db
624	Ъ	605	Qy
136156	GAACTGGGGGGGGTTATGCAACCGATGTCGGTCTGACCGCTCTGACCGCCAGTTGGCGT	136212	DЬ
604	lnIleGlyLeuGlyTrpGlySerAspThrGlyThrArgLeuValThrLysPheGlu	585	Qy
136213		136213	Ър
584	${\tt ValTyrGlnSerLysLysValProLeuTyrValPheValAlaSerAspLysProArgAsp}$	565	Qy
136213	AATACCGTC	136221	Ър
564	nGluValIleAspLeuProGluArgThrAlaLeuAlaAsnArgLysThrProAlaAsp	545	Qy
136222		136245	Db
544		525	Qy
136246		136246	Db
524	${\tt MetProAspAspArgValLeuAlaIleAsnHisAspAspGlyValAsnArgSerIleLeu}$	505	Qy
136246		136246	рь
504	${\tt SerAsnLeuIleGlnAspLysLeuAsnLeuValAlaAlaLysAlaArgHisLeuTyrAsp}$	485	Qy
136246	ATTTTACCGCTTGAT	136260	Дb
484	PheSerAla	465	Qy
136261	GCCAAAGAGAGTAAA	136275	Db
464	erSerSerSerArgThrGluProAlaGlnValAspGluSerThrLeuGluProValIle	445	Qy
136276	GTTGTTTCGCCGGATTTCCAAGAT	136299	Дb
444	${\tt ArgGluGlnIleGlnAsnAspGlnValSerPheGluGln}$	425	Qy
136300		136356	Db
424	Asn	405	Qy
136357	ATCCGAGAGGATTATCTGCAGAATTTAGTGCCGTTCCATGAGGGGGAATTCTATACCTCT	136416	Вр
404		385	γo
136417	ATTTTCCAAGGCTCACAA	136434	Db
384		365	Qy
136435	CACGAGGCGTTCTGGGATATTGATTTCGACAGTGGGCAACGTTACCGCTTTGGTAAGGTT	136494	Db
364		345	Qy
136495	CGCCGTGGCTATTTCGACGCCAATATGATCAAAAGCCAGCTCGGTGTTTGCCGCTCAATTA	136554	DЬ
344		325	Qy
136555	TCGGTCCTCAACCATGGTGATTTTGATAATTTCACCAGTTCTCTTACTGGTTTAGCGTTA	136614	Db
324		305	Qy

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REFERENCE
AUTHORS
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SOURCE
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                                                                                                                                                                                                                                                   ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   135861 CTGTATCCGGGGGTGAGTATTAATCGTACCCGCCAACGTGGTGGGGGCGATGCCGGTCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ValLysGluGlyAsnProIleLysLeuHisPhePheIleGly 916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PheGlyAspIleGlyAsnAlaTyrAspLysGlyPheThrAsnAspThrLysIleGlyAla 881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTGGCAACGGGCTCTCTTGAATATCAATATAACTTCACGGGTAGATGGTGGGGGGGCCCGTT 135463
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                                                             McClelland, M., Sanderson, K.E., Spieth, J., Clifton, S.W., Latreille, P., Courtney, L., Porwollik, S., Ali, J., Dante, M., Du, F., Hou, S., Layman, D., Leonard, S., Nguyen, C., Scott, K., Holmes, A., Grewal, N., Mulvaney, E., Ryan, E., Sun, H., Florea, L., Miller, W., Stoneking, T., Nhan, M., Waterston, R., and Wilson, R.K.
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Salmonella typhimurium LT2
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AE008906.1 GI:16
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    (6858),
                                                                                                                                                                                                                                                                                                                                                                                typhimurium
                                                                                                                                                                                                                                                                                                                   GI:16422950
                                                  sequence of Salmonella enterica
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 24892)
The Salmonella typhimurium Genome Sequencing Project.
Direct Submilsion
Submitted (29-MAR-2001) Genome Sequencing Center, Dep
Genetics, Washington University School of Medicine, 4
Park Boulevard, St. Louis, MO 63108, USA
COMMENT Supported by NIH grant 5U 01 AI43283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Coding sequences below are predicted from manually evaluated computer analysis, using similarity information and the programs; GLIMMER; http://www.tigr.org/softlab/glimmer/glimmer.html and GeneMark; http://opal.biology.gatech.edu/GeneMark/
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11677609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EC numbers were kindly provided by Junko Yabuzaki and the Kyoto Encyclopedia of Genes and Genomes; http://www.genome.ad.jp/kegg/.and Pedro Romero and Peter Karp at EccCyc; http://ecocyc.PangeaSystems.com/ecocyc/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://kinich.cifn.unam.mx:8850/db/regulondb_intro.frameset
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                                                                                                                                                                                                                                                                                                                                                       /note="560...7
                                                                                                                                                                                                                                                                                                                560.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="similar to E. coli (AAC77156.1); Blastp hit identity in aa 1 - 91"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(95.
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/gene="rpsF"
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                                                                                                                                                                                                                                                                                                                                                                                                                       complement(378. .383)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="putative outer membrane
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/db_xref="GI:16422951"
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                                                                                                                                                      /transl_table=11
                                                                                                                                                                                               /note="hypothetical
                                                                                                                                                                                                                        /gene="STM4390"
                                                                                                                                                                                                                                                                   /note="putative
                                                                                                                                                                                                                                                                                       /gene="STM4390"
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                                                                                                                               protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QAWCQMPVIVSGHENQAITHSITVGSRITVQGFISCHKAKNGLSKMVLHAEQIELIDS
GD"
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                                                                                                                                     /note-"similar to E. coli 50 (AAC77160.1); Blastp hit to identity in aa 1 - 149"
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828. .833
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                                                                                                                       /codon_start~1
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/gene⇔"rplI"
                                                                                                                                                                                                                                                                /note::"STM4394"
1819. .1824
                                                                                                                                                                                                                                                                                               /geneo"rplI"
                                                                                                                                                                                                                                                                                                                                 /translation~"maryfrrrkfCRFTAEGVQEIDYKDIATLKNYITESGKIVPSRI
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1547. .1552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="mrhyelvfmyhpdqseqvpgmiervsaaitgaegkihrledwgr
RQLAYPINKLHKAHYVLMNVEAPQEVIDELETTFRFNDAVIRSMVMRTKHAVTEASPM
VKAKDERRERRDDFANETADDAEAGDSEE"
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/transl_table~11
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/protein_ide"AAL23211.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /genee"rpsF"
/notee"putative
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1562. .1789
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Best Local Similarity:
Query Match:
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 16671
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TTATGTTGGGTTAGCTTACTGTGCCTGAGCAGTTCTGCGGTAGCC-----
                                                                                                                                                     CGCGCCCGAGTTGATGATGCGATTCGCGAAGGGCTTAAAGCGTTAGGCTATTACGAACCC
                                                                           ACTATCAAATTCGACTTGCTTCCACCGCCTGCGAAAGGACGGCAGGTATTAATCGCCAGG 16670
                                                                                                                                                                                                                                AACGTTCGCGCACAGCTCTCTACGATTCAGAGCGATGAGGTGACGCCGGATCGGCGCTTT 16550
                                                                                                                                                                                                                                                                    AspLeuAsnGlySerIleProArgLeuArgGlnThrAlaLeuValAlaAlaArg-----
                                                                                                               ---IleAspLeuSerIleIleArgAsnSerIleGlyGluValAspValIleIleHisAsp
                                                                                                                                                                                                                                                                                                                                            ThrGluProTyrAlaAsnIleLysAlaAlaLeuGluAspIleThrGlnGluSerAlaMet
                                                                                                                                                                                                                                                                                                                                                                                                                        LysPheTyrGlnSerSerGlnSerGlyGluThrSerAlaIleGlySerSerHisGlnLys
                                   -GlyGluProValTyrIleAspTyrArgAlaValGluValArgGlyGluGly
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/gene="yifz"
/note="similar to E. coli orf.
(AAC74606.1); Blastp hit to A/
identity in aa 20 - 250"
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/gene="ytfB"
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VFGGTLTIHGESSVAILVYLTLLSSVAFALWSILLKYNRVGMIAPENFLIPVSGAALS
AIFLGENILEWKYMIALVLYCSGIWWVNKVKR"
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/db_xref="Gi:16422957"
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/gene="ytfB"
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FYIGLAFTSGVKGSIMNATGTFFSVLLAHFIYQNDRLSYNKTLGCILGFAGVMVVNVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="similar to E. coli orf, hypothetical
(AAC77163.1); Blastp hit to AAC77163.1 (224
identity in aa 13 - 224"
/codon_start=1
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2428. .3354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="STM4395"
2417. .2422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="AAL23216.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="putative cell envelope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="STM4396"
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/gene="yifZ"
                                                                                                                                                                                                                                                                                                          GCAAATGTTCGTCTGAAAGTCGAAGGGCTATCCGGAGAGCTGGAAAAA 16490
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486.50
36.90%
22.45%
10.29%
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                           ----AlaValGlyTyrTyrAsp---
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174
112
270
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aa), 85%
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aa), 25%
16730
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645 17366	GlyValLysLeuTyrAlaThrLysProLeuSerHisProLeuAsnAspGlnLeuArg:::	627 17307	Ф
626 17306	LeuIleAsnArgAspGlyTyrGlnAlaGlyAlaGluLeuArgLeuSerGluAspLysLys :::       ::: TGGATGAACTCTTACGGTCATAGCCTGACCACCAGCACCAGTATTTCTGCGCCCGGAACAG	607 17247	ОУ
606 17246	IleGlyLeuGlyTrpGlySerAspThrGlyThrArgLeuValThrLysPheGluHisAsn	587 17187	g 99
17186	-GAA	17184	Db
586	ln	567	Qy
17183	T	17181	Db
566	${\tt IleAspLeuProGluArgThrAlaLeuAlaAsnArgLysThrProAlaAspValTyr}$	547	Qγ
546 17180	THESE TAS PATAYAL SETATAYALALARIGATE THE SETAS PATAYAL SETATAYALALARIGATE THE SETAS PATAYALAS PATAYALAS THE SETAS PATAYALAS THE SETAS PATAYALAS PATAYANAS PA	17145	용 5
7		17144	, B
526	AspAspArgValLeuAlaIleAsnHisAspAspGlyValAsnArgSerIleLeuGlyArg	507	Qy
17144		17144	망
506	LeuIleGlnAspLysLeuAsnLeuValAlaAlaLysAlaArgHisLeuTyrAspMetPro	487	Qy
17144		17144	망
486	${\tt ValGluLeuThrAspGlyIleLeuMetAspIleSerProIleGluPheSerAlaSerAsn}$	467	Qy
17144	AAAACAAAAATTCTGCCGAAAACAAAAATTCTGCCG	17127	망
466	${\tt laGlnValAspGluSerThrLeuGluProValIleGluThr}$	447	Qy
446 17126	IleValPheProGluArgGluGlnIleGlnAsnAspGlnValSerPheGluGlnSerSer:::	427 17097	D Q
7	ACCGGATGGTTTAATTCTGTC	4.	Вb
426	pLeuIleAlaThrArgTyrPheAsnMetValAsnThrGlu	407	Qγ
406 17045	ArgGluLeuLeuGluGlnLeuLeuThrValAsnMetGlyGluAlaTyrAsnLeuGlnAla	387 16986	рь Оу
16985	GAAGGTTCGCAGATTCGT	16968	뮹
386	\spLysLeuProValLys	367	Qy
366 16967	AlaAspValSerLeuIleTyrAspThrGlyThrGlnTyrArgPheAspGluValValPhe	347 16908	Db Qy
346 16907	GlyTyrPheAspGlyArgTrpLeuAspArgSerValAspValIleLeuProAspAsnThr 	327 16848	망 양
16847	:::	16788	DЬ
326	HisHisGlyLysTyrGluThrLysLysAsnLeuIleGluAsnAlaSerAlaGluHis	307	Q
306 16787	AlaAspAspLysAlaPheThrThrValAlaAspGluValProLeuLeuIleGlyAspVal	287 16731	Db Qy

67 GTACAGGGCGGTTTTAAACGTACC	<pre>r serovar Typn1 division; Enterobacteriaceae; f Thomson, N.R., Pickard, D., Bentley, S.D., Holden, M.T.G., prooks, K., Chillingworth, T., Davies, R.M., Dowd, L., White, N</pre>	M Salmonelia enterica subsp. enterica Salmonelia; Proteobacteria; gamma sub Salmonelia.  1 (bases 1 to 249050)  Parkhill,J., Dougan,G., James,K.D., Wain,J., Churcher,C., Mungall,K.L., Sebaihia,M., Baker,S., Basham,D., E Connerton,P., Cronin,A., Davis,P.,	ANIS ENCE HORS	REF C
17367 GTACAGGGGGGTTTTAÀACGTACC	erovar Typh	AL627283 AL513382 AL627283.1 GI:16505370 Salmonella enterica subsp. enteric	SION ON RDS	
17367 GTACAGGGGGTTTTÄÄÄCCTACC	NA linear BCT 06- almonella typhi) strain	AL627283 AL627283 AL627283 Salmonella enterica serovar Typhi (	LT 17283	81 00 00 73
17367 GTACAGGGCGGTTTTAAAGGTACC	T 1809	GACAAAGACGAACACGGTTTACA	.806	DЬ
17367 GTACAGGGCGGTTTTAAAGGTACC	Ly 91	alLysGluGluGlyAsnProIleLysLeuHi 	0	Qу
17367 GTACAGGGGGGTTTTNAAGGTACC	SPValAlaThrGly 9 	yValArgTrpAlaSerProValGly 	884 8000	Qy Db
17367 GTBACAGGGCGTTTTAAACGTACC	AAAACCGGGACCGGGGTC 17	ATAGCGGCGAGGCGTGAGTGATATTCGCCGTAG	794	DЬ
17367 GTACAGGGGGTTTTAAACGTACC	LysIleGlyAlaGlyVal 88	spIleGlyAsnAlaTyrAspLysGlyPheThrAsı	o	Qy
17367 GTACAGGGCGTTTTAAAGCTACCGATTTGAATGATACGGAGCAC 17 666 ThrArgThrLeuGluHisGluIleSerArgSerIleIleGlnAsnGlyGlyTrpAsnArg 687 TCGACCACGCTTGCCGTGCGCGTTACTGGGACCTTTCCAGTTGGCAGCGG 17 686 ThrTyrSerLeuArgTyrArgLeuAspLysLeuLysThrGlnAlaProProGluThrTrp 706 GlnAspLeuProValAspPheValAsnGlyLysProSerGlnGluAlaLeuLeu	ArgLeuAlaValPheGly 86           TGGGGGGCAGTGTTTGTC 17	<pre>}!uTyrAsnTyrGluPheMetLys            AGTACCAGTATAACGTCACCGGT</pre>	844 7880	Db Qy
17367 GTACAGGGCGGTTTTTAAACGTACC	nValLeuAla 84         AAAACTGGCA 17	AspSerLeuSerProIleSerAsp    :::        AAATCTATTTCGCCTAAAGATAGC	82 782	ОУ
17367 GTACAGGGCGGTTTTAAACCTACCGATTTGAATGATACGAGCAGGAC 1 666 ThrargThrLeuGluHisGluIleSerArgSerIleIleGlnAsnGlyGlyTrpAsnArg 666 ThrargThrLeuGluHisGluIleSerArgSerIleIleGlnAsnGlyGlyTrpAsnArg 67415 TCGACCACGCTTGCCGTGTCGCGTTACTGGGACCTTTCCAGTGGTTGGCAGCGG 686 ThrTyrSerLeuArgTyrArgLeuAspLysLeuLysThrGlnAlaProProGluThrTrp 71469 GCGATTAATCTGCGCTGGAGTTTCGAC 706 GlnAspLeuProValAspPheValAsnGlyLysProSerGlnGluAlaLeuLeu 707 GlnAspLeuProValAspPheValAsnGlyLysProSerGlnGluAlaLeuLeu 708 GlnAspLeuProValAspPheValAsnGlyLysProSerGlnGluAlaLeuLeu 709 GlnAspLeuProValAspPheValAsnGlyLysProSerGlnGluAlaLeuLeu 709 GlnAspLeuProValAspPheValAsnAsnAcGTCACCAATACCACCATGCTGTTCTAC 709	GCAGTATTCGCGGCTATAAA 1	AAGTTCCGCCGGATTTACGTTTCTTCGCCGGGGGCC	776	₽ 5
17367 GTACAGGGCGGTTTTAAACGTACCGATTTGAATGATACGAGCAGGAC 1 666 ThrargThrLeuGluHisGluIleSerArgSerIleIleGlnAsnGlyGJYTrpAsnArg 666 ThrargThrLeuGluHisGluIleSerArgSerIleIleGlnAsnGlyGJYTrpAsnArg 671 TCGACCACGCTTGCCGTGTCGCGTTACTGGGACCTTTCCAGTGGTTGGCAGCGG 686 ThrTyrSerLeuArgTyrArgLeuAspLysLeuLysThrGlnAlaProProGluThrTrp 786 GCGATTAATCTGCGCTGGAGTTTCGAC	ATAGAAACCGGTGATTTCGAC 1	CACCGTTTTGTGATGCGCGCCAATTTGGGCT	770	₽ ₽
17367 GTACAGGGGGGTTTTAAACGTACCGATTTGAATGATACGGACCAGGAC 1 666 ThrargThrLeuGluHisGluIleSerArgSerIleIleGlnAsnGlyGlyTrpAsnArg 6 :::        17415 TCGACCACGCTTGCCGTGTCGCGTTACTGGGACCTTTCCAGTGGTGCCAGCGG 1 686 ThrTyrSerLeuArgTyrArgLeuAspLysLeuLysThrGlnAlaProProGluThrTrp 7:::     ::     17469 GCGATTAATCTGCGCTGGAGTTTCGAC	[leTrpSerAspAsnPheAsn 8	rgAlaHisGlnMetThrGlyGlyI	78	Qy
17367 GTACAGGGCGGTTTTTAAACGTACCGATTTGAATGATACGGAGCACGAC 666 ThrArgThrLeuGluHisGluIleSerArgSerIleIleGlnAsnGlyGlyTrpAsnArg 686 ThrTArgThrLeuGluHisGluIleSerArgSerIleIleGlnAsnGlyGlyTrpAsnArg 687 TCGACCACGCTTGCCGTGTCGGCTTACTGGGACCTTTCCAGTGGTTGGCACCGG 686 ThrTyrSerLeuArgTyrArgLeuAspLysLeuLysThrGlnAlaProProGluThrTrp 706 GCGATTAATCTGCGCTGGAGTTTCGAC	AspAsnAlaTyrGlySerAsn 78     GATCGC17	leAlaArgAlaGlyIleSerGlyValTyrSerPhec: :: ::   TGCTGCAGGCGCAAAACGTCTGGATTCGGACTTTGT	76 766	Qy Db
17367 GTACAGGGCGGTTTTAAAAGTACCGATTTGAATGATACGAGCAGGAC 17 666 ThrArgThrLeuGluH1sGluIleSerArgSerIleIleGlnAsnGlyGlyTrpAsnArg 686 ThrTyrSerLeuArgTyrArgLeuAspLysLeuLysThrGlnAlaProProGluThrTrp 686 ThrTyrSerLeuArgTyrArgLeuAspLysLeuLysThrGlnAlaProProGluThrTrp 706 GCGATTAATCTGCGCTTGCAGTTTCGAC	ValSerAspAlaAsnMetAla 76         ::: ::: GGCTCCGACGTGGATTTCTCC 17	rgGlnArgTyrSerLeuGluValGlySerSerGly             :::::  GCAGCGCTATTCAGTAGACTATTCGAATACGGCC	74 760	ОУ
17367 GTACAGGGCGGTTTTTAAAGGTACC	ValAsnProMetArgGlyTyr 74 :::         CTGATGCCAACCTGGGGCGAT 17	laGlyValAlaValHisLysThrValAlaAspAsnL        ::: ::    ::: CGGCGTGATGATCAGCCGAACCCGCTCGCGAGGGG	754	Db 24
17367 GTACAGGGCGGTTTTAAACGTACCGATTTGAATGATACGGAGCAC 17 666 ThrargThrLeuGluH1sGluIleSerArgSerIleIleGlnAsnGlyGlyTrpAsnArg 68 :::       17415 TCGACCACGCTTGCCGTGTCGCGTTACTGGACCATTCCAGTGGTTGGCAGCGG 17 686 ThrTyrSerLeuArgTyrArgLeuAspLysLeuLysThrGlnAlaProProGluThrTrp 70 686 ThrTyrSerLeuArgTyrArgLeuAspLysLeuLysThrGlnAlaProProGluThrTrp 70 17469 GCGATTAATCTGCGCTGGAGTTTCGAC	E::    AATACCACCATGCTGTTCTAC 17		749	Db
17367 GTACAGGGCGGTTTTAAAGGTACCGATTTGAATGATACGGAGGAC 17 666 ThrArgThrLeuGluHisGluIleSerArgSerIleIleGlnAsnGlyGlyTrpAsnArg 68 :::	GlnGluAlaLeuLeu 72	lnAspLeuProValAspPheValAspGlvLvsPro	70	0 6
17367 GTACAGGGCGGTTTTAAACGTACCGATTTGAATGATACGGAGCAGGAC 17 666 ThrargThrLeuGluHisGluIleSerArgSerIleIleGlnAsnGlyGlyTrpAsnArg 68 :::	rGlnAlaProProGluThrTrp 70	TyrSerLeuArgTyrArgLeuAspLysLeuLysT :::     ::: ATTAATCTCCTTCCACTTTCCAC	68 746	P 29
17367 GTACAGGGCGGTTTTAAACGTACCGATTTGAATGATACGGAGCAGGAC 17	GlnAsnGlyGlyTrpAsnArg 68 :::  {         CTTTCCAGTGGTTGGCAGCGG 17	hrArgThrLeuGluHisGluIleSerArgSerIleI ::        CGACCACGCTTGCCGTGTCGCGTTACTGGG	66 741	Оy
	AATGATACGGAGCAGGAC 17	TACAGGGCGGTTTTAAACGTACCG	736	Db

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PUBMED
REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Details of S. typhi sequencing at the Sanger Centre on the World Wide Web. \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (25-OCT-2001) Submitted on behalf of the Salmonalla sequencing team, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, UK E-mail: parkhill@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Farrar,J., Feltwell,T., Hamlin,N., Haque,A., Hien,T.T., Holroyd,; Jagels,K., Krogh,A., Larsen,T.S., Leather,S., Moule,S., O'Gaora, Parry,C., Quail,M., Rutherford,K., Simmonds,M., Skelton,J., Stevens,K., Whitehead,S. and Barrell,B.G.
Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18
Nature 413 (8858), 848-852 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Parkhill, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11677608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.sanger.ac.uk/Projects/S_typhi/)
                                                                              /note-"Pfam match to entry PF00817 IMS, impB/mucB/samB family, score 545.70, E-value 3.1e-160" complement(join(1753. .1830,35386. .35730))
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                                                                                                                                                                                                      WVKGHRYAKAGCMLNDFTPTGISQLNLFDEVQPHERSEQLMKVLDSINHSGMGKVWFAGRGIAPEWQMKRELLSPAYTTRWAELPVARLR"
complement(695. .1741)
                                                                                                                                                                                                                                                                                GVLALTSGNPKRTEKLLSLQPVDEIWGYGRRISKKLHTWGITTALQLARANPTEIRKN
FSVVLERTVRELNGESCISLEEAPPKQQIVCSRSFGERVTTYEAMRQAVCQYAERAA
EKLRGEROFCRHYAVFVKTSPFAVNEPYYGNVASEKLTTPTQDTRDIIAAAVKALDRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"Similar to Salmonella typhimurium cryptic 60-MDa plasmid SamB protein SW:SAMB_SALTY (P23832) (424 aa) fasta scores: E(): 0, 89.6% id in 423 aa, and to Shigella flaxneri ImpB impB TR:Q32A91 (EMBL:AF079316) (423 aa) fasta scores: E(): 0, 71.7% id in 421 aa Paralogue of E. coli umuC (UMUC_ECOLI); Fasta hit to UMUC_ECOLI (422 aa), 63% identity in 420 aa overlap"
     complement(join(1753.
                                                                                                                                                                                                                                                                                                                                                         /translation-"mfaladvnsfyascekvfrpdlrntpvvvlsnndgcviarskea
KQLGIKMGVPWFQLKTTEFPVPVVAFSSNYELYASMSNRVMAHLEELAPRVEQYSIDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="SPTREMBL:Q8Z1G9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"samB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product-"hypothetical protein"
/protein_id="CAD06718.1"
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/codon et=
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/transl_table=11
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.1830,35386. .35730))
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O'Gaora, P.,
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misc_feature
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                                                                                                                                                                                                                                                                                                                                               /note-"Similar to Bacteriophage P2 late gene control protein D SW:VPD_BPP2 (P10312) (387 aa) fasta scores: E(): 0, 54.3% id in 370 aa and to Bacteriophage 186 late gene control protein D SW:VPD_BP186 (P21679) (389 aa) fasta scores: E(): 0, 54.7% id in 371 aa" /codon_start=1
NRTYANRGNAERAAKMQWERLQRGVASFSLQLAEGRADLYTEMPVKVSGFKQPIDDAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="SPTREMBL:Q821G7"
/translation="MMNCPKCGHSAHTRSSFQVTDSTKERYCQCQNINCGSTFVTHET
VVRFIVTPALVUNAPPHPTYSQQHMNF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /notee "Similar to Escherichia coli prophage P2 Ogr protein SW:OGRX_ECOLI () (72 aa) fasta scores: E(): 4.8e-15, 55.7% id in 70 aa and to Bacteriophage 186 late gene control protein B SW:VPB_BP186 (P08711) (72 aa) fasta scores: E(): 2.1e-17, 64.2% id in 67 aa."
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/translation="MNKPLIALLITSFSASADKIPSSIQNLIAVYDTRTHSLEDGGL
TIRYNKRLLLVDAAESMEQGICNDYYMNKWKPGTIKRITLLNVTSDQGFEINAGGDEC
RKAGTMKDGARTYRTSEIKPLQ"
complement(2437. .2655)
/gene="STY4600"
                                      ADRGAYTGVIASWLHTREPKKKETTQVKRRHKKVATPKEPEAKQGDYLVGTDENVLVL
                                                               {	t ESDASFLMKLARQYGAIASVKDGNLLFIRQGQGRTASGKPLPVITITKKAGDGHRFTL}
                                                                                         /db_xref="SPTREMBL:08z1G6"
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/translation="MNFSSDLFGLNSRSPAFSITIEGKDVTTALDARLMSLTLTDNRG
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IRARSADFRETLNTRREKSWHQTTVGEVVKEIAARHNLKVALGKDLTDKVLDHMDQTN
                                                                                                                                                                                                                         /product="putative regulator of late
/protein_id="CAD06723.1"
/db_xref="GI:16505375"
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/gene="STY4601"
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/gene="STY4601"
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/product="putative
transcription"
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/gene="STY4600"
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1973. .2350
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                                                                                                                                                                                                                                                                                                                            /transl_table=11
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/db_xref="GI:16505374"
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/protein_id="CAD06721.1"
/db_xref="GI:16505373"
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/codon_start=1
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1973. .2350
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/transl_table=11
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/db_xref="PSEUDO:CAD06720.1"
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/EC_number="3.4.21.-"
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Query Match:
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153390 ACTATCAAATTCGACTTGCTTCCACCGCCTGCGAAAGGACGGCAGGTATTAATCGCCAGG 153449
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                                                                                                                                                                                                                                                                                                                                                                206
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                                                ---IleAspLeuSerIleIleArgAsnSerIleGlyGluValAspValIleIleHisAsp 268
                                                                                                     CGCGCCCGAGTTGATGATGCGATTCGCGAAGGGCCTTAAAGCGTTAGGCTATTACGAACCC 153389
                                                                                                                                                                                                        AACGTTCGCGCACAGCTCTCTACGATTCAGAGCGATGAGGTGACGCCGGATCGGCGCTTT 153329
                                                                                                                                                                                                                                                                                                                                                          ThrGluProTyrAlaAsnIleLysAlaAlaLeuGluAspIleThrGlnGluSerAlaMet 225
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/translation="MSDNNLRLQVVLGAVDKLTRPFKNAQAGSKELASAIRQTRDQIK
/translation="MSDNNLRLQVVLGAVDKLTRPFKNAQAGSKELASAIRQTRDQIK
KLSDAGGQLKSFDQLTQSVSRTGAELDQARLRAQMMTREMSSLESPTKKQTQALEAQW
KLSDAGGQLKSFDQLTQSVSRTGAELDQARLRAQMATREMSLARETERYNRQLAEQERR
RAVSRLEQKQQQGTRQMAAARAELYRLGLSAGGGARETARIJARETERYNRQLAEQER
LREVGERQRKLNAIKAKAEKTRELRNSLAGNCAGAMAAGVTTGMTLLAPVKAYSESEN
AANQLAGSMMGPGGKVAPEFEKINRLAVALGDKLPGTTADFQNMMTMLRRQGMSAQVI
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/gene="STY4603"
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/protein_id="CAD06725.1"
/db_xref="GI:16505377"
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/gene-"STY4603"
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/gene="STY4602"
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(EMBL:U32222) (812 aa) fasta scores: E(): 1.4e-14, 24.5%
id in 694 aa"
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PDNDPLTLSGVLLPEVTGGRLSLLALEQMAELGKAWPLIEGSGTIYGMFVIESLSQTK
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/transl_table=11
protein_fa="cab06724.1"
/db_xref="GI:16505376"
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/gene="STY4602"
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NMLQGFSKISSAMNIINKKGLEAVKTFAPLLVMADQGSMAGESAGNAYRKIFQAALDA
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                                                                                                                                                                                                                                                                                                          GCAAATGTTCGTCTGAAAGTCGAAGGGCTATCCGGAGAGCTGGAAAAA 153269
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486.50
36.90%
22.45%
10.29%
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Matches:
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Indels:
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174
112
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G E	TGGATGAACTCCTACGGTCATAGCCTGACCAGCAGCAGCAGTATTTCTGCGCCGGGACAG	N G	Db
626	i.eu.ileAsnArgAspG]vTvrG]nA]aG]vAlaG]uI.eu.ArgI.euSerG]uAspI.vsI.vs	607	0
154025	ACCGGGGTGGGGTACTCCACCGACGTCGGGCCGCGCGTGAAAGCCGTCGTGGAAAAAACCG	153966	Дb
606	IleGlyLeuGlyTrpGlySer AspThrGlyThrArgLeuValThrLysPheGluHisAsn	587	Qy
153965	GAA	153963	Db
586	GlnSerLysLysValProLeuTyrValPheValAlaSerAspLysProArgAspGlyGln	567	Qy
153962	ATT	153960	Db
566	ValIleAspLeuProGluArgThrAlaLeuAlaAsnArgLysThrProAlaAspValTyr	547	Qy
153959	TTAAAAAGGCGTGGTATCACCGCGAACCGAAAAAAAGGCGTGGTATCACCGCGAACCGAAAAAAAA	153924	Db
546	IleSerAspAlaValSerAlaValAlaArgAlaIleLeuProAspGluSerGluAsnGlu	527	Qy
153923		153923	Db
526	Asp Asp Arg Val Leu Ala Ile Asn His Asp Asp Gly Val Asn Arg Ser Ile Leu Gly Arg Asp Asp Arg Val Leu Ala Ile Asn His Asp Asp Gly Val Asn Arg Val Leu Ala Ile Asn His Asp Asp Gly Val Asn Arg Val Leu Ala Ile Asn His Asp Asp Gly Val Asn Arg Val Leu Ala Ile Asn His Asp Asp Gly Val Asn Arg Val Leu Ala Ile Asn His Asp Asp Gly Val Asn Arg Val Leu Ala Ile Asn His Asp Asp Gly Val Asn Arg Val Leu Ash Val Val Val Asn Arg Val	507	Qy
153923		153923	Db
506	LeuIleGlnAspLysLeuAsnLeuValAlaAlaLysAlaArgHisLeuTyrAspMetPro	487	Qy
153923		153923	Db
486	ValGluLeuThrAspGlyIleLeuMetAspIleSerProIleGluPheSerAlaSerAsn	467	Qy
153923	AAAACAAAATTCTGCCG	153906	DЪ
466	SerSerArgThrGluProAlaGlnValAspGluSerThrLeuGluProValIleGluThr	447	Qy
153905	TIGGTGGCGCCGGAATTTGAGAAATCGCGT	153876	Db 45
,			<b>)</b>
426 153875	ValArgAlaLeuSerAsnAspLeuIleAlaThrArgTyrPheAsnMetValAsnThrGlu:::	407 153825	Qy Db
153824	AIGNIUMEULHULUUTILHEULHIITTYVAIASIMECSIYSIVALATYIASILEUSINAIA        :::         :::      GATGAATATTTACAAAATCTGTTGCCGTTTAAAGAGGGTGATGAGTACGAATCGAAAGAT	153765	Db VY
, U		4 0	au Db
86	heThrIleAspProLysThrAsnGlnLeuThrThrAspP	ι . ω	Qy
Ġ.	GCTTTTGGGATATTGATTATGATAGCGGTGAGCGCTATCGCTTCGGGCCTGTCACCTTC	153687	DЬ
366	AlaAspValSerLeuIleTyrAspThrGlyThrGlnTyrArqPheAspGluValValPhe	347	Qy
153686		153627	Db
346	$\verb GlyTyrPheAspGlyArgTrpLeuAspArgSerValAspValIleLeuProAspAsnThr \\$	327	Qy
153626	CTCAACCAGGGGGACTATGACAATTTTAAAAAAGTCGTTAACCAGCGTGTCGCTACGCAAA	153567	рь
326	PheHisHisGlyLysTyrGluThrLysLysAsnLeuIleGluAsnAlaSerAlaGluHis	307	Qy
153566	CGTACGGACAAAGATTATCTGGCCTTACTGAAAACGCGTCCGGCAATCGGCACGGTG	153510	Db
306	AlaAspAspLysAlaPheThrThrValAlaAspGluValProLeuLeuIleGlyAspVal	287	Qγ
286 153509	LeuGlyGluProValTyrIleAspTyrArgAlaValGluValArgGlyGluGly:::     :::          :::           :::	269 153450	ОУ

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                                                                                                                                                                                       GACAAAGACGAACACGGT-----TTACAGTTTTATATCGGT 154874
                                                                                                                                                                                                        ValLysGluGlyAsnProIleLysLeuHisPhePheIleGly 916
                                                                                                                                                                                                                                        GCCGTGCGCTGGGCGTCGCCGGTTGGGCCTGTCAAACTCGATTTTGCCGTACCGGTCCGC
                                                                                                                                                                                                                                                          GlyValArgTrpAlaSerProValGlyGlnValArgValAsp-----ValAlaThrGly
                                                                                                                                                                                                                                                                                             GATAGCGGCGAGGCGGTTAGTGATATTCGCCGTAGCGATTTCAAAACCGGGGACCGGGGTC
                                                                                                                                                                                                                                                                                                                    AspIleGlyAsnAlaTyrAspLysGlyPheThrAsnAspThrLysIleGlyAlaGlyVal
                                                                                                                                                                                                                                                                                                                                                {\tt ValGlyThrAlaGluTyrAsnTyrGluPheMetLysAspLeuArgLeuAlaValPheGly}
                                                                                                                                                                                                                                                                                                                                                                                                   TACAAATCTATTTCGCCTAAAGATAGCGACGGCAATCTTAAAGGCGCCTCAAAACTGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                           HisaspSerLeuSerProIleSerAspLysGlyTyrLeuThrGlyGlyGlnValLeuAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAAGTTCCGCCGGATTTACGTTTCTTCGCCGGGGGGGGCGACCGCAGTATTCGCGGCTATAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HlsvalProTyrArgLeuArgPhePheAlaGlyGlyAspGlnSerIleArgGlyTyrAla 823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ArgAlaHisGlnMetThrGlyGlyIleGlnAlaGlyTyrIleTrpSerAspAsnPheAsn 803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTACTGCAGGCGCAAAACGTCTGGATTCGGACTTTGTACGATCGC-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     {\tt IleAlaArgAlaGlyIleSerGlyValTyrSerPheGlyAspAsnAlaTyrGlySerAsn}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----CACCGTTTTGTGATGCGCGCCAATTTGGGCTGGATAGAAACCGGTGATTTCGAC 154538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCGCAGCGCTACTCGGTAGACTATTCGAATACGGCCTGGGGCTCCGACGTGGATTTCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCGGGCGTGATGATCAGCCGAACCCGCTCGCGAGGGGGGACTGATGCCAACCTGGGGGCGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlnAspLeuProValAspPheValAsnGlyLysProSerGlnGluAlaLeuLeu-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCGATTAACCTGCGCTGGAGTTTCGAC-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ArgGlnArgTyrSerLeuGluValGlySerSerGlyLeuValSerAspAlaAsnMetAla
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                                              Vibrio cholerae.
Vibrio cholerae
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                 Bacteria; Proteobacteria;
1 (bases 1 to 14390)
                                                                                                                        Vibrio cholerae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   {\tt ThrTyrSerLeuArgTyrArgLeuAspLysLeuLysThrGlnAlaProProGluThrTrp}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCGACCACGCTT-----GCCGTGTCGCGTTACTGGGACCTTTCCAGCGGTTGGCAGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         {\tt AlaThrLeuGlyTyrGlnGluValPheGlyHisSerThrAsnGlyPheAspLeuSer}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTGCTGGATTTTAGTTATAAAATGCCGCTGCTGAAAAACCCCGCTGGAGCAATACTATCTG 154145
                                                                                        AE004323 AE003852
AE004323.1 GI:969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTACAGGGCGGTTTTAAACGTACC------GATTTGAATGATACGGAGCAGGAC
                                                                                                                   chromosome
                                                                                                                                              AE004323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -------CACTTTACCCAGGGAACGTCACCAATACCACCATGCTGTTCTAC 154319
                                                                                     GI:9657119
 Eisen, J.A., Nelson, W.C.,
                                                                                                                          14390 bp
some I, se
                      gamma subdivision; Vibrionaceae;
                                                                                                                        section
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Clayton, R.A.,
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of 251 of
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Gwinn, M.L.
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complete
                         Vibrio
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JOURNAL
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MEDLINE
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                                                                           /note="similar to GB:D10483 PID:1786254; identified by s
                                                                                                                    complement(1492. .3084)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center Dr, Rockville,
Location/Qualifiers
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/transl_table=11
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PID:1786253; identified by s
                                                                                                                                                                                                                                                                                                                                                                 /gene="VC2537"
                                                                                                                                                                                                                                                           putative"
                                                                                                                                                                                                                                                                     /product="thiamine
                                                                                                                                                                                                                                                                                                                                                complement(764. .1498)
                                                                                                                                                                                                                                                                                   transl_table=11
                                                                                                                                                                                                                                                                                                 /codon_start=1
                                                                                                                                                                                                                                                                                                                                        /gene="VC2537"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="VC2536"
80. .661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="VC2536"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="biotype:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /chromosome="I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:666"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Vibrio cholerae"
/strain="N16961"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /serotype="01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .14390
                                                                                                                                               .3084)
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2 (bases 1 to 14390)
Heidelberg, J. F., Eisen, J.A., Nelson, W.C., Clayton, R.A., Gwinn, M.I. Dodson, R.J., Haft, D.H., Hickey, E.K., Peterson, J.D., Umayam, L.A., Gill, S.R., Nelson, K.E., Read, T.D., Tettelin, H., Richardson, D., Ermolaeva, M.D., Vamathevan, J., Bass, S., Qin, H., Dragoi, I., Sellers, P., McDonald, L., Utterback, T., Fleishmann, R.D., Nierman, W.C., White, O., Salzberg, S.L., Smith, H.O., Colwell, R.R., Mekalanos, J.J., Venter, J.C. and Fraser, C.M.
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/db_xref="01:9657121"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="mmknmarknokapweeeeeeliwvsrtelknomlaloklgeelve
LKPSALAKFPLPEDLAEAIKDAORFKNEARROLQYIGKLMRHIDPEPLQAALDKLRN
KHSQTTALLHKLEQLKDRIVAEGDSAIEVAMEQYPEADRORLRLLARQASKEKAGNKP
PKSSREIFOLLKEAMLAKQEIEEESEDDLDSAE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="conserved hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              by Glimmer2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABC transporter,
                                                                                                                                           transporter,
                                                                                                                                                                                                                                             sequence
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                                                                                                                                                                                                                                                                             SP: P31549
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                                                                                                                                           permease
                                                                                                                                                                                                                                          similarity;
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                                                                                                                                           protein,
                                                                                                                                                                                                                                      putative"
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putative"
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meso-diaminopimelate ligase"

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APKODEALADVLORGCWSETEFSGEOGEWQAEKITADGSQFHYLLKGERVGOVNWSLU

DRAWGENAINATAAAHUTUNDEI AFBSTGICHWALKGERVGOVNWSLU

CHANGENAINATAAAHUTUNDEI AFBSTGICHWALKAU

CHAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="msmnnnrtitlawtgasgapyglrllqcllaadyqyyllissaa
RVVLatehglklpanpeaaqaalvehlgcasdklvvcgkedwfspvasgsaapkomvv
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SWRAKVWDASWIVAACVLVLPPLVMVVLAGLNSKLGKVLTSGDFWSAVSHSLQVASLA
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PID:1790680; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(4990. .6345)
/gene="VC2542"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VTIMPAAPGFYHQPQSIDDLVDFMVARILDHLGIEQALVPRWGYDQRVRGE"
complement(4990. .6345)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="3-octapreny1-4-hydroxybenzoate carboxy-lyase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity; putative"
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PRTSTPGQGLLLWMKSVYGDQAPQAWKQLASKTVTVTKGWSEAYSMFLGGEADLVLSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="similar to GB:D10483 PID:497658; identified by se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="VC2539"
complement(3094, .4086)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(3094. .4086)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMSVGWFYVIERLFAQRPLTKC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LRKPLSHAFAIGFLLSMGDLSAIALFGSQDFRTLPLYLYQLLGSYQMDTAAVVALAML
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            {f SSLALASGIAMLLTSRALRLKAAHRRANGVEWIATLILVTPGLVVSTGLFLLLRNITD}
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GDHNVSNALMAIAAARHVGVAPELACEALGLFVNTKRRLELKGEINGVTVYDDFAHHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="VC2542"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="VC2540"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="VC2540"
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                                                                                                                                                                                                                                                                                                                                   AACGTGGAGGCGTATCTCTCATCGATC------GCGGCACAAGACTATTCCACCAGT 14097
                                                                                                                                                                                                                                                                                                                                                                        AsnIleLysAlaAlaLeuGluAspIleThrGlnGluSerAlaMetAspLeuAsnGlySer
                                                                                                                                                                TACCACCCCAGTATCGATTTTACTGTCTCTGAAGATAACCAGCGTTTACGCGCCGCAGTG
                                                                                                                                                                                                        Tyr-----AspIleAspLeuSerIleIleArgAsnSer----
                                                                                                                                                                                                                                                                                             Ile---
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                                                                               ACCTTGGGCGAAGTGACCCGTTTGAGCGAGGTTGATATTGTGATC ---
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WSVEEVAKQCQQPAQVSANMDEFVAMIAKEAQAGDQILVMSNGGFEGIHGKLLAALQQ
K"
                                                                                                                                                                                                                                                                                         --ProArgLeuArgGlnThrAlaLeuValAlaAlaArgAlaValGlyTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="VC2544"
/note="similar to SP:P09200 GB:X12545 PID:41416 PID:537074
GB:U00096; identified by sequence similarity; putative"
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6651. .7661
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7831. .8361
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ELNKNAKYVVLMDPLDGSSITOVNVSVGTIESIYRVSSPOPTOGDFLQPGNKQVA
AGYVIYGSSTMLVYTTGNGVNGFTYDDSLGTFYLSHENMRIDBNGKIYSI NEGNVIF
PTGVKKYIKFCQENVPEEGRPYTSRYIGSLVADFHRNLLKGGTYLYPSTQSHPNGKLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="VC2543"
6334. .6597
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similar to GB:U14003 SP:P17288 PID:450373 PID:537068 GB:U00096; identified by sequence sim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="fructose-1,6-bisphosphatase"
/protein_id="AAF95685.1"
/db_xref="GI:9657128"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPSVSSIPVKRSKFYNSLQTRCIAQSIPSEDPIILLNPFVALH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="hypothetical protein"
/protein_id="AAF95684.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="VC2545"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLYECNPMAFLIEQAGGLASDGARRIMDIKPTELHQRVPFFVGSKNMVHKVETFLETY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="GI:9657127"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="inorganic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           translation="MQKMRTLGEFIVEKQHDFPHASGELSSLLASIRLAAKIVNREIn/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  translation="MNVHKNPAFLLCDWNGSIIPIRYAKASAAVQRGVNSKWSTIKVR/
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22.40%
9.60%
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                                                                                                                      IleGlyGluValAspValIleIleHisAspLeuGlyGlu
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CGCGGTGAAGCCGAAGGCGATCGCGAT 13905
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13266	5 TACAAGATCCCACT	1332	Db
551	2 AlaThrLysProLeuSerHisProLeuAsnAspGlnLeuArgAlaThrLeuGlyTyrGl	63	Qy
13326	GGCACAGTTTTGACAGCAGTTTCTCTCTTTCTATACCAGAGCAGACCATTACGGCGG	1338	Db
531	2 GlyTyrGlnAlaGlyAlaGluLeuArgLeuSerGluAspLysLysGlyValLysLeuTyr	61	Qy
511 13386	92 GIYSETASPTRIGIYThrArgLeuValThrLysPheGluHisAsnLeuIleAsnArgAsp 6 :::                15 TCCACGGACGTTGGAGTACGTGGTTCATTAAAATGGAAGAACCTTGGGTGAACAGCCAA 1	1344	р у У
w			) }
591	2 ProLeuTyrValPheValAlaSerAspLysProArgAspGlyGlnIleGlyLeuGlyTrp	υī	Q
71	52 GluargThrAlaLeuAlaAsnArgLysThrProAlaAspValTyrGlnSerLysLysVal	1351	Db Qy
13515	15	1351	DЬ
551	32 SerAlaValAlaArgAlaIleLeuProAspGluSerGluAsnGluValIleAspLeuPro	S	ργ
531 13515	23GATGAGGGG	1352	Db 43
13524	24		) DB
511	92 LeuAsnLeuValAlaAlaLysAlaArgHisLeuTyrAspMetProAspAspArgValLeu	4	Ş.
13524	324	135	Db
491	72 GlyIleLeuMetAspIleSerProIleGluPheSerAlaSerAsnLeuIleGlnAspLys	4	Qy
13524	24	135	дg
471	52 ProAlaGlnValAspCluSerThrLeuGluProValIleGluThrValGluLeuThrAsp	4	Оу
13524	35 TTATCGCAGTTG	135	дд
451	32 ArgGluGlnIleGlnAsnAspGlnValSerPheGluGlnSerSerSerSerArgThrGlu	4	γο
<b></b> (	86 CAAAATCTTTCCAATACAGATTGGTTCTCTTCGGTGTTTGTT	135	Дb
w	12 AsnAspLeuIleAlaThrArgTyrPheAsnMetValAsnThrGluIleValPheProGlu	۵	ογ
411 13587	92 GlnLeuLeuThrValAsnMetGlyGluAlaTyrAsnLeuGlnAlaValArgAlaLeuS 	136	Db 04
13647	94GAGCGACCACGGTCGAAGGCAGTCAAATCGATGAAAATCGCC	136	ф
391	72 LysThrAsnGlnLeuThrThrAspProAspLysLeuProValLysArgGluLeuLeuGl	w	γo
13695	24 CACTTTGATAGCGGGATCCGTTACCTGTTT	137	В
371	52 IleTyrAspThrGlyThrGlnTyrArgPheAspGluValValPhePheThrIleAsp	w	γo
13725	84 GATTTTCAGGCCAGCCGGCTGGAAGTGATTCCAGAG	13	Db .
1	32 ArgTrpLeuAspArgSerValAspValTleLeuProAspAspThral=AspValSov	ω	Q V
331 13785	312 TYPGJUTTALYSLY9ASALGUIIGGLUASAAJASGEAJAGUHISGJYTYYPHEASPGJY	138	Db 49
13845	04 FITCAACGTTTGATCCGCCGCAGTGGTTTGAGAGTGGAT	1.	, 10
311	92 PheThrThrValAlaAspGluValProLeuLeuIleGlyAspV		, Q

REFE AU TI	SOURCE	RESULT 1 AX033468 LOCUS DEFINITI ACCESSIO VERSION KEYWORDS	Db	Óγ	Фр	Db	Оу	Оy	Db	Qy	Оy	DЬ	Qy	Db	Qy	Qу	Db	o Db	Qy	Db	Qy	Db	Qy	DЪ	Qy
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1 (bases 1 to 1737) 1 (bases 1 to 1737) 1 (bases 1 to 1737) Ruelle, J. L. and Thonnard, J. Haemophilus influenzae rd outer membrane sequences used as vaccine Patent: WO 0047737-A 1 17-AUG-2000; RUELLE JEAN LOUIS (BE); SMITHKLINE BEECHAM BIOLOG (BE); THONNARD JOELLE (BE)	Haemophilus influenzae. Haemophilus influenzae Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae; Haemonhilus	AX033468 1737 bp DNA linear PAT 21-SEP-2000 Sequence 1 from Patent WO0047737. AX033468 AX033468.1 GI:10280229	CCGGCGATGAGTTCAAAATCCACTTCACTTTAGGG 12552	luGlyAsnF	ArgTrpAlaSerProValGlyGlnValArgValAspValAlaThrGlyValLysGlu 904                     :::               ::: CGCTGGATTTCGCCCGTTGGCCCTATTCGGCTCGATTTCGCATGGGGGGCTGGATGCCGCG 12588	CCTGAATGGAAGAAAGGGGTCGGTACTGGGATC 12	➣	TyrAsnTyrGluPheMetLysAspLeuArgLeuAlaValPheGlyAspIleGlyAsnAla 868		E œ	LeuArgPhePheAlaGlyGlyAspGlnSerIleArgGlyTyrAlaHisAspSerLeuSer 828	TTAGTTCGCGTTGATGGTGGAGCCAACTTGGTGGATGAATTTGACCAACTCTCGCCCTCG 12873	ThrClyGlyIleGlnAlaGlyTyrIleTrpSerAspAsnPheAsnHisValProTyrArg 808	CTTCTTGGTTACGAACTTATGCGCGCAATCACCGCGCC 12	laTvrGlvSerAspArgAlaHisGlnMet 788	LeuGluValGlySerSerGlyLeuValSerAspAlaAsnMetAlaIleAlaArgAlaGly 768	LySThrValAlaAspAsnLeuValAsnProMetArgGlyTyrArgGlnArgTyrSer 748 :::    CGTACGCGGACTCGCTCCAACAGTGGCTTACTGACTTGGGGCGATAAACAGACGATTACC 13032	- :	ValAspPheValAsnGlyLysProSerGlnGluAlaLeuLeuAlaGlyValAlaValHis 729	ACAA 1	rgTyrArgLeuAspLysL	CTTGAACGCCATTGGCAGTTGGATGGCGGCTGGCATCGCACGGTCTTTATT 1	erIleIleGlnAsnGlyGlyTrpAsnArgThrTyrSerLeu 68	GCGTGATACCGAGAGCTTGGAATCT 13	GlnGluValPheGlyHisSerThrAsnGlyPheAspLeuSerThrArgThrLeuGluHis 671

744	500 ArgHisLeuTyrAspMetProAspAspArgValLeuAlaIleAsnHisAspAspGlyVal 51	Db 724 71AGTTCAGCCTAATGTTAAT 744	Qy 480 IleGluPheSerAlaSerAsnLeuIleGlnAspLysLeuAsnLeuValAlaAlaLysAla 499	Db 723 723	723	${\tt GlnSerSerSerArgThrGluProAlaGlnValAspGluSerThr}$	Oy       420 PheAsnMetValAsnThrGluIleValPheProGluArgGluGlnIleGlnAsnAspGln 439               :::                     Db       712 TTTAGCTCAGTA723	Oy 400 GluAlaTyrAsnLeuGlnAlaValArgAlaLeuSerAsnAspLeuIleAlaThrArgTyr 419 :::         ::::::::::::::::::::::::::	Qy 380 ProAspLysLeuProValLysArgGluLeuLeuGluGlnLeuLeuThrValAsnMetGly 399    Section	Qy 360 ArgPheAspGluValValPhePheThrIleAspProLysThrAsnGlnLeuThrThrAsp 379 :::	QY 340 ValileLeuProAspAsnThrAlaAspValSerLeuIleTyrAspThrGlyThrGlnTyr 359 :::      :::::::::   :::    :::    Db 514 ATCAGCCCTGAAACCCATCAAGCATGGTGGCGAATGTTATTTGATAGTGGTGTCCGTTAT 573	QY 320 GIDASDAIGSETALAGIUHJSGJYTYPPREASPGJYARGTTPLEUASPARGSETVALASP 339 Db 454 TCACGTTTAGCATTAAATCGTGGGTATTTTGATGGGAACTTTAAAATTTCACGTTTAGAA 513	300 PROLEULEULJASPVALPHEHISHJSJVYSJVYGJUTATLYSLYSASHLEULLE			262 ValAspValileIleHisAspLeuGlyGluProValTyrIleAspTyrArgAla	Qy 243 ArgAlaValGlyTyrTyrAspIleAspLeuSerIleIleArgAsnSerIleGlyGlu 261	914-168-2 (1-919) x AX033468 (1-1737)	Watch: 9.23% Indels:  Match: 6 Gaps:	milarity: 436.50 Matches: 35.64% Conservati	l9 Lenath:	BASE COUNT 517 a 309 c 380 g 531 t ORIGIN	organism="Haemophilus influenzae" /organism="Haemophilus influenzae" /db xref="taxon:727"	FEATURES Location/Qualifiers
Qy 864 AspIleGlyAsnAlaTyrAspLysGlyPheThrAsnAspThrLysIleGlyAlaGlyVal 883	dy 044 valstynikalogutykasnyksturnemethysaspheuakgheuakgheuakgheusy 863	844 ValClvThralaCluTvrascTvrCluDhavatIvrascTonalavalavalaboClu	Qy 824 HisaspSerLeuSerProlleSerAspLysGlyTyrLeuThrGlyGlyGlyClnValLeuAla 843	13	804 HisValProTyrArgLeuArgPhePheAlaGlyGlyAspGlnSerIleArgGlyTyrAla	Oy 784 ArgAlaHisGlnMetThrGlyGlyIleGlnAlaGlyTyrIleTrpSerAspAsnPheAsn 803	Db 1282 AAAGTGCAAGCATCTAGCGCGTTGGGTTCGTACTTATGCAGAAAAT	/45GIDATGTTYSETLEUGIUWAIGIYSETSETGIYLEUVAISETASPALAASHMETAIA     ::::::::::::::::::::::::::::::::	/39 FIGHERINGS TYPERING TO THE CONTROL OF THE CONTR		1126 CAAGCGGAT	Db: 1069 AATGCGCATGGTTGGCAATATTTTGGCGGACTTCGTATGCGATACGACAGTTTTACA 1125  Ov 699 GinAlaProProGluThrTrpGlnAspLeuProValAspPheValAspGlvLvsProSer 718	Db 1015 GAGAATGATACCAATACGAGAGTGCTTACGTTGTCAGCGTTACTTGGAAT 1068  Qy 679 GlnAsnGlyGlyTrpAsnArgThrTyrSerLeuArgTyrArgLeuAspLysLeuLysThr 698	Db 967 CCATTAAATTATTACTATGATTTTGCCGTCGGTTGGGAAGGGGAAAAA 1014  Oy 659 ThrasnGlyPheAspLeuSerThrargThrLeuGluHisGluIleSerArgSerIleIle 678	Oy 639 ProLeuAsnAspGlnLeuArgAlaThrLeuGlyTyrGlnGlnGlnValPheGlyHisSer 658	620 ArgLeuSerGluAspLysLysGlyValLysLeuTyrAlaThrLysProLeuSerHis	OY 600 VALTITITYSPINGTUHISASTILEUTITEASTATGASPGTYTYTGITATAGTYALAGTULEU 619 :::	787 CGTAAAAAAATGCGATGGAACTCGGTGTGGGCTTTTCTACTGATGGCGGCGTTCACGGA	Qy 580 AspLysProArgAspGlyGlnIleGlyLeuGlyTrpGlySerAspThrGlyThrArgLeu 599	Db 745CATAAAAGCAAAACTGTGGAGATTATTCTTTATCCA 786	744	540 ProAspGluSerGluAsnGluValIleAspLeuProGluArgThrAlaLeuAlaAsnArg	Db 744 744	Oy 520 AsnargSerIleLeuGlyArgIleSerAspAlaValSerAlaValAlaArgAlaIleLeu 539

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                                                                                                                                                                                                   Submitted (27-SEP-1997) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA
The H. Influenzae sequence has been updated by R. Fleischmann. New database matches have been assigned, product names have been improved, and a number of frame shifts have been corrected. We gratefully acknowledge the work of Tatusov et. al. We have incorporated their annotation into the /notes fields of the corresponding H. influenzae genes

(bases 1 to 11833)
White,O., Clayton,R.A., Kerlavage,A.R., Fleischmann,R.D., Peterson,J., Hickey,E., Dodson,R. and Gwinn,M.
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                                                                                                                                                               Submitted (28-MAY-1998) The Institute for Genomic Research, 9712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (25-JUL-1995) The Institute for Genomic Research, Medical Center Dr. Rockville, MD 20850, USA 4 (bases 1 to 11833) White,O., Clayton,R.A., Kerlavage,A.R. and Fleischmann,R.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tatusov,R.L., Mushegian,A.R., Bork,P., Brown,N.P., Hayes,W.S., Borodovsky,M., Rudd,K.E. and Koonin,E.V. Metabolism and evolution of Haemophilus influenzae deduced from whole-genome comparison with Escherichia coli Curr. Biol. 6 (3), 279-291 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             White, O., Clayton, R.A.,
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                                                               ical Center Dr, Rockville, MD 20850, USA whole genome was shifted by 588 nucleotides for a new Sep 30, 1996 this sequence version replaced gi:1221393 Location/Qualifiers
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IMALTDDGNGVPRGPLAPLLIGILIAVIGGAMGPLTGFAMNPARDFGPKFFAYLAGWG
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145. .939
                                                                                                                                                                                                                                                                codon_start=1
                                                                                                                                                                                                                                                                                                                                           'note="similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (gptB)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="xanthine-guanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="similar to SP:P26972 GB:X52093 GB:X63336 PID:47695 percent identity: 74.03; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similarity; putative"
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percent

Ωy	Length: 11833 Matches: 142 Conservative: 105 Mismatches: 235	1.22e-17 436.50 35.64% 20.49%	Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity:
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o, b o, b	Complement(6088. 9884)  'genee" HI0696"  'foote="similar to GB:U14003 Sp:p39322 PID:537063 GB:U00096  'foote="similar to GB:U14003 Sp:p39322 PID:537063 GB:U00096  'foote="similar to GB:U14003 Sp:p39322 PID:537063 GB:U00096  'footential ty: putative"  'codon_start=1  'footensl_table=11  'protein_id="conserved hypothetical protein"  'protein_id="AAC23356.1"  'db_xref="GI:1573699"  'db_xref="GI:1573699"	complement(608899 /gene="HI0696" /note="similar to GB /note="similar to GB percent identity: 34 similarity: putative /codon_start=1 /transl_table=11 /product="conserved /product="G:1573699 /thanslation="MTEQIO /translation="MTEQIO	
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Quer DB: US-0 QY	42614983 /gene="HI0694" /note="similar to GB:U00096 SP:P75966 PID:1787380 percent identity: 66.29; identified by sequence similarity; putative" /codon_start=1 /transl_table=11 /product="conserved hypothetical protein" /product="conserved hypothetical protein 1d="AAC22354.1"	42614983 /gene="HI0694" /note="similar t /note="similar t identity: 66.29; putative" /codon_start=1 /transl_table=11 /product="conser /product="GI-157 /profin_id="AAC	CDS

Ωу	Qy	Qy Db	оу Оу	Оу	Db C	g B	Qy g	P 09	Qy Db	оу Оу	ОУ	Db Oy	Оу	Оy	Db Qy	Оу	Qу Db	Query DB: US-09
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i LysThrProAlaAspValTyrGlnSerLysLysValProLeuTyrValPheValAlaSer ::::::           ::: ::: CATAAAAGCAAAACTGTGGATGTGGAGATTATTCTTTATCCA	ProAspGluSerGluAsnGluValIleAspLeuProGluArgThrAlaLeuAlaAsnAr	AsnArgSerIleLeuGlyArgIleSerAspAlaValSerAlaValAlaArgAlaIleLeu	ArgHisLeuTyrAspMetProAspAspArgValLeuAlaIleAsnHisAspAspGlyVal	IleGluPheSerAlaSerAsnLeuIleGlnAspLysLeuAsnLeuValAlaAlaLysAla       ::	- Pendatni Ananti katatni katatni en in anana katatni anana katatni anana katatni anana katatni anana katatni	10:001:00:00:00:00:00:00:00:00:00:00:00:	ValSerPheGluGlnSerSerSerSerArgThrGluProAlaGlnValAsp	PheAsnMetValAsnThrGluIleValPheProGluArgGluGlnIleGlnAsnAspGl	GluAlaTyrAsnLeuGlnAlaValArgAlaLeuSerAsnAspLeuIleAlaThrArgTyr:::	ProAspLysLeuProValLysArgGluLeuLeuGluGlnLeuLeuThrValAsnMetGly::::::      :::     ::	ArgPheAspGluValValPhePheThrlleAspProLysThrAsnGlnLeuThrThrAsp::: !!! CATTATGGCAATATTACTTTT	ValileLeuProAspAsnThrAlaAspValSerLeuIleTyrAspThrGlyThrGlnTyr::: :::       :::   :::   :::   :::   :::     :::     :::       :::	GluAsnAlaSerAlaGluHisGlyTyrPheAspGlyArgTrpLeuAspArgSerValAsp:::               TCACGTTTAGCATTAAATCGTGGGTATTTTGATGGGAACTTTAAAATTTCACGTTTAGAA	ProLeuLeuIleGlyAspValPheHisHisGlyLysTyrGluThrLysLysAsnLeuIle	ValGluValArgGlyGluGlyAlaAspAspLysAlaPheThrThrValAlaAspGluValIII:::::	ValaspValIleIleHisAspLeuGlyGluProValTyrIleAspTyrArgAla	ArgAlaValGlyTyrTyrAspIleAspLeuSerIleIleArgAsnSerIleGlyGlu 	ch: 9.23% Indels: 211 Gaps: 14 -168-2 (1-919) x U32752 (1-11833)
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                           GATAAAGATAACAGCAAAAATATTCAATTTTACATCGGA 10012
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                                                     GluGluGlyAsnProIleLysLeuHisPhePheIleGly 916
                                                                                  GGTGTGCGTTGGGCATCGCCAGTTGGTGCGATTAAATTTGATATTGCCACACCCATTCGT 10051
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Makino,K., Yokoyama,K., Kubota,Y., Yutsudo,C.H., Kimura,S., Kurokawa,K., Ishi,K., Hattori,M., Tatsuno,I., Abe,H., Iida,T., Yamamoto,K., Ohnishi,M., Hayashi,T., Yasunaga,T., Honda,T., Sasakawa,C. and Shinagawa,H. Complete nucleotide sequence of the prophage VT2-Sakai carrying twerotoxin 2 genes of the enterohemorrhagic Escherichia coli 0157: derived from the Sakai outbreak Genes Genet. Syst. 74 (5), 227-239 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPUNZODB 243184 bp DNA line Escherichia coli O157:H7 DNA, complete genome, APPUNZ568 BA000007 APPUNZ568.1 GI:13364484
                                                                                                                                                                                                                                                                                                                                                                            Submitted (26-JUN-2000) Ken Kurokawa, Osaka University, Ge Information Research Center; 3-1, Yamadaoka, Suita, Osaka Japan (E-mail:ken@gen-info.osaka-u.ac.jp, URL:http://www.gen-info.osaka-u.ac.jp/, Tel:81-6-6879-8365 Fax:81-6-6879-2047)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12 DNA Res. 8 (1), 11-22 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hayashi,T., Makino,K., Ohnishi,M., Kurokawa,K., Ishii,K., Yokoyama,K., Han,C.-G., Ohtsubo,E., Nakayama,K., Murata,T., Tanaka,M., Tobe,T., Iida,T., Takami,H., Honda,T., Sasakawa,C. Ogasawara,N., Yasunaga,T., Kuhara,S., Shiba,T., Hattori,M. ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete nucleotide sequence of the prophage VT1-Sakai carrying the Shiga toxin 1 genes of the enterohemorrhagic Escherichia coli 0157:H7 strain derived from the Sakai outbreak
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Comparative analysis of the whole set of rRNA operons between an enterohemorrhagic Escherichia coli 0157:H7 Sakai strain and an Escherichia coli K-12 strain MG1655
Syst. Appl. Microbiol. 23 (3), 315-324 (2000)
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Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                                                                                                    project
                                                                                             /gene="ECs5008"
466. .2115
/note="similar to PGI_ECOLI gi|1790457 percent identity 100 in 549 aa (Conserved in E.coli K-12)"
                                                                                                                                                                           /db_xref="taxon:83334
                                                                                                                                                                                                         /sub_strain="RIMD 0509952"
                                                                                                                                                                                                                                      /organism="Escherichia
/strain="0157:H7"
                                                                   /gene="ECs5008"
                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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Yasunaga,T., Yokoyama,K., Makino,K., Shinagaw
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7:H7
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'LTANSJALION" "MKNINTOTAAWQALQKHFDEMKDVTIADLFAKDGDRFSKFSAT
FDDOMLVDYSKNRITEETLAKLQDLAKRCDLAGA, KSMESGEKINRTENRAVLHVALR
NRSNTPILVDGKDVWPEVNAVLEKMKITSESA II SGEWKGYTGKAITDVVNIGIGGSDL
GPYMVTBALRPYKNHLNMHFVSNVDGTHIAEVLKKVNPETTLELVASKTETTQETMTN
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AHSARDWFLKAAGDEKHVAKHFAALSTHAKAVCBEGIDTANMFEFNDWVGGRYSLWSA
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ILLYDQYMHRFAAYFQGNMESNGKYVDRNGNVDYQTGPIIWGEPGTNGQHAFYQLI
HQGTKWYPCDFIAPAITHNPLSDHHQKLLSNFFAQTEALAFGKSREVYEQEYRDQGKD
BATLDYUVPFKVFEGNRFTNSILLERITPFSIGALIALVEHKIFTQGVILNIFTFEDQW
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OIQALKVTGROKINLDPDIVKVAERANDPLOGNYTLWVGPPPSTVTLFGLISRPGNQP
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3619
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99 in 698 aa (Conserved in E.coli K-12)"
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97 in 245 aa (Conserved in E.coli K-12)"
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96 in 222 aa (Conserved in E.coli K-12)"
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2954. .3622
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2628. .2870
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/transl_table=11
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Db 211481 CGCGCACGCGTCGATGATGCTATCCGCGAAGGTCTGAAAGCGCTGGGTTATTACCAGCCG 211540
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CDS

CDS gene

gene

CDS

gene

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US-09-914-168-2 (1-919) x AP002568 (1-243184)
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231 IleProArgLeuArgGlnThrAlaLeuValAlaAlaArgAlaValGlyTyrTyr-----
                                                                                                                                  211 AsnTleLysAlaAlaLeuGluAspIleThrGlnGluSerAlaMetAspLeuAsnGlySer 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MYSLSRPRVEFISTILQTVLNLGLLCLGLILVVFLGKETVHLAD VLFAPEQASKYELVEGLVVYFLYFEFIALIVKYFQSGFHFPLRYFVYIGITAIVRLII VDHKSPLDVLIYSAAILLLVVTLMLCNSKRLKRE" complement(7501. .8976) /gene="ECS5014" complement(7501. .8976)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(9348.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TVPBSPRWIMSRGKOEOABGITAKIMGNTLATQAVOEIKHSLDHGRKTGGRLIMFGVG
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VLLSEIFPNAIRGKALAIAVAAQWLANYFVSWTFPMMDKNSWLVAHFHNGFSYWIYGC
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GKLVSFNOFALIFGQLLVYCVNYFIARSGDASWLNTDGWRYMFASECIPALLFLMLLY
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7047. .7457
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LGHETKLAQKRVEDYVPKSTEOGWYIDKSRFDPHIDPYLNQSVGGPENRYMYDLKOVMG
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QANYEQHLGNGFYGDYTGYLETMFGGAGAEVLYRPLDSNWAFGLDANYKQRDWRSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to XYLE_ECOLI gi|1790463 percent identity
100 in 491 aa (Conserved in E.coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98 in 136 aa (Conserved in /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGYATITNVSKEEYGEGDFTKGVYVSVPLDLFSSGPTRSRAAIGWTPLTRDGGQQLGR
KPQLYDMTSDRSVNFR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KLEYEGNNYQODFAGKLEQKSKFNVGAIYRVTDWADVNLSYERANTFMEGVTLRTNEN
DLRPSYNDNARPQYQPQPQDAILQHSVVANQLTLLKYNAGLADPQIQAKGDTLYVTGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MKKRHLLSLLALGISTACYGETYPAPIGPSQSDFGGVGLLQTPTAMAEGELSLNYEDWIDVYRYSASVQLFEPWLETTLRYEDVRTRQYSSVEAFSGDQTYKONDAYAFDKUFLDQVAVGARDIGGTGLFDAFYLVASKAWGPEDFLGLGWGYLGTSGNVKNPLCSASDKYCYRDNSYKQAGSIDGSQMFHGPASLFGGVEYQTPWQPLRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGVLAALFMWKFVPETKGKTLEELEALWEPETKKTQQTATL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="ECs5013"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /transl_table=11
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434.50
36.92%
22.94%
9.19%
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212176	TECLY DEBUCKY LEPCTY SET ASPIRED BY STITLED BY SET BY SE	212117	B 3
> ⊦	GAA	20	? ?
86	spGlyGln	567	3 8
	C	212111	рь
566	${\tt IleAspLeuProGluArgThrAlaLeuAlaAsnArgLysThrProAlaAspValTyr}$	547	Ŷ
212110		212096	В
546	rGluAsnGlu	527	γ
212095		212095	Дb
526	IleLeuGlyArg	507	δ
212095		212095	DЪ
506	Leu Ile Gln Asp Lys Leu Asn Leu Val Ala Ala Lys Ala Arg His Leu Tyr Asp Met Property Control of the Control o	487	Q
212095	TTGACGGGCGTGGTTTTCGCCG	212075	Ъ
486	pGlyIleLeuMetAspIleSerProIleGluPheSerAlaSerAsn	467	Οy
212074	GAAACGAAAGTATTACCAGAAACGAAAGTATTACCA	212057	рь
466	ArgThrGluProAlaGlnValAspGluSerThrLeuGluProValIleGluThr	447	οy
212056	TTTGATAAAGCGCG	212027	В
446	$\verb"neProGluArgGluGlnIleGlnAsnAspGlnValSerPheGluGlnSerSer"$	427	Ş
212026	ACTGAACCGCCGACTTTCTGCTACCGGCTGGTTTAACTC	211976	рь
426	$alarg \verb AlaleuSerAsnAspLeuIlealaThrargTyrPheAsnMetValasnThrGlu$	407	δ
406 211975	ArgGluLeuLeuGluGlnLeuLeuThrValAsnMetGlyGluAlaTyrAsnLeuGlnAla	387 211916	в 6
211915		9	В
386	heThrIleAspProLysThrAsnGlnLeuThrThrAspProAspLysLe :::	36	δ
211897	GCCTTCTGGGATATTGATTATAACAGTGGCGAACGTTACCGCTTTTGGGCATGTGACCTTT	211838	Ъ
366	pValSerLeuIleTyrAspThrGlyThrGlnTyrArgPheAspGluValValPh	347	Š
346 211837	G1yTyrPheAspG1yArgTrpLeuAspArgSerValAspValI1eLeuProAspAsnThr             	327 211778	g 8
211777	SATTATO	211718	ДЬ
326	HisHisGlyLysTyrGluThrLysLysAsnLeuIleGluAsnAlaSe	307	δ
306 211717	AlaAspAspLysAlaPheThrThrValAlaAspGluValProLeuIleuIleGlyAspVal	287 211661	B 64
$\vdash$	CACGCCAGGCGTGCCGGTGTTAATTGGCGGCACCGATGTGGTATTGCGCGGGGGGCGC	211601	DЬ
286	coValTyrIleAspTyrArgAlaValGluValArgGlyG	267	οy
266 211600	AsplieAspLeuSerIleIleArgAsnSerIleGlyGluValAspValIleIle::: :::    :::    ::: ACCATTGAATTTGATCTCCGTCCACCGCCAAAGAAAGGGCGGCAGGTATTGATCGCCAAA	249 211541	B 6

	AE000493 U00096 AE000493.1 GI:2367360 Escherichia coli K12.	E B S S I	SEE
DEC-	z	RESULT 15 AE000493 LOCUS DEFINITIO	DE PE
	LysGluGluGlyAsnProIleLysLeuHisPhePheIleGly 916    :::	903 212990	dd 6
902 21298	GlyvalArgTrpAlaSerProValGlyGlnValArgValAspValAlaThrGlyVal	884 212930	D Qy
883 2129	ASPIleGlyAsnAlaTyrAspLysGlyPheThrAsnAspThrLysIleGlyAlaGlyVal	864 212870	Дb
863 21286	ValGlyThrAlaGluTyrAsnTyrGluPheMetLysAspLeuArgLeuAlaValPheGly    ::	844 212810	Db Qy
843 21280	HisaspSerLeuSerProIleSerAspLysGlyTyrLeuThrGlyGlyGlnValLeuAla 	824 212750	Db Qy
823 21274	HisValProTyrArgLeuArgPhePheAlaGlyGlyAspGlnSerIleArgGlyTyrAla        	804	Дy
803 21268	ArgAlaHisGlnMetThrGlyGlyTleGlnAlaGlyTyrIleTrpSerAspAsnPheAsn     ::: :::    :::  CATCGTTTTGTGACACGCGGCACGCTGGGCTGGATTGAAACCGGTGATTTCGAC	784 212636	Оy
783 21263	IleAlaArgAlaGlyIleSerGlyValTyrSerPheGlyAspAsnAlaTyrGlySerAsn   :::	764 212591	Db
763 21259	ArgGlnArgTyrSerLeuGluValGlySerSerGlyLeuValSerAspAlaAsnMetAla 	744 212531	ОУ
743 2125	A ALAGLYVALALAVALHISLYSTHYVALALAASPASNLEUVALASNPYOMETAYGGLYTYY	724	Дb
723 2124	GlnAspLeuProValAspPheValAsnGlyLysProSerGlnGluAlaLeuLeu	706	da Vo
705 2124	<pre>5 ThrTyrSerLeuArgTyrArgLeuAspLysLeuLysThrGlnAlaProProGluThrTrp :::     ::         6 CCATTAACCTGCGCTGGAGTCTCGAC</pre>	212399	dd Qy
685 21239	5 ThrArgThrLeuGluHisGluIleSerArgSerIleIleGlnAsnGlyGlyTrpAsnArg :::	212345	Оy
665 2123	<pre>5 AlaThrLeuGlyTyrGlnGlnGluValPheGlyHisSerThrAsnGlyPheAspLeuSer</pre>	212297	ОУ
645 2122	7 GlyValLysLeuTyralaThrLysProLeuSerHisProLeuAsnAspGlnLeuArg	212237	dq VQ
626 2122	LeuIleAsnArgAspGlyTyrGlnAlaGlyAlaGluLeuArgLeuSerGluAspLysLys	607	dd Vo

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                      AL Submitted (13-OCT-1998) Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA ON Sep 9, 1997 this sequence version replaced gi:1790660. This sequence was determined by the E. coli Genome Project at the University of Wisconsin-Madison (Frederick R. Blattner, director). Supported by NIH grants HG00301 and HG01428 (from the Human Genome Project and NCHGR). The entire sequence was independently determined from E. coli K12 strain MG1655. Predicted open reading frames were determined using GeneMark software, kindly supplied by Mark Borodovsky, Georgia Institute of Technology, Atlanta, GA, 30332 [e-mail: markdamber.gatech.edu]. Open reading frames that have been correlated with genetic loci are being annotated with CG Site Nos., unique ID nos. for the genes in the E. coli Genetic Stock Center (CGSC) database at Yale University, kindly supplied by Mary Berlyn. A public version of the database is accessible (http://cgsc.biology.yale.edu). Annotation of the genome is an ongoing task whose goal is to make the genome sequence more useful by correlating it with other data. Comments to the authors are appreciated. Updated information will be available at the E. coli (thtp://www.genetics.wisc.edu). *** The E. coli K12 sequence and its annotations are periodically updated; this is version M54. No sequence changes. Annotation updates: updated gene identifications and products; all new functional assignments courtesy of Monica sequences described in reference 1. The unique numeric identifiers beginning with a lowercase 'b' assigned to each gene (protein or labels. This should allow them to be searched for in Entrez as gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (02-SEP-1997) Guy Plunkett III, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA. Email: ecoll@genetics.wisc.edu Phone: 608-262-2534 Fax:
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                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                 /note="central position to predicted
/bound_moiety="IlvY predicted site"
                                                                                                                                                                                                                                                                     /sub_strain="MG1655"
                                                                                                                                                                                                                                                                                                        /strain="K12"
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                                                                                           /note='
                                                                                                                                                                                                                                         /db_xref="taxon:83333"
                                                                                           factor Sigma70;
                                                                                           predicted +1 start at 4435250"
                                                                                                                                                                             promoter: -73.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
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/note="f447; 100 pct identical amino acid seque
equal length to YTFL_ECOLI SW: P39319"
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DLVGQGLEEQIVARDENSWLIDGGTPIDDVMRVLDIDEFPQSGNYETIGGFMMFMLRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(2320. .3663)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(2320.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEFDKGKILIPKVKDKLHLSVMSEVNRQVMRLQTEMA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="factor Sigma54; predicted +1 start
complement(1882. 1910)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(1790. .1807)
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WAKDGALTPEEVQQYMDLLQKLLK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MTLRKILALTCLLLPMMASAHQFETGQRVPPIGITDRGELVLDK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="f184; 100 pct identical amino acid sequence and equal length to YTFJ_ECOLI SW: P39187"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNYDSLLTLREFFRCATQIDKSGYQVLSSKNETVHAMDKFLISFSLKDNGAEYTMTLR
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/gene="ytfK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="orf, hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="b4217"
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . 656
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .3663)
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
5121 GTCACGCCAGGCGTGCCGGTGTTAATTGGCGGCACCGATGTGGTATTGCGCGGCGGCGCG 5180
                                                                                          5061
                                                                                                                                                                  5001 CGCGCACGCGTCGATGATGCCATCCGCGAAGGTCTGAAAGCGCTGGGTTATTACCAGCCG 5060
                                                                                                                                                                                                                                                    4941 AACGTTCGTGCGCAGCTTTCTACGATTGAAAGTGATGAAGTGACGCCAGACCGTCGCTTT 5000
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                                                  267
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                                                                                                                                 249
                                                                                                                                                                                           231 IleProArgLeuArgGlnThrAlaLeuValAlaAlaArgAlaValGlyTyrTyr-----
                                                                                                                                                                                                                                                                                           211 AsnIleLysAlaAlaLeuCluAspIleThrGlnGluSerAlaMetAspLeuAsnGlySer 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
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                        HisaspLeuGlyGluProValTyrIleAspTyrArgAlaValGluValArgGlyGluGly 286
                                                                                 ACCATTGAATTTGATCTCCGTCCACCGCCAAAGAAAGGGCGGCAGGTATTGATCGCCAAA 5120
                                                                                                                           -----AspileAspLeuSerIleIleArgAsnSerIleGlyGluValAspValIleIle 266
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Tiesdevtpdrrfrarvddaireglkalgyyqptiefdlrpppkkgrqvliakvtpgv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="factor Sigma70; predicted +1 start at 4439826" complement(4687...4718) /note="factor Sigma70; predicted +1 start at 4439809" 4751...4762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ....c--KEP (repetitive extragenic palindromic) element; contains 1 REP sequence" complement(3986. .4624) /gene="msrA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="0577; 100 pct identical amino acid sequence equal length to YTFM_ECOLI SW: P39320"
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4830. _6563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"factor Sigma70; predicted +1 start at 4438844" complement(3785. .3813) /note-"factor Sigma70; predicted +1 start at 4438907" 3905. .3938 /note-"REP (repetitive extragenic palindromic) element
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="peptide methionine sulfoxide reductase"
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433.50
36.92%
22.94%
9.17%
                                                                                                                                                                                                                                                                                                                                                                                                       Conservative:
Mismatches:
Indels:
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Matches:
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164
100
262
189
18
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Escherichia.  REFERENCE 1 (bases 1 to 11760)  AUTHORS Perna, N. T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D.,  Rose, D. J., Mayhew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A.,  Posfai, G., Hackett, J., Klink, S., Boutin, A., Shao, Y., Miller, L.,  Grotbeck, E.J., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K.,	SOURCE Escherichia coli 0157:H7 EDL933. ORGANISM Escherichia coli 0157:H7 EDL933 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;	AE005654 AE0	z	SULT 16	Oy 903LysGluGluGlyAsnPrOIleLysLeuHisPhePheIleGly 916	Db 6450 GGCGTGCGCTGGGAATCGCCGGTCGGGCCAATCAAACTCGATTTTGCCGTACCGGTCGCG 6509	Qy 884 GlyValArgTrpAlaSerProValGlyGlnValArgValAspValAlaThrGlyVal 902	QY 004 ASPLIEUTYASHALATYTASPLYSGLYPNETTRASHASPTRTUYSILGGLYALIGGLYVAL 883	6330 ACCGGATCGCTGGAATACCAGTACAACGTGACCGGAAAATGGTGGGGGGGG	Qy 844 ValGlyThrAlaGluTyrAsnTyrGluPheMetLysAspLeuArgLeuAlaValPheGly 863	Db 6270 TACAAATCTATCGCTCCGAAATACGCCAACGGTGACCTGAAAGGGGCCTCGAAGTTGATA 6329	6210 AAAGTACCGCCGGATCTGCGTTTCTTCGCCGGGGGCGACCGCAGTATTCGTGGCTACAAA	Qy 804 HisValProTyrArgLeuArgPhePheAlaGlyGlyAspGlnSerIleArgGlyTyrAla 823	Db 6156CATCGTTTTGTTACACGCGGCACGCTGGGCTGGATTGAAACCGGTGATTTCGAC 6209	6111 GTTTTCCAGGCGCAGAACGTCTGGATCCGCACACTGTACGATCGC	Oy 764 IleAlaArgAlaGlyIleSerGlyValTyrSerPheGlyAspAsnAlaTyrGlySerAsn 783	QY       /44 AFGCINAFGTYPSETLEUGLUVALGLYSETSETGLYLEUVALSETÄSPÄLAÄSNMETÄLA 763	5991 CCTGGGGTGATGATTAGCCGCACGCGTTCTCGTGGTGGCCTGATGCCAACCTGGGGCGAC	724 AlaGlyValAlaValHisLysThrValAlaAspAsnLeuValAsnProMetArgGlyTyr	Db 5946CACTTTACTCAGGGTGAAATTACCACGATGCTGTTTTAT 5990	ysProSerGlnGluAlaLe	5919 GCCATTAACCTGCGCTGGAGTCTCGAC	Qy 686 ThrTyrSerLeuArqTyrArqLeuAspLysLeuLysThrGlnAlaProProGluThrTrp 705	Qy 666 ThrArgThrLeuGluHisGluIleSerArgSerIleIleGlnAsnGlyGlyTrpAsnArg 685 :::         bb 5865 TCCACTACGCTGGTGGCTTCTCGCTACTGGGATCTCTCCAGCGGCTGGCAGCGT 5918	Db 5817 GTGCAGGGCGGTTTTAAGCGCACTGACCTGAACGATACCGAATCTGAC 5864	Qy 646 AlaThrLeuGlyTyrGlnGlnGluValPheGlyHisSerThrAsnGlyPheAspLeuSer 665
410	Gomplement(20792033)  CDS complement(20792633)	AIGUVSLGYALLUUIVS FALKIYGGDERFRNGSS DITKEKICEKYKSTIEA	/translation="MLPRIRHNNFIGAVELFVKSSYTKTHSNNFFNNIHHAFKKKDWI SNYDSLLTLREFFRCATQIDKSSYQVLSSKNETVNAMDKFLISFSLKDNGAEYTMTLR GSGFBYEEIPITINBYNSFMDFKNREFPLEQNRRLYAWDILQKKOSDIPKRIKGYIHQ	/transcare= /protein_id="AAG59413.1" /db_xref==GI:12519214"		/function="orf; Unknown function" /note="Residues 1 to 133 of 312 are 98.49 pct identical to residues 1 to 133 of 166 from Escherichia coli K-12 Strain		gene HVHDWQKPLDYTPRESFLNPGFRVSIY"  1078 2016 /gene="z5826"	ALIDEKR PLIGVYA RVMINYSKA EGKAWEVKUMORI MUVULA KEET IKMUEET IVITAALISE KANDELE IVITAALISE	/UD_XIET= GI: 1279213 /translation="MIDDVCQLARNAGDAIMQVYDGAKPMDVVSKADNSPVTAADIAA umvrupci ppr madravi spenancesvandundvari vadr norvestrandcesvant	3'-phosphoadenosine-5'-phosphosultate in pathway of sulfite synthesis" /protein_id="AAG59412.1"		240	n="pnenotype; central intermediary metabolism: btabolism tabolism 1 to 246 of 246 are 99.18 pct identical	CDS 126866 /gene="cysQ"	/note="25825" /gene="25825"	/ser /db_; /not	/organism="Escherichia coli O157:H7 EDL933" /strain="EDL933"	FEATURES Location/Qualifiers source 111760	TITLE Direct Submission  JOURNAL Submitted (22-OCT-2000) Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA	3	Posfai, G., Hackett, J., Klink, S., Boutin, A., Shao, Y., Miller, L., Grotbeck, E.J., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K.,	Perna, N.T., Plunkett, G		TITLE Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7  JOURNAL Nature 409 (6819), 529-533 (2001)	Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C.,

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5770. .7503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(3260..4603)

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Strain MG155: B4218"

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/function="orf; Unknown function"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Z
2919. .3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene~"msrA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene-"ytfL"
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gene CDS

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CDS

QΥ DЬ Qγ Дb ρ DЪ Qγ DЬ δÃ Дb Qy

В

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US-09-914-168-2 (1-919) x AE005654 (1-11760)
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DB:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                              249
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                                                                                                                                                                                                                                GTCACGCCAGGCGTGCCGGTGTTAATTGGCGGCACCGATGTGGTATTGCGCGGGGGGGCGCG 6120
                                                     PheHisHisGlyLysTyrGluThrLysLysAsnLeuIleGluAsnAlaSerAlaGluHis 326
                                                                                                                                                                  AlaAspAspLysAlaPheThrThrValAlaAspGluValProLeuLeuIleGlyAspVal 306
                                                                                                                                                                                                                                                                                  HisAspLeuGlyGluProValTyrIleAspTyrArgAlaValGluValArgGlyGluGly 286
                                                                                                                                                                                                                                                                                                                                          ACCATTGAATTTGATCTCCGTCCACCGCCAAAGAAAGGGCGGCAGGTATTGATCGCCAAA 6060
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGCGCACGCGTCGATGATGCTATCCGCGAAGGTCTGAAAGCGCTGGGTTATTACCAGCCG 6000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AsnIleLysAlaAlaLeuGluAspIleThrGlnGluSerAlaMetAspLeuAsnGlySer
                                                                                                                CGGACCGATAAAGACTATTTGAAATTGCTCGATACTCGCCCG----GCTATTGGCACGGTA
                                                                                                                                                                                                                                                                                                                                                                                               -----AspIleAspLeuSerIleIleArgAsnSerIleGlyGluValAspValIleIle 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AACGTTCGTGCGCAGCTTTCTACGATTGAAAGTGATGAAGTGACGCCAGACCGTCGCTTT 5940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scores:
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/gene="ytfN"
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433.50
36.92%
22.94%
9.17%
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Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps:
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164
100
262
189
18
                                                                                                                   6177
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y 685 r 6858	ThrArgThrLeuGluHisGluIleSerArgSerIleIleGlnAsnGlyGlyTrpAsnArg: ::	6805	Db Qy
68	GTGCAGGGCGGTTTTAAGCGCACTGACCTGAACGATACCGAGTCTGA	σ,	B 5
G 6756	ACCCTCGACTTCAGCTATAAAATGCCGCTGCTGAAGAATCCACTGGAACAATATTATTT	6697	D D
g 645		62	Qy
66	:::         ::: TGGATGAACTCATACGGTCACAGTCTGACCACCAGTACCAGTATTTCCGCGCCGGAA	6637	Db
s 626	AsnArgAspGlyTyrGlnAlaGlyAlaGluLeuArgLeuSerGluAspLysI	607	δÕ
3 6636	GCG	6577	Db
n 606	lleGlyLeuGlyTrpGlySerAspThrGlyT	587	γO
: A 6576		6574	Вb
586	${\tt GlnSerLysLysValProLeuTyrValPheValAlaSerAspLysProArgAspGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyG$	567	Qy
- 6573	ATC	6571	Db
r 566	ValīleAspLeuProGluArgThrAlaLeuAlaAsnArgLysThrProAlaAspValTyr	547	οy
r 6570		6556	DЬ
1 546	IleSerAspAlaValSerAlaValAlaArgAlaIleLeuProAspGluSerGluA	527	δδ
- 6555		6555	Db
J 526	AspAspArgValLeuAlaIleAsnHisAspAspGlyValAsnArgSerIleLeuGlyArg	507	γo
6555		6555	рь
506	LeuIleGlnAspLysLeuAsnLeuValAlaAlaLysAlaArgHisLeuTyrAspMetPro	487	Οу
6555	TTGACGGCGTGGTTTCGCCG	6535	В
n 486	ValGluLeuThrAspGlyIleLeuMetAspIleSerPr	467	Qy
6534	GAAACGAAAGTATTACCA	6517	Db
r 466	erArgThrGluE	447	γQ
6516	GTGGTGGCTCCACAATTTGATAAAGCGCGC	6487	Ъ
r 446	IleValPheProGluArgGluGlnIleGlnAsnAspGlnValSerPheGluGlnSe	427	Qγ
64	:::     :::	w	В .
4	ValArqAlaLeuSerAsnAspLeuIleAlaThrArqTvrPheAsnMet1	407	Q Q
F 6435	GAT	6376	рь
1 406	${\tt ArgGluLeuLeuGluGlnLeuLeuThrValAsnMetGlyGluAlaTyr}$	387	γo
6375		6358	Db
386	PheThrIleAspProLysThrAsnGlnLeuThrThrAspProAspLysL	367	γo
1 6357	ALASPVALSETLEULLETYKASPTATGLYTTATGLOTYKASPVALSELUVALVALPHE 	6298	₽ 5
0	. Galiuliicaulwacauuliiuncuuwacachaciaaachiiacacicacachii	, ,	, 8
, ω	GlyTyrPheAspGlyArgTrpLeu	327	3 5

Db 6859 CCCATTACCTCCCCTCACTCCCCCCCACCACCACCACCAC	Qy	686	ThrTyrSerLeuArgTyrArgLeuAspLysLeuLysThrGlnAlaProProGluThrTrp 705
GINASPLEUPTOVALASPÉNVALASNGLYLYSPTOSETGINGLUALISHELEUT		85	ATTAACCTGCGCTGGAGTCTCGAC
AlaGlyValAlavalHisLysThrValAlaAspAsnLeuValAsnProMetArgGlyTyr 743 CCTGGGGTGATGTTTACCGGACGGTTCCTGTGTCTTAT CCTGGGTGATGTTTACCGGACGGTTCCTCGTGGTGGCCTGGTGCCAACCTGGGGAC ArgGlnArgTyrSerLeuGluValGlySerSerGlyLeuValSerAspAlaAsnMetAla 763 TCCCAACCCTCTCTTTGCACTACTCCAACTCCACACGCTGGCCTGGGCTGCCAACCTGGGGAC ArgGlnArgTyrSerLeuGluValGlySerSerGlyLeuValSerAspAlaAsnMetAla 763 TCCCAACCCTTCTCTTTGCACTACTCCAACTCCACACGCTGGGCTTCCACATGGCCTGGGTTTCTCC 7050 TLeAlaArgAlaGlyTleSerGlyValTyrSerPheGlyAspAsnAlaTyrGlySerAsn 783 TCCCAACCCTTCTCTTTGCACTGGATCCCACACCTGGCCTTCCACATGTGCTCCACATGGCTTCTCCCCCACACTTGCTTCCACATGTGCTTCCACATGTGCTTCCACATGTGCTTCCACATGTGCTTCCACATGTGCTTCCACATGTGCTTTCCACAGGTTGCTTCTCCACATGTGCTTTCCACAGGTTGCTTCTCCACAGGTTGCTTTCTCCACAGGCCTGACTTTCTCACACGGCTTATTCCGCCTTAAACTCACATGAACTCACATGAACTCACTTAAACGCCTTAAATGCCTTAAACGCTTAACGCTTAAATGTTCCACACGTTATTCCACAGGCCTTATTCCACAGGTTGTTTCTCCCACAGGCCACAGTTATTCCACATGTTTTCTCCCACAGGCCACAGTTATTCCACAGTTGTTTTCTCCCACAGGCCACAGTTTCTCTCTTTTCTCCCACAGGTTATTCCACAGTTGTTTTCTCTCCACAGGCCACAGTTATTCCACATGTTTTTCTCCTCAAATTCACTTTAAATCCCTTAAATTCTTC	Qy	0	lnAspLeuProValAspPheValAsnGlyLysProSerGlnGluAlaLeuLeu 7
AlaGlyValAlavalHisLysThrValAlaAspAsnLeuValAspProMetArgGlyTyr 743  CCTGGGGGGGGGATGATTGGCGGCGGGTTCTCGTGGTGGCGTGCCTTGCCGGGGGAC  ArgGlnArgTyrSerLeuGluValGlySerSerGlyLeuValSerAspAlaAssmAetAla 763  IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII		88	
CCTGGGGTGATGGTTTGGCGGCGGTTCTCGTGGTGGCCTTTTGCTGCTGGCGGGCGAC ArgGlnArgTyrSerLeuGluValGlySerSerGlyLeuValSerAspAlaAsnMetAla 763	Qy		laGlyValAlaValHisLysThrValAlaAspAsnLeuValAsnProMetArgGlyTyr 74
ArgGlnArgTyrSerLeuGluvalGlySerSerGlyLeuValSerAspAlaAsnMetAla 763		93	CTGGGGTGATGATTAGCCGCACGCGTTCTCGTGGTGGCCTGATGCCAACCTGGGGCGAC 699
TCCCAACGGTACTACTCAACAGGGCTTGGGGTTCAATTTCTCCC 7050  IleAlaArgAlaGlyIleSerGlyValTyrSerPheGlyAspAsnAlaTyrGlySerAsn 783 ::::::   GTTTTCCAGGCGCAAAACGTCTGGATCCGACTCGCACTCGCC	Qy	744	gGlnArgTyrSerLeuGluValGlySerSerGlyLeuValSerAspAlaAsnMetAla 76
IlealaargalaGlyIleSerGlyValTyrSerPheGlyAspAsnAlaTyrGlySerAsn 783 ::::::   :::::   ::::   ::::   ::::   ::::   ::::   ::::   ::::   ::::   :::::   ::::   ::::   ::::   ::::   ::::   ::::   ::::   ::::   :::::   ::::   ::::   ::::   ::::   ::::   ::::   ::::   :::::   :::::   ::::		9	CGCAACGCTACTCTATCGACTACTCCAACACGGCCTGGGGGTTCAGATGTCGATTTCTCC 705
ArgalaHisGlnMetrhrGlyGlyIleGlnAlaGlyTyIleTrpSerAspAsnPheAsn 803 ArgalaHisGlnMetrhrGlyGlyIleGlnAlaGlyTyIleTrpSerAspAsnPheAsn 803 Hill:::CANCGTTTGGACACGCGGCACGCGGGCGGATGGAATGGAA	Qy	64	gAlaGlyIleSerGlyValTyrSerPheGlyAspAsnAlaTyrGlySerAsn 78
ArgAlaHisGlnMetThrGlyGlyIleGlnAiaGlyTyrIleTrpSerAspAsnPheAsn 803CARTCGTTTTGTGACACGCGGCACGCTGGGCTGGATTGAAACCGGTGATTTCGAC 7149 HisvalproTyrAsgleuArghebehalaGlyGlyAspGlnSerIleArgGlyTyrAla 823		051	GGCGCAGAACGTCTGGATCCGCACACTGTACGATCGC709
HisvalProTyrArgLeuArgPhebhalaGlyGlyAspGlnSerIleArgGlyTyrAla 823	Qy	8	gAlaHisGlnMetThrGlyGlyIleGlnAlaGlyTyrIleTrpSerAspAsnPheAsn 80
HisValProTyrArgLeuArgPhePheAlaGlyGlyAspGlnSerTleArgGlyTyrAla 823		09	CATCGTTTTGTGACACGCGGCACGCTGGGCTGGATTGAAACCGGTGATTTCGAC 714
AAAATCTATCGCCGGATCTGCGTTTTTCTCCCCGGGGGCGATCGGAGTTTGCAAA 7209 HisaspSerLeuserProlleSerAspLysGlyTyrLeuThrGlyGlyGlnValLeuAla 843 ::     :: ::	Qy		82
HisAspSerLeuSerProIleSerAspLysGlyTyrLeuThrGlyGlyGlnValLeuAla 843 ::		5	720
ValclyThralacluTyrAsnTyrGluPheMetLysAspLeuArgGaGGCCTCGAAGTTGATA 7269  ValclyThralacluTyrAsnTyrGluPheMetLysAspLeuArgLeuAlaValPheGly 863    ::::  -  -  -  -  -  -  -  -  -  -  -	Qy	N	isAspSerLeuSerProIleSerAspLysGlyTyrLeuThrGlyGlyGlnValLeuAla 84
ValGlyThralaGluTyrAsnTyrGluPheMetLysAspLeuArgLeuAlaValPheGly 863    :::		21	ACAAATCTATCGCCCCGAAATACGCTAACGGTGACCTGAAAGGGGCCTCGAAGTTGATA 726
ACCGGATCGCTGGAATACCAGTACAACGTGACAGGAAAATGGTGGGGGGGG	Qy	4	lGlyThrAlaGluTyrAsnTyrGluPheMetLysAspLeuArgLeuAlaValPheGly 86
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GATAGTGCCAAGCGGTAAGCGATATTCGCCGCAGCACTTTAAAAACCGGTACCGGGGTC 7389  GIYVALArgTrpAlaSerProValGlyGlnValArgValAspValAaThrGlyVal 902	Qy	0	IleGlyAsnAlaTyrAspLysGlyPheThrAsnAspThrLysIleGlyAlaGlyVal 88
GlyValArgTrpAlaSerProValGlyGlnValArgValAspValAlaThrGlyVal902		$\omega$	AGTGGCGAAGCGGTAAGCGATATTCGCCGCAGCGTTTAAAACCGGTACCGGGGTC 738
GGCGTACGCTGGGAATCGCGGTCGGCCAATCAAACTCGATTTTGCCGTACCGGTCGCG 7449LysGluGluGlyAsnProIleLysLeuHisPhePheIleGly 916	Qy	84	.aSerProValGlyGlnValArgValAspValAlaThrGlyVal 90
GATAAAGACGAACACGGGTTACCAGTTTTACATCGGT 7485  ECOUW93  ECOUW93  ESCherichia coli K-12 chromosomal region from 92.8 to 00.1 minute 014003.1 GI:1263172  Escherichia coli Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia coli Escherichia coli Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia coli Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia coli Genome VI: DNA sequence of the Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia coli genome VI: DNA sequence of the Nucleic Acids Res. 23 (12), 2105-2119 (1995) 9534462 7610040 2 (bases 1 to 338534) Plunkett,G. I.I.I. Direct Submission Submitted (22-AUG-1994) Guy Plunkett III, Laboratory of Genetics, Proteobacteriaceae; Escherichia Coli Genetics, VIII Submission, 445 Henry Mall, Madison, WII 53706, USA.		390	ATCGCCGGTCGGGCCAATCAAACTCGATTTTGCCGTACCGGTCGCG 744
ECOUW93  ECOUW93  ESCherichia coli K-12 chromosomal region from 92.8 to 00.1 minute U14003.1 GI:1263172  Escherichia coli. Escherichia coli Escherichia coli Escherichia coli Escherichia coli Escherichia coli Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.  1 (bases 1 to 338534) Burland, V., Plunkett, G. III, Sofia, H.J., Daniels, D.L. and Blattner, F.R. Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.8 through 100 minutes Nucleic Acids Res. 23 (12), 2105-2119 (1995) 9534362 7610040 2 (bases 1 to 338534) Plunkett, G. I.I. Direct Submission Submitted (22-AUG-1994) Guy Plunkett III, Laboratory of Genetics, Presil. Coli deposition 445 Henry Mall, Madison, WI 53706, USA.	Qy	0	LysGluGluGlyAsnProIleLysLeuHisPhePheIleGly 91
ECOUW93  BCOUW93  BSCherichia coli K-12 chromosomal region from 92.8 to 00.1 minute 014003.1 GI:1263172  Escherichia coli.  Escherichia coli  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.  Chases I to 338534)  Burland, V., Plunkett, G. III, Sofia, H.J., Daniels, D.L. and Blattner, F.R.  Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.8 through 100 minutes  Nucleic Acids Res. 23 (12), 2105-2119 (1995) 9534362 7610040  Chases I to 338534) Plunkett, G. I.I.  Direct Submission Submitted (22-AUG-1994) Guy Plunkett III, Laboratory of Genetics, Pmail, Madison, WI 53706, USA.  Franchis Colideratics with the coli general Park Franchis Colideratics of USA.		45	ATAAAGACGAACACGGGTTACAGTTTTACATCGGT 748
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	JOU	KNAL	Submitted (22-AUG-1994) GUY PIUNKETT III, Laboratory of Genetic University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA Fmail: ecoligamentics wisc edu phone. 608-262-2534 Fmy.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entry ECOUW89 (U00006) by 1885 bp.
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                                                                                                                      complement(1985.
                                                                                                                                                                                                                  /note="predicted bend of 75.87 degrees"
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                                                                                                                                                                                                                                                                                                                                               809.
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Number J05260 (ECOPHNAQ)
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                  AlaAspValSerLeuIleTyrAspThrGlyThrGlnTyrArgPheAspGluValValPhe 366
                                                                            GGTTATTTCGATAGCGAATTTACCAAAGCGCAGCTGGGCATTGCGCTCGGCCTGCATAAA 133740
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GCCTTCTGGGATATTGATTATAACAGTGGCGAACGTTACCGCTTTGGGCATGTGACCTTT 133800
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/protein_id="AAA96993.1"
/db_xref="GI:536938"
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/gene="phnN"
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PNMRYHLALLDGEVVGMIGLHLQFHLHHVNWIGEIQELVVMPQARGLNVGSKLLAWAE
EEARQAGAEMTELSINVKRHDAHRFYLREGYEQSHFRFTKAL"
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/gene="phn0"
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/note="predicted bend of 75.60 degrees"
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134373	CACTTTACTCAGGGTGAAATTACCAATACCACGATGCTGTTTAT	134329	Db
723	GlnAspLeuProValAspPheValAsnGlyLysProSerGlnGluAlaLeuLeu	706	Qy
134328	GCCATTAACCTGCGCTGGAGTCTCGAC	134302	Db
705	ThrTyrSerLeuArgTyrArgLeuAspLysLeuLysThrGlnAlaProProGluThrTrp	686	Qy
685 134301	ThrargThrLeuGluHisGluIleSerArgSerIleIleGlnAsnGlyGlyTrpAsnArg:::	666 134248	Qy
665 134247	AlaThrLeuGlyTyrGlnGlnGlnValPheGlyHisSerThrAsnGlyPheAspLeuSer	134200	ДУ
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626 134139	LeuIleAsnArgAspGlyTyrGlnAlaGlyAlaGluLeuArgLeuSerGluAspLysLys :::    ::::: TGGATGAACTCTTATGGTCACAGTCTGACCACCAGTACTAGTATTTCCGCGCCCGGAACAG	607 134080	Qy Db
606 134079	IleGlyLeuGlyTrpGlySerAspThrGlyThrArgLeuValThrLysPheGluHisAsn	587 134020	Qy
134019		134017	Db
586	GlnSerLysLysValProLeuTyrValPheValAlaSerAspLysProArgAspGlyGln	567	Qy
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134013	:::       CGAACAGAAAACACC	133999	Db
546		527	Qy
133998		133998	Db
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133998		133998	Db
506	LeuIleGlnAspLysLeuAsnLeuValAlaAlaLysAlaArgHisLeuTyrAspMetProduction and the state of the state	487	Qy
133998	TTGACGGCCTGGTTTCGCCG	133978	Db
486		467	Qy
133977		133960	Db
466	${\tt aGlnValAspGluSerThrLeuGluProValIleGluThr}$	447	Qy
133959		133930	Db C's
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426		407	Qy
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133818	G :	133801	Db
386	PheThrIleAspProLysThrAsnGlnLeuThrThrAspProAspLysLeuProValLys	367	Оу

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JOELLE
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Ruelle, J.L. and Thonnard, J.
Haemophilus influenzae rd outer membrane sequences
Patent: WO 0047737-A 3 17-AUG-2000;
RUELLE JEAN LOUIS (BE); SMITHKLINE BEECHAM BIOLOG
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Sequence 3 from Patent WO0047737
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Bacteria; Proteobacteria; gamma
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Haemophilus influenzae
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AspLysProArgAspGlyGlnIleGlyLeuGlyTrpGlySerAspThrGlyThrArgLeu CGTAAAAAAATGCGATGGAACTCGGTGTGGGCCTTTGCTACTGATGGCGGCGTTCACGGA LysThrProAlaAspValTyrGlnSerLysLysValProLeuTyrValPheValAlaSer ProAspGluSerGluAsnGluValIleAspLeuProGluArgThrAlaLeuAlaAsnArg ValGluValArgGlyGluGlyAlaAspAspLysAlaPheThrThrValAlaAspGluVal AsnArgSerIleLeuGlyArgIleSerAspAlaValSerAlaValAlaArgAlaIleLeu ArgHisLeuTyrAspMetProAspAspArgValLeuAlaIleAsnHisAspAspGlyVal 519 LeuGluProValIleGluThrValGluLeuThrAspGlyIleLeuMetAspIleSerPro ValSerPheGluGlnSerSerSerSerArgThrGluProAlaGlnValAspGluSerThr GATCCATATTTAATGAATAATTTGTCGGATTTAACCAGCGATTTTTCATCTTCAAATTGG GluAlaTyrAsnLeuGlnAlaValArgAlaLeuSerAsnAspLeuIleAlaThrArgTyr ProAspLysLeuProValLysArgGluLeuLeuGluGlnLeuLeuThrValAsnMetGly ::::: ||| ::: ||| ArgPheAspGluValValPhePheThrIleAspProLysThrAsnGlnLeuThrThrAsp GluAsnAlaSerAlaGluHisGlyTyrPheAspGlyArgTrpLeuAspArgSerValAsp :::: GTGCAAATTGAGGGGGAAGCCGCACAAGATGAAAATTTTGATGCGCTACGTAAAAACTTG CGCGATTTATTGATTGCTCATGTTACACCAGGCGAGCCAACAAAAATTGCGGGGACTGAT ValAspValIleIleHisAspLeu-----GlyGluProValTyrIleAspTyrArgAla CGTGTGTTTGGTTATTATGAATCTTCCGTGCGTTTTGAACGAAAACAGCGTCAAGGCAAA ArgAlaValGlyTyrTyrAspIleAspLeuSerIleIleArgAsnSer---IleGlyGlu IleGluPheSerAlaSerAsnLeuIleGlnAspLysLeuAsnLeuValAlaAlaLysAla ATCAGCCCTGAAACCCATCAAGCATGGTGGCGAATGTTATTTGATAGTGGTGTCCGTTAT ValIleLeuProAspAsnThrAlaAspValSerLeuIleTyrAspThrGlyThrGlnTyr TCACGCTTGGCATTAAATCGTGGGTATTTTGATGGGAACTTTAAAATTTCACGTTTAGAA CCA---AAAGAAGGCGTTTTGGTTGAACACCAAACTTACGATGATTACAAAACAGCGATT ProLeuLeuIleGlyAspValPheHisHisGlyLysTyrGluThrLysLysAsnLeuIle ---AGCCATTCACAAATCCGTGACGATTATCTCAATAATATTCTTAACATCAAATCTGGC CATAAAAGCAAAACTGTGGATGTGGAGATTATTCTTTATCCA TTAGTTCAGCCTAATGTTAAT ........ 379 299 780 539 499 479 459 439 419 738 738 399 359 447 738 717 705 645 507 717 717 588 567 339 319 390 261

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                                                                                                                                                                                                                                           GluGluGlyAsnProIleLysLeuHisPhePheIleGly 916
                                                                                                                                                                                                                                                                                                                             GlyValArgTrpAlaSerProValGlyGlnValArgValAspValAlaThrGlyValLys
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                                                                                                                                                                                                                                                                                                     GGTGTGCGTTGGGCATCGCCAGTGGGTGCGATTAAATTTGATATTGCCACACCCATTCGT
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Chambergo, F., Ciapina, L. P., Cicarelli, R. M. B., Coutinho, L. L.,
Cursino-Santos, J. R., El-Dorry, H., Faria, J. B., Ferreira, A. J. S.,
Ferreira, R. C. C., Ferro, M. L. T., Formighieri, E. F., Franco, M. C.,
Greggio, C. C., Gruber, A., Katsuyama, A. M., Kishi, L. T., Leite
Jr., R. P., Lemos, E. G. M., Lemos, M. V. F., Locali, E. C., Machado, M. A.,
Madeira, A. M. B. N., Martinez-Rossi, N. M., Martins, E. C., Meidanis, J.,
Menck, C. F. M., Miyaki, C. Y., Moon, D. H., Moreira, L. M., Novo, M. T. M.,
Okura, V. K., Oliveira, M. C., Oliveira, V. R., Pereira, Jr., H. A.,
Rossi, A., Sena, J. A. D., Silva, C., de Souza, R. F., Spinola, L. A., F.,
Takita, M. A., Tamura, R. E., Teixeira, E. C., Tezza, R. I. D., Trindade (
Santos, M., Truffi, D., Tsai, S. M., White, F. F., Setubal, J. C. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (28-NOV-2001) Departmento de Bioquimica, Sao Paulo, Av. Prof. Lineu Prestes 748, Sao Paulo,
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Kitajima,J.P.
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Xanthomonas campestris pv. campestris str. ATCC 33913
Bacteria; Proteobacteria; gamma subdivision; Xanthomo
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480. .2099
                                                                                                                                                                                                                                                                                                                                                                                                                   480.
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33913"
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located using Blastx/Glimmer/Genemark"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="ATCC 33913"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to 11870)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              campestris str.
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SP 05508-900,
                                                                                                                                                                                                                                                                                               putative;
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YGSVEGPVAGPLTLRNVDFRYQDIHFTAERVYLEPDLRPLLGRKLQLDÄVQVSNÄTLN
LGRSDEPTLPSWPESLPQINVPLAIQADHIGVDLRITTLGRKLQLDÄVQVSNÄTLN
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LDKMEVAIAGRAPAPLRASLVETGRDDPTWAFNAVTEALDTSLLIPARAGQETPPATP
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                                                                   DAWALRQPAQFSTEGAAFTLSDTCLGAATGGALCASANWPREGMVVHGGALPLSLVQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="XCC4084"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MOILILEGEOSDAIPVAPLPLCAGRDLRTLACADLASLIAGIQA AGGDSDVELVLLDSGDLPLHERTCATALRAAVDALPTPYIELHADAGQELEPWLHPQH APLAVVITPHOAPRAYMASLGIAARCLPALHALMRVAA" complement (3616 . . 7572)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="XCC4083"
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/geneo"XCC4083"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation-"MILRGPEAASSLYRGPQALPRAVITQLYRCARDAGKTVALRACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(2282. .2587)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGASVWGOVAIDPISRRLYFGTGNNYNIPAGVGNCVSNARSYRGSELTVODELNCMAP
DNYVDSVVALMUDTGKLAWADBAQGYDAWNLSCIVABPTGGLEVBYQATNLTG9DYDFG
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FDPYKSQVYVAINNSSNATYTLGPDNTVSHNGGSWAALDAATGKIKWQVKVPGVNSVN
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located using Blastx/Glimmer/Genemark"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="identified by sequence similarity; putative;
located using Blastx/Glimmer/Genemark"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
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ARPVQWLVLLFGDTVIPAELLGVRGDRITRGHRFMHDGDIALAAPGDYIDALRAAHVL
VDADARRARIYEEVDAAARQAGGSARISDDNLEQVVNLVEWPSAVLCSFERAFLAVPQ
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FFDEDLKQGLEAMGAGLASVTYQAKLGTVADKVARVARLAEAIAPQVGARDAA
ELAKNDLQSRMNNEFPELQGIAGRHYAKAAGEPSEISLAIDEAYQPFRAGDDIALSPL
GKVLAIAERLDTLAGGFAAGLKPTGNKDPFALRRNALGLARTVIESGFDLDLPKLIDV
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complement(9598. 11694)
/gene="glyS"
/note="identified by second
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GDNGRVILRGEGGTTWTSDLVAMPPSLRFFAGGPNSIRGYAFREVGPRTPKPDEFALG
AKNVVTASAEYEHYLKGGPWGGAVFVDSGSAFDDTPDWRTGIGFGLRWRSPVGPVRVD
                                                                                                                                                                                                                                   /translation-"MSEQLPLLIELGTEELPVKALPGLAQAFFDGVLAGLEKRGVAVT
RGDAKPLSTPRRLAVLLPGVATEQPEQRSEVLGPYLNIALDAEGKPTRALAGFAAKAG
IDWTALERTSDAKGERFVHRAVTPGAQAAALLPEILREAIAAMPIPKPMRWGAHEYAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(9598. .11694)
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EGSYYHEGKLDRLRESLTKLDYFSTIDIQPKPEEADDQGRVPVDVKLTRAKRTVYTSG
LSYGSESGAGVRGGVERRYVNSRGHKMDTQLDYAQNRKSLTTSYRVPAFRWLDGWYTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MPHRVRRPDRLPCEDLCMYVHDVHAYMTHGMALSTPRRPINRPS RSSRYBAMRFILRPSLLLCILAGAEGAFARGTIDKIEILELAGAEGATENLEVS LSLVEAVGKEGGESKLEVLLAGAEGAFARGTBEFGYYSSTIDIAAPROGERCHTVVITV NRGEEPVRVRGSHISITGWAEGDRYLGQDLKQFEPREGQVFSHPQYEASKVRITRRLAE
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RFDALPDGSAKITASAKSGDGTLNIDGGLSWFGTSTPLLLNIRGENVLAYNTSELRIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       located using
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located using Blastx/Glimmer/Genemark"
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using Blastx/Glimmer/Genemark"
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                                                                                                                                                                                                                                Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                  Score:
                                                                                                                                                                                                                                                                                                             Alignment
   8915
                                                                                                                           9032
                                273
                                                                                                                                                                                                                                                                                               No . :
                                                                                           253
                                                                                     SerIleIleArgAsnSerIleGlyGluValAspValIleIleHisAspLeuGlyGluPro 272
                                                                                                                                        ArgGlnThrAlaLeuValAlaAlaArgAlaValGlyTyrTyrAsp-----Il@AspLeu
GTGCGGGTGCGGCAGTCTCATATTTCGATCACCGGCTGGGCCGAGCAAGACCGCTATCTG
                            ValTyrīleAspTyrArgAlaValGluValArgGlyGluGlyAlaAspAspLysAlaPhe
                                                            GCCGCGCGCGACGGCGAGCGCCTGACCGTGGTGATCACGGTGAACCGTGGCGAGCCG
                                                                                                                        CGGCAGACGCGC --- GAGGCACTGGAGCCGTTTGGTTATTACTCGCCCACCATCGACATC
                                                                                                                                                                                                                                                                                                             Scores:
                                                                                                                                                                                                                               8.56e-14
375.50
35.29%
23.00%
7.94%
                                                                                                                                                                                                                Mismatches:
Indels:
Gaps:
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Matches:
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 8856
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647 8232	628 ValLysLeuTyrAlaThrLysProLeuSerHisProLeuAsnAspGlnLeuArgAlaThr	9d 4d
627 8292	608 IleAsnArgAspGlyTyrGlnAlaGlyAlaGluLeuArgLeuSerGluAspLysLysGly ::::	Db Oy
607 8352	gLeuValThrLysPheGluHisAsnLeu       rerGCGCGGGGGCGTGGAGCGGCGCTAT	P 09
8412		Db
587	ysValProLeuTyrValPheValAlaSerAspLysProArgAspGlyGlnIle	Qy
4	32	Db
8433	ProGluArqThrAlaLeuAlaAsnArqLvsThrProAlaAspValTvrGln	0 0
47	528 SerAspAlaValSerAlaValAlaArgAlaTleLeuProAspGluSerGluAsnGluVal	γ
8439	8439	В
527	$. Leu \verb AlaTleAsnHisAspAspGlyValAsnArgSerTleLeuGlyArgIle $	Qy
8439	8439	Db
507	euAsnLeuValAlaAlaLysAlaArgHisLeuTyrAspMetProAsp	Qy
8439		рь
487	LeuThrAspGlyIleLeuMetAspIleSerProIleGluPheSerAlaSerAsnLeu	Ş
8448		В
467	hrGluProAlaGlnValAspGluSerThrLeuGluProValIleGluThrVal	Qy
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447	${\tt rgGluGlnIleGlnAsnAspGlnValSerPheGluGlnSerSerSer}$	Q
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387	sArg	Ş
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8676	8735 TTCACCCAGCGCGGTGGCGGTGACGCGTGCCGAGCATGCCGCCGACATCGATCTGAAC	DЬ
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1		<b>)</b>

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rThrasnGlyPheAspLe	axonopodis pv. e genome. 2008923 GI:21110627 s axonopodis pv. s axonopodis pv. roteobacteria; tt 10839) C.R., Ferro,J.A. Monteiro-Vit	aThrGlyValLysGluGlu      :::  CACGGCTTGAACGACCCC	's Ileg :   CACCG	gLeuAlaValPheGlyAsı           CGGGCGGTGTTCGTCGA	ValLeuAlaValGl ::: AACGTGGTCACCGC	aHisAspSerLeuSer ;;;   ATTCCGCGAAGTGGGC	AsnHisValProTyrArgLeuA :::    GTGGCGATGCCGCCGAGCCTGC	rAsnArgAlaHisGlnMetThrGl      CCTGCGTGGC	tAlaIleAlaArgAlaGlyIleSe ::: CGGTCAGCTCTACGGCCAGCTACG	TyrArgGlnArgTyrSerL ;;; GTGTCCGGGCAGATGTTCA	HisLysThrValAlaAspA ::: TATCCGCAGCTGCAGGCCA	alAspPheValAsnGlyLysF     :::    TTCAGCAGTGGCAGCG	ArgTyrArgLeuAspLysLeuLy	GluHisGluIleSerArgSerIl :::           AAACTCACCGGCAGCGCAGTGG	lnGlnGluValPheGlyH ::::: GCGCGCCTGTACGACG
	p bp DNA line citri str. 306, see citri str. 306. citri str. 306 amma subdivision; xa rello,C.B., Van Sluy	<pre>snProIleLysLeuHisPh :: CGCAGTTCCAGCTCTACAT</pre>	pAlaSerProValG1 	<pre>snAlaTyrAspLysGly ::   :::    STGCCTTCGATGAC</pre>	TyrGluE	erAspLysG ::     cgcccaagccggacg	PG AA	lyIleGlnAlaGly :::     GAAGGTGGC	lyValTyrSerPheGly      GGTTCCTGGGCGCCGGC	SerSerGly :::       GCCGAGGGC	CGATGACCGGC	SerGlnGluAlaLeuLeu- :::   ::: TTCACCGATGCCGTGTACG	ThrGlnAlaProF	IleGlnAsnGlyGlyTrpAs          :: CAGATCAACGAGCGCTGGAG	SerThrAsnGlyPheAspL      CAGACCGAATACATCGACC

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
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3B 31va,A.C.R., Ferro,J.A., Reinach,F.C., Farah,C.S., Furlan,L.R.,

Quaggio,R.B., Monteiro-Vitorello,C.B., Van Sluys,M.A., Almeida

Jr.,N.F., Alves,L.M.C., do Amaral,A.M., Bertolini,M.C.,

Camargo,L.E.A., Camarotte,G., Cannavan,F., Cardozo,J.,

Chambergo,F., Ciapina,L.P., Cicarelli,R.M.B., Coutinho,L.L.,

Cursino-Santos,J.R., El-Dorry,H., Faria,J.B., Ferreira,A.J.S.,

Ferreira,R.C.C., Ferro,M.I.T., Formighieri,E.F., Franco,M.C.,

Greggio,C.C., Gruber,A., Katsuyama,A.M., Kishi,L.T., Leite

Jr.,R.P., Lemos,E.G.M., Lemos,M.V.F., Locali,E.C., Machado,M.A.,

Madeira,A.M.B.N., Martinez-Rossi,N.M., Martins,E.C., Meidanis,J.,

Menck,C.F.M., Miyaki,C.Y., Moon,D.H., Moreira,L.M., Novo,M.T.M.,

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Rossi,A., Sena,J.A.D., Silva,C., de Souza,R.F., Spinola,L.A.F.,

Takita,M.A., Tamura,R.E., Teixeira,E.C., Tezza,R.I.D., Trindade dos

Kitajima,J.P., L.,

Kitajima,J.P., Setubal,J.C., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chambergo, F., Ciapina, L.P., Cicarelli, R.M.B., Coutinho, L.L., Cursino-Santos, J.R., El-Dorry, H., Faria, J.B., Ferreira, A.J.S., Ferreira, R.C.C., Ferro, M.I.T., Formighieri, E.F., Franco, M.C., Greggio, C.C., Gruber, A., Katsuyama, A.M., Kishi, L.T., Leite Jr., R.P., Lemos, E.G.M., Lemos, M.V.F., Locali, E.C., Machado, M.A., Madelra, A.M.B.N., Martinez-Rossi, N.M., Martins, E.C., Meidanis, J., Menck, C.F.M., Miyaki, C.Y., Moon, D.H., Moreira, L.M., Novo, M.T.M., Okura, V.K., Oliveira, M.C., Oliveira, V.R., Perceira, J.H.A., Rossi, A., Sena, J.A.D., Silva, C., de Souza, R.F., Spinola, L.A.F., Rossi, A., Sena, J.A.D., Silva, C., de Souza, R.F., Spinola, L.A.F., Santos, M., Truffi, D., Tsai, S.M., White, F.F., Setubal, J.C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brazil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (28-NOV-2001) Departmento de Bioquimica, Sao Paulo, Av. Prof. Lineu Prestes 748, Sao Paulo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Comparison of the genomes of two Xanthomonas pathogens with differing host specificities Nature 417 (6887), 459-463 (2002) 22022145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "idnK"
                                                                                                                                                                                                                                                                                    ORF located using Glimmer/Genemark"
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US-09-914-168-2 (1-919) x AE012071 (1-10839)
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  235 ArgGlnThrAlaLeuValAlaAlaArgAlaValGlyTyrTyrAspIleAspLeuSerIle 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                        255 IleArgAsnSerIleGlyGlu---ValAspValIleIleHis---AspLeuGlyGluPro 272
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LQLALGANSR INAKGKVGDQLLD LAQCLQPLQLLDVLPGATGVVRGQLQVSGKRDAPDIT
ADIALMGLERWITY SAQNI ISLBGRLPWRGSDGQLALGGTA IEAGVVLDSS YRVQARGAVE
ALRLADDI ANSMASVALQGDVRRNGERWQGQVATLRI APAKGDAWSLRQPAQFSTDGA
AFTLSDTCLGAATGGALCASANWPRESENVYGDALPLSI VQPAULFKQEGRQI YLRGEL
SLDGSSFK PRGNAWEGSLRIASPEGGI FILGETY KAAVAGNBURGELLRYLDGTSVQADFI
GQQIQGKLGIGFQGAGFVDAKENTGWDAYAFLNGELY INMSRLYWLELV IADVVRPKG
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DFRLHGDYLPNDDY RADLTAFAVLPANGRTPASLGIVARGDLDKMEVQIAGGRAPAPL
QASLVETGRDDPTWAF KAVTEALDTSLLIPAREGQANPDL IANNCASGKGRADLL
HGSLKQGELSATLQPSHIALADQVLTVEPLVIDTFEGRTQLRGTADFRDVDPSFRFA
VNASGLRFTPAADPATPDAPLVPVELQDARLGVAGTLKAWAAIGRATVERDGQQAELV
FDSRGNDRGAQLKQVQAKTPGGSLDLTGEVAWAPALQWDVSAQLAKFDPGYFAPGWNG
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/gene="XAC4204"
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VSLRAERKIGDVTAGIDVSGRAESPRADVWSEPAMSQSEALSYLVLGRGLSTASSDET
QQVSAASAALSAGSSLIASQIGAKLGLDEAGVSQSSTLGSVVGFGKYLSPKLYVGYGV
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KSGPGTLTVDGGLSWFGTSTPLLLNIRGDNVLAYNTSELRIIANPDMQFGITDNTMQL
RGKVTVPEADIDLERLDRGTSVSEDVVVLDPVDPEQTPASPLDMDLAIVLGDKVNMSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GWYTASARLYDEQTEYIDLRNVKLTGSRSGQINERWSAIASINALRERWRFSSGDDFE
GAVYETSTLIYPQLQANYVNVDDRLFPRSGVSAQMFIRGGAEGAGSDTNFGQLYGQLR
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NIQVSLSLYEAVGKEQGESRLEVLLAQAERQTREALEPFGYYSPTITLAAPRAGDKYT
VVITVDRGEBVRVRTSHISITGWAEGDDRYLGQDLKQDEBPEGQVFSHPGYEASKVRIT
RRLAERGYFDADETQRRVAITRAEHAADIDLNWDSGRRYDMGKVRFDYDYFRDGLFDP
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/protein_id="AAM39039.1"
/db_xref="GI:21110635"
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/gene="XAC4204"
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located using Blastx/Glimmer/Genemark"
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10035 GAAGCCAGCAAGGTCCGCATCACCCGGCGTCTGGCCGAGCGTGGCTACTTCGATGCCGAC 9976

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9337	63AACGCCTTGCGCGAGCGTTGGGGGTTTC	Db	
712		Qy	
9364	9414 GGCAGCCGCAGCCAGATCAACGAGCGCTGGAGCGCGATCGCCTCGATC	Db	
692	euArgTyrArg	Qy	
9415	9468 CGGCTGTACGACGAGCAGAGCAGTACATCGACCTGCGCAACGTCAACCTCACC	Db	
672		Qy	
9469	9516 CGCGTGCCGGCGTTCCGTTGGCTGGATGGCTGGTACACCGCCTCGGCG	Db	
652	euGlyTyrGlnGln	Qy	
9517	9576 CACAAGATGGACACGCAGCTGGATTACGCGCAGAACCGCAAGAGCCTGACCACCAGTTAC	Db	
632		Qy	
9577	9636 AGCGAAAGCGGCGCCGGTGTGCGCGCGCGTGGCGTGAACGTGAACGCGCGCG	Db	
612		Qy	
9637		Db	
592		Qy	
9652		Db	
572	553 ArgThrAlaLeuAlaAsnArgLysThrProAlaAspValTyrGlnSerLysLysValPro	Оу	
9670		Db	
552	LeuProAspGluSerGluAsnGluValIleAspLeuProGlu	Qy	
9679	9679	Db	
532	513 IleAsnHisAspAspGlyValAsnArgSerIleLeuGlyArgIleSerAspAlaValSer	Qy	
9679	9679	Db	
512	493 AsnLeuValAlaAlaLysAlaArgHisLeuTyrAspMetProAspAspArgValLeuAla	Qy	
9679	9679	Db	
492	473 IleLeuMetAspIleSerProIleGluPheSerAlaSerAsnLeuIleGlnAspLysLeu	Qy	
9679	9726 GAAGAGGCGGACGACCAGGGCTGCCGTGCCGGTGGACGTCAAACTCACC	Db	
472		Qy	
9727		Db	
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9736		Db	
432		Оу	
9778		Db	
412		Qy	
9838	9873GACTACGACTACTTCCGCGATGGCCTGTTCGACCCG	Db	
392	oValLysArgGluLeuLeuGluGln	Qy	
9874	9915 TGGGACAGCGGCCGCTACGACATGGGCAAGGTGCGCTTC	Db	
372		Qy	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCTTCGGCCTGGCGCTCGCCGGTGGGCCCGGTGCGCGTGGATATCGCACATGGC
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                                                                         Goel, A.K., Rajagopal, L.,
Direct Submission
Submitted (18-OCT-2000)
                 3 (bases 1 to 20310)
Goel,A.K., Rajagopal,L.,
Direct Submission
                                                                                                                                                                                           1 (bases 1 to 20310)
Goel,A.K., Rajagopal,L., Nagesh,N. and Sonti,R.V.
Genetic locus encoding functions involved in biosynthesis
membrane localization of xanthomonadin in Xanthomonas oryz
                                                                                                                                                                                                                                                                                                                                   Xanthomonas oryzae pv. or
cluster, partial seqence.
AY010120
AY010120.2 GI:15055553
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Xanthomonas oryzae pv. oryzae
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                               Nagesh, N. and Sonti, R.V.
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Habshiguda, Hyderabad,
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A. P.
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/evidence=not\_experimental

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REMARK
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WELGAGDNSRLLRGEGGTTWFSDLVAWPPSLRFFAGGSNSLRGYAFREVGPRTPKPD
                                                                                                                                                                                                                                                                                                                     GPGTLTVDGGLSWFGTSTPLLLNIRGDNVLAYNTSELRIIANPDMQFGITDNTMHLRG
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frameshift mutation"
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LRAERKIGDITAGIDVSGRAESPRADVWSEPAMSQSEALSYLVLGRGLSTASSDETQQ
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PVRVDIAHGLMDPDAQFQLYIDIGANL"
                                                                                                                                                        IGGGSVLTLKYLLSRGFDIEAESSTVETKGSVNWRREK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . 5853
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(11662. .11949)
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ANGEPHAGT"
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PAVLAAAVQGSGAQLLDLKDASESLVAAYRGRVLGALVLAALLLAVTVAIALRSPRRI
VRVLLPMALTTVLILAILRGTGVELNLFHLIALILAAGLGLDYALFFDHAGDDHADQL
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SEQLRPRLDALVRNGDLLGYDMAARYLPSAKTQHARQAALPDAAQARAFTETAVATTP
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CDS

CDS

CTGGTGTACTGGGACGAGGGCAGCTACTACCACGAAGGCAAGCTGGATCGGCTACGCGAG 931

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US-09-914-168-2 (1-919) x AY010120
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LeuLeuThrValAsnMetGlyGluAlaTyrAsnLeuGlnAlaValArgAlaLeuSerAsn 412
                                                                                                                                                                                                                                                                                                            TrpLeuAspArgSerValAspValIleLeuProAspAsnThrAlaAspValSerLeuIle
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                                                                                                                                                                                                       TyrAspThrGlyThrGlnTyrArgPheAspGluValValPhePheThrIleAspProLys 372
                                                                                                                                                                                                                                                         TTTACCCAACGCCGCGTAGCGATCACGCGCGCGCGAGCACGCGGCCGATATCGATCTGAAT 793
                                                                                                                                                                                                                                                                                                                                                              GAAGCCAGCAAGGTGCGCATCACCCGGCGCGCCTGGCCGAGCGTGGCTACTTCGATGCCGAC
                                                                                                                                                                                                                                                                                                                                                                                                            GluThrLysLysAsnLeuIleGluAsnAlaSerAlaGluHisGlyTyrPheAspGlyArg 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGCAGGACCTCAAGCAGTTCGAGCCGCGCGCGAGGGGCAGGTCTTCAGTCATCCGCAGTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IleArgAsnSerIleGlyGlu---ValAspValIleIleHis---AspLeuGlyGluPro
                                                                                                  ThrAsnGlnLeuThrThrAspProAspLysLeuProValLysArgGluLeuLeuGluGln
                                                                                                                                                       TGGGACAGCGGCCGCCTACGACATGGGCAAGGTGCGCTTC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTGCGGGTGCGCACCTCGCATATTTCGATCACCGGCTGGGCCGAGCAGGACCGTTATCTA 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTGCGCCACGCGCGGGCGACAAGGTGACCGTGGTGATCACGGTGGATCGTCGAGAGCCG
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SSQTAAERELAELLVESLNLEDVQPADIDPEAPLFNTGLGLDSIDALELALAISKRYG
FQLRSDNDENRRIFASLRALSAHVEANKTV"
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/protein_id="AAG38843.1"
/db_xref="GI:11693122"
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VEGLYGQAGMPVTPEQRRYTRRLTLAWALLLCGLTLANLVLGLCAEPSGVLTQLGYAS
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/protein_id="AAG38842::
/db_xref="GI:19483795"
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GTRSRTGALLPFKVGLLQAAIDAGVQVVPVALDGCGRVLPVDGLFRVRPGIIRVRIGT
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TyrSerLeuGluValGlySerSerGlyLeuValSerAspAla :::	ъ У У
731 ThrvalalaaspAsnLeuvalasn	β 5
70 TTCAGCAGCG	, B 2
ArgLeuAspLysLeuLysThro	8 8 8
92 ACC	) B 5
38 GCGCGCTTTACGACGAGCAGACCGATTACATCGACCTGCGCAACGT	o p
7. ATTILL PYSPTOLEUSERHISPTOLEUASAASPGInLeuArgalaTh	o B 2
12 SIYIYKUINALAGIYALAGIULeu	D
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43 ACGGTCTACACC	g
GGGCGCGTGCCGGTGGACGTCAAACTCACCCGC	0 <b>v</b>
VAGCCGACGACCAG	δο 20 20 20 20 20 20 20 20 20 20 20 20 20
33 AlaValAlaArgAlaIleLeuProAspGluSerGluAsnGluValIleAspLeuPr	γ <sub>0</sub>
76Yourstyout teledutyArgileSerAspAla	В
13 IleAsnHisAspAspG vValAspAspGovTley	Q
พValAlaAlaLysAlaArgHisLeuTyrAspMetProAspAspArgVal	\$ 5
65GATATCCAGCCC	2 2
<pre>letAspIleSerProIleGluPheSerAlaSerAsnLeuIleGlnAspLy</pre>	Qy
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aGlnValAspGluSerThrLeuGluProValIleGluThrValG]uThrVa	Qγ
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433 GluGlnIleGlnAsnAspGlnValSerPheGluGlnSerSerSerSerArgThrGl	οy
932 TCGCTGACCAAGCTGGATTACTTCAGCACCATC	Db
413 AspLeuIleAlaThrArgTyrPheAsnMetValAsnThrGluIleValPhaProg	õ

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2 (bases 1 to 10074)

2 impson,A.J.G., Reinach,F.C., Arruda,P., Abreu,F.A., Acencio,M., Alvarenga,R., Alves,L.M.C., Araya,J.E., Bala,G.S., Baptista,C.S., Barros,M.H., Bonaccorsi,E.D., Bordin,S., Bove,J.M., Briones,M.R.S., Carrer,H., Colauto,N.B., Colombo,C., Costa,F.F., Costa,M.C.R., Costa-Neto,C.M., Coutinho,J.L., Cristofani,M., Dias-Neto,E., Costa-Neto,C.M., Coutinho,J.L., Cristofani,M., Dias-Neto,E., Docena,C., El-Dorry,H., Facincani,A.P., Ferreira,A.J.S., Ferreira,V.C.A., Ferro,J.A., Fraga,J.S., Franca,S.C., Franco,M.C., Frohme,M., Furlan,L.R., Garnier,M., Goldman,G.H., Goldman,M.H.S., Gomes,S.L., Gruber,A., Ho,P.L., Hoheisel,J.D., Junqueira,M.L., Kemper,E.L., Kitajima,J.P., Krieger,J.E., Kuramae,E.E., Laigret,F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                         Aylella

1 (bases 1 to 10074)

1 (bases 1 to 10074)

Simpson, A.J., Reinach, F.C., Arruda, P., Abreu, F.A., Acencio, M., Alvarenga, R., Alves, L.M., Araya, J.E., Baia, G.S., Baptista, C.S., Barros, M.H., Bonaccorsi, E.D., Bordin, S., Bove, J.M., Briones, M.R., Benno, M.R., Camargo, A.A., Camargo, L.E., Carraro, D.M., Carrer, H., Colauto, N.B., Colombo, C., Costa, F.F., Costa, M.C., Costa-Neto, C.M., Coutinho, L.L., Cristofani, M., Dias-Neto, E., Docena, C., El-Dorry, H., Fraga, J.S., Franca, S.C., Franco, M.C., Ferro, J.A., Fraga, J.S., Franca, S.C., Franco, M.C., Frohme, M., Furlan, L.R., Garnier, M., Goldman, G.H., Goldman, M.H., Gomes, S.L., Gruber, A., Ho, P.L., Hoheisel, J.D., Junqueira, M.L., Kemper, E.L., Kitajima, J.P.
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                                                                                                                                                                                                                                                                                                                                   The genome sequence of the plant pathogen Xylella fastidiosa. The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing and Analysis
Nature 406 (6792), 151-157 (2000)
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Xylella fastidiosa 9a5c
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Xylella fastidiosa 9a5c, section 103 of 229 of the complete genome.
AE003957, AE003849
AE003957.1 GI:9106207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Xanthomonas
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FEATURES
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Lopes, C.R., Machado, J.A., Machado, M.A., Madeira, A.M.B.N.,
Madeira, H.M.F., Marino, C.L., Marques, M.V., Martins, E.A.L.,
Martins, E.M.F., Matsukuma, A.Y., Menck, C.F.M., Miracca, E.C.
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lr"
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9291...9446
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similarity; putative; ORF located using Glimmer/RBSfinder"
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GQMQIRARPGHEMTANGGLDVRGRYKAYGQDLTIIRGQLVWSNMIVSDPRVNIRAQRR
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VLTLKYLLSRGFDLEVESSTVETKGSVNWRKEK"
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/note=similar to SP|P77541 (percent identity: 62 %/query
alignment coverage: 98.3 %/subject alignment coverage:
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complement(6826. .6945)
/gene="XF1233"
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complement/07^^
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7500. 8396
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Best Local Similarity:
Query Match:
DB:
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   1817 AAGCTGGATCGCCTGCGTGAGTCC----
                                                                                                                                        1751 TATTTCCAC-----AAGGGCTATTTAATCCA 1777
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                                                                          1778 CTGGTGTACTGGGACGAAGGTAGC-
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ys 498 1885	479 ProIleGluPheSerAlaSerAsnLeuIleGlnAspLysLeuAsnLeuValAlaAlaLy ::::::::::::::::::::::::::::::	Qy Db

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RESULT 23
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AATACGAGAGCGCTTACGTTGTCAGCGTTACGTTATTGGAATAATGCGCGTGGTTGGCAA 284
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Haemophilus influenzae
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
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Novel compounds
Patent: WO 0232946-A 9 25-APR-2002;
SmithKline Beecham Biologicals s.a.
Location/Qualifiers
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909	roValGlyGlnValArgValAspValAlaThrGlyValLysGluGluGlyAsnProIle	Оу 890 Р	_
ũ.	TAT-TACACAGCAAAAGAGCTGCGTTATGGCGCAGGCGTTGGTGTGCGTTGGGCATCG	777	m
889	aser	Qy 870 <i>i</i>	_
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809		Qy 790 с	0
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Boucher, C.A.
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PROTEIN"
                                                                                                                                                                                                                                                                                                                                           predicted by Codon_usage
predicted by Homology
predicted by FrameD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="mktiqksaklnnvcydirgpvlekakqmeeeghqiiklnignla
PFGFDAPEEIQQDMIRNLPNSAGYSDSKGIFAARKAVMHYTQQQGIKNVTLDDIYLGN
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IRAKITPNTKGIVVINPNNPTGALYSDALLHDIIAIAREHGLVIFADEVYDKVLFDDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                      hote "Product confidence :
                    VVTANKALLAVHGNE I FKAAQDKGVMVAFEAAVAGG I PI I KALREGLTGNR I EWI AG I
I NGTTNF I LSEMROKGLDFGTYLAEAQRLGY AEADPTFD I EGFDAAHKLTLMSA I AFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene-"RSc1327"
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/note="RS02849"
1538. .2857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GRIARFLERYRQRHGTGIRAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CANVPGQWAIQTALGGYQSINDLVAPGGRMRRQRDLAYELITAIPGVSCVKPKAALYM
FPRLDPSVYPIDDDQTFIRQLLEEERVLLVQGTGFNWHSPDHFRIVFLPHEDDLREAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RHTAMASLSEDVLTVTFNSLSKSYRSCGYRAGWMVVSGDKRPAKDYIEGLNMLSSMRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product-"PROBABLE ASPARTATE AMINOTRANSFERASE PROTEIN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   predicted by Homology predicted by FrameD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene name confidence : hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 biosynthesis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="RS02848"
206. .1447
VPVQFERAYVEG1TKLEAVDIRYAEELGYRIKLLGLTRRAEAGIELRVHPTLVPATRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'function∾"small molecule metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /evidence-not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Product confidence :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="RSc1326"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:305"
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/strain="GMI1000"
                                                                                                                                                                                                                                                                                                                    'codon_start≃1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        codon_start-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="RSc1326"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                           name confidence : hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acid
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/note="RSc1330; 1
5037. .6296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="RS02851"
4361. .4957
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /function="miscellaneous; hypothetical/global homology"
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Gene name confidence: hypothetical
predicted by Codon_usage
predicted by Homology
predicted by FrameD"
                                                                                                                                                                                                                                                                                  Gene name confidence : putative predicted by Codon_usage predicted by Homology predicted by FrameD"
                                                                                                                                                                                                                                                                                                                                                                                                       /function="small molecule metabolism; biosynthesis of
cofactors, carriers; molybdopterin"
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Fyfdllgrdparlaglfrdvdekggfsmtgkpefdriaefgfvsgrsthedrvytird
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5037. .6296
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Gene name confidence : probable
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                                                                                                                                                                                             /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="CONSERVED HYPOTHETICAL PROTEIN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /evidence=not_experimental
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/db_xref="GI:17428343"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /evidence=not_experimental
/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2889. .4334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGEPOTDIIMLSHVVVEKOVNAAIAAIEALPTVLSKVTRLRMEELN"
                                                                                                                                                                                                                                                      codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IANVEGAMNAVVVQGDAVGPTLYYGKGAGAEPTASAVVADLVDVTRLHTADPEHRVPH
LAFQPDALSNTPLLPIEEVRSAYYLRMRVADETGVLADITRILAESGISIDAMLQKES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                codon_start=1
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gene

gene

CDS

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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                             100027 TGGATCCGCGCCATGCCCGAGCAGAACGCCTCGATCGACATCCTGCGCGATGGCCTGCCG 100086
                                          100189 GAACTGATCCGCGACGAG----CCGGTCCATGCACTGGGGCATGCG------
                                                                                                                               100129
                                                                                                                                                                                                             99967 GGCGACCAGATCGTCCGCTTCGCCGGCCAACCCGCCGACCAGGCTTCCGACCTGATCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99907 CCGGTCACCATTGCCGAGGTTCTGCCCGGCAGCGCGGCGAGCGCGCGGACTGCGTCGC
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107 LeuAspMetSerValIleGluGluThrThrProLeuSerLeuGlu------
                                                                                      87
                                                                                                                                                                       78
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                                                                                                                                                                                                                                                                                                                                              38
                                                                                                                                                                                                                                                                                                                                                                                                                                   23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 ProValAlaLeuAlaAlaTyrLeuPro-----
                                                                                                                          AATCCGGGCGGGCCGAAGCTCGGCAAGCTCGGCGCGCAGCTCTCGCAGCATGTGGAAACC
                                                                                                                                                                    LysPro-----
                                                                                ValAsnPheAspAspGlnSerProIleSerArgIleGlyGluGlnSerProProLeuGly 106
                                                                                                                                                                                                                                                     ProValLeuLeuThrProGluGlnIleGlnAlaArgLeuAsnAlaAlaGlyLeuAsnAla
                                                                                                                                                                                                                                                                                                                          IleIleAsnHisValProAlaHisAspThrAlaIleAsnGlnAlaLysAlaGlyAsnPro
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GTRLGAQOLGLAASVGCAGLQVVRRPRVAVFTGDELAMPGEPLKPGAIYNSNRFTLR
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RLLGVDDVTPKRIPMRADFALPKGDRRNEFLRARINAGGGLDLFPNQSSGVLTSTVWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene name confidence : probable predicted by Codon_usage predicted by Homology predicted by FrameD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /function="small molecule metabolism; biosynthesis cofactors, carriers; molybdopterin" /note="Product confidence: probable Gene name confidence: probable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="RSc1332; RS02854" 6586. .7116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cofactors, carriers; molybdopterin"
/note="Product confidence : probable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="RSc1331; RS02853" 6310. .6573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="CAD15033.1"
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/function="small molecule metabolism; biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="moaD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="moaE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="PROBABLE MOLYBDOPTERIN MPT CONVERTING FACTOR (SUBUNIT 1) PROTEIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /evidence=not_experimental
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="moaE"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MDMQIELRFFASVREQLGTSHEAAAVPDTVRTVGELRRWLAARG"
                                                                                                                                                                                                                                                                                                                                                                                                                            ---LeuMetThrSerGlnAlaLeuAlaGlnGlnAsnAsnProAlaAsn
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268.00
35.55%
21.18% .
5.67%
                                                                                                                                                                  ------GlnSerGlnAlaLeuAspVal 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
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233
158
450
261
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-GluLeu 123
                                          100230
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Score:

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0	CGCCAAGATCGCCAGATCAACATCGTCGCCAAGACAAGGCCTTCTCC	10123	B X
385	ProLysThrAsnGlnLouThrThrAsnDroAsnLvsLouProVal	, 370	Š
101237	ACCACCGTCACGCCAGTCGATGCCAACCGGTGTCCGTCACGTTCACGGTG	10118	Db .
369		, 351	γo
101186	TCTCGCGCGGCTACTACGCCGCCGACGTGCAG	101	מם
350	roAspAsnThrAlaAspValSer	337	γQ
101126	ASILEGITASINATASETATAGIUHISGIYTYPPRASPETYATGTTPLEUASPATG :::	101067	da An
101066	\GCTGGAATTCATCGGCATCAAGGAATTCGACAAGGACACGCTGCGCCGC	101007	Дb
١	LysLys		, Q
101006	AAGGATGTACAGATCCGCGCGAGGGCAACGTGCTGGTGGTGCGCGTGGAGGAGCGTCCG	100947	Db
314		/ 314	Qy
100946	ACCTTCACCGACGACAAGGGCGCCGAATCGATCCGCGCGCTGTACAACACCGGTTTCTTC	100887	Db
314		/ 306	Qy
305 100886	GlyAlaAspAspLysAlaPheThrThrValAlaAspGluValProLeuLeuIleGlyAsp	286	Оy
100826		100	뫄
285	IleHisAspLeuGlyGluProValTyrIleAspTyrArgAlaValGluValArgGlyGlu	7 266	γQ
265 100793	AspLeuSerIleIleArgAsnSerIleGlyGluValAspValIle	251 0 100734	dg Yo
100733		5 100674	gg.
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238	AsnGlySerIleProArgLeuArgGlnThrAla	/ 228	γQ
100613	:::    ::: CACTTCGCTCGCCTTGTACAACGACTTGAGCCGGCTGTTCCTGGCTCACGGCTAGGCTGT	100554	Дb
227		7 208	Qy
100553	GCCGGAATCCTGGCAAGCGGTACTTCAAAAGATCGGCATCGCCTGCATCCTGCTTCT	0 100497	망
207		7 193	δõ
100496	GGTATTGGATGGGGGCATTTGCTGTATTATTGCGTGGAATTTTTGACAGGCAAGCCTGT	0 100437	망
192		/ 183	Qy
100436	CTTGATCAGCGTGAGTCTCGGGGTGCTGAACTTGTTGCCCGTTCC	100392	DЪ
182		/ 164	Qy
163 100391	GlyGluGlnProAsnSerGluValValValProProThrLeuGluProGluLysProGly	7 144 5 100344	Оу
100343	ATCGTGGGGCAGGCGTCGCAGAACCTGAGCGG-TCCGATCACCGTCGCCGACTTCGC	100	B 2
100284		, 100231	Ş 5
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02325	GGAACCGATACCGTGTTCTTCGGCATCGGCTA 1	Db 10227	
93	4 SerArgSerlleIleGlnAsnGlyGlyTrpAsnArgThrTyrSerLeuArgTyrArgLeu 6	0у 67	
73 02277	4 ValPheGlyHisSerThrAsnGlyPheAspLeuSerThrArgThrLeuGluHisGluIle 6	Qy 65 Db 10221	
53 02217	9	Qy 63 Db 10216	
38 02166	LeuArgLeuSerGluAspLysLysGlyValLysLeuTyrAlaThrLysProLeuSerHis 6	Оу 619 рь 102108	
18 02107	1 ThrLysPheGluHisAsnLeuIleAsnArgAspGlyTyrGlnAlaGlyAlaGlu 6	Qy 60 Db 10204	
00 02047	81 LysProArgAspGlyGlnIleGlyLeuGlyTrpGlySerAspThrGlyThrArgLeuVal 6	Oy 58	
.80 .01990	1 ThrProAlaAspValTyrGlnSerLysLysValProLeuTyrValPheValAlaSerAsp 5	Qy 56 Db 10194	
60 01942	1 ProGluarg	Qy 55 Db 10188	
50 01882	4 ValAlaArgAlaIleLeuProAspGluSerGluAsnGluValIleAspLeu 5	Qy 53 Db 10182	
01822	9	Qy 51 Db 10176	
18 01762	5 MetProAspAspArgValLeuAlaIleAsnHisAspAspGly 5	Qy 50 Db 10170	
04 01702	81leGlnAspLysLeuAsnLeuValAlaAlaLysAlaArgHisLeuTyrAsp 5	Oy 48	
.87 .01642	1 Glu	Oy 48	
80 01582	1 GluProValIleGluThrValGluLeuThrAspGlyIleLeuMetAspIleSerProIle 4 ::: ::: ::: ::: ::: ::: ::: ::: :::	Oy 46 Db 10152	
60 01522	1 SerPheGluGlnSerSerSerSerArgThrGluProAlaGlnValAspGluSerThrLeu 4	Oy 44 Db 10146	
40 .01465	1 AsnMetValAsnThrGluIleValPheProGluArgGluGlnIleGlnAsnAspGlnVal 4 :::	Oy 42 Db 10141	
20 01 <b>4</b> 17	3AsnLeuGlnalaValArgAlaLeuSerAsnAspLeuIleAlaThrArgTyrPhe 4 :::   :::     :::	Oy 40 Db 10135	
02 01357	6 LysArgGluLeuLeuGluGlnLeuLeuThrValAsnMetGlyGluAlaTyr 4 ::: :::	Oy 38	

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Giullani,M.M., Pizza,M., Rappuoli,R.
85kda neisserial antigen
Patent: WO 0138350-A 6 31-MAY-2001;
Chiron Spa (IT); Statens Institutt f
Location/Qualifiers
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Sequence 6 from Patent W00138350.
AX155443
AX155443.1 GI:14536771
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Neisseria meningitidis
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae;
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                                                                                                                                                              /organism="Neisseria meningitidis"
/db_xref="taxon:487"
755 c 596 g 392 t
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429	LeuSer Asn Asp Leu IleAla Thr Arg Tyr Phe Asn Met Val Asn Thr Glu IleVal Phenomen Control of the Control of t	410	Qy
909	CTGGAAAAACTGCTGACCATGAAGCCCGGCAAATGGTACGAACGCCAGCAGATGACCGCC	850	Db
409	uGluGlnLeuLeuThrValAsnMetGlyGluAlaTyrAsnLeuGlnAlaValArgA	390	Qy
849	GAAGGCGACACCAACGAA	817	Db
389	spProLysThrAsnGlnLeuThrThrAspProAspLysLeuProValLys 	370	Qy
816	AAAATCACCGTCCACGAAGGCGGACGTTTCCGCTGGGGCAAAGTGTCGATT	766	DЬ
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765	GATTTCCGTATCCTCGATACCGACATCCAAACCAACGAAGACAAAACCAGGCAGACCATC	706	DЬ
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645	ATGTCGCTGACCGAAGGCGGCATTTGGACATGGCTGACACGAAGCGACCGGTTCGACCGC	586	рь
309	aPheThrThrValAlaAspGluValProLeuLeuIleGlyAsp\	290	Qy
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289	ArgAla	270	Qy
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489	AAA	430	Db
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236	LeuAsnGlySerIle	225	Qy
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318	GTTATCGAACGCCCCACCATCGGCTCGCTCAACATCACCGGCGCCCAAAATGCTGCAAAAC	259	Db
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258	ACCGGTTTCTTTGACGACGTACGAGTCGAAACTGCGGACGGGCAGCT	199	DЬ
186	laArgLeuPheAsnAspGlyValAsnLysValPro	170	Qy
198		163	DЬ
169	luProGluLysProGlyLeuIleLysi	150	Qy
162	ACCGAGCCGAGCACCGTATTCAACTACCTGCCCGTCAAAGTCGGCGACACCTACAAC	106	ДЪ
149	spTyrIleProGluTyrGlnGlyGluGlnF	136	Qy
105	TCGCCTTTGGCATTTGCCGACTTCACCATCCAAGACATCCGTGTCGAAGGCTTGCAGCGT	46	Дb
135	roLeuSerLeuGluGluLeuPheAlaGlnGluSerT	116	Qy
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	th: 5.62% Indels: 259	ry Mat	Que DB:
	milarity: 34.28% Conservative: 1	re:	Sco

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1682	AAACG	1623	Db
719	pGlnAspLeuProValAspPheValAsnGlyLysProSerGl	705	Qу
1622	CTGACCGT	1563	Db
705	ThrT	691	Оу
1562	TATAAAACCACCACCGCCGCCGGCGGCGTAAGGATGGG-TATCCCCGT	1516	Db
690	IleIleGlnAsnGlyGlyTrpAsnArgThrTy	671	Qy
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1293		1270	da
590		573	Qy
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960	GAGATTCAGAACCGCATGGGCTCGGCAGGCTACGGCATACAGC	919	Db
449	lnSers	430	Qy
918	::: GTTTTGGGT	910	Db

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	Pred.   Score:	Al ignment	BASE C	q	FEATURES	JOURNAL	AUTHORS TITLE	פיישפיישפיים	SOURCE ORGANISM	VERSION	AX202493 LOCUS DEFINITION ACCESSION	Db 2: RESULT	Оy		Oy 2		Db 2	Qy		V VQ			Qy		Db 1	Qy	Db 1	9	Qy Db 1	Db 1
•			COUNT	Car	3				MSIN		Z	322	903 sgJ		2202 TT/			865 eGJ		854 t			817 nS		1860 CT:	791	1824 C-	773 rs		1743 CG
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1622	 	В
705	yrargLeu-AspLysLeuLysThrGlnAlaProProGluThrTr	δ
1562		Dъ
069	isGluIleSerArgSerIleIleGlnAsnGlyGlyTrpAsnArgThrTyrSerLeuArg	Оy
1515	::: CGCAAAGCATCGACCAGCGTCAAACAA	рь
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630	yTyrGlnAlaGlyAlaGluLeuArgLeuSerGluAspLysLysGlyValLysLeu	Qy
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449	${\tt lnIleGlnAsnAspGlnValSerPheGluGlnSerSerSerArg}$	Qy
918	910 GTTTTGGGT	DЬ

REFERENC AUTHOR TITLE JOURNA MEDLIN PUBME REFERENC AUTHOR	RESULT ACO1049 LOCUS LOCUS ACCESSI ACCESSI VERSION KERNORD KOURCE SOURCE	Qу	Qу	Ф	Оу	dd Qy	ФУ	Qу	Qу	Qу	Оу	Qy
AUTHORS TITLE TOURNAL AEDLINAL E PUBMIED PERENCE TERENCE	z Oze e o	903 2322	883 2262	867 2202	865 2142	854 2082	837 2022	817 1971	797 1918	791 1860	773 1824	753 1774
Bacteria; Fusobacteria; Fusobacterium.  CE 1 (bases 1 to 10029)  RS Kapatral, V., Anderson, I., Ivanova, N., Reznik, G., Los, T.,  Lykidis, A., Bhattacharyya, A., Bartman, A., Gardner, W., Grechkin, G.,  Zhu, L., Vasieva, O., Chu, L., Kogan, Y., Chaga, O., Goltsman, E.,  Bernal, A., Larsen, N., D'Souza, M., Walunas, T., Pusch, G.,  Genome sequence and analysis of the oral bacterium Fusobacterium  nucleatum strain ATC 25586  AL J. Bacteriol. 184 (7), 2005-2018 (2002)  NE 2188394  ED 11889109  CE 2 (bases 1 to 10029)  R Kapatral, V., Anderson, I., Ivanova, N., Reznik, G., Los, T.,  Lykidis, A., Bhattacharayya, A., Bartman, A., Gardner, W., Grechkin, G.,  Zhu, L., Chu, L., Kogan, Y., Chaga, O., Goltsman, E., Bernal, A.,  Larsen, N., D'Souza, M., Walunas, T., Pusch, G.D., Haselkorn, R.,  Fonstein, M., Kyrpides, N. and Overbeek, R.	AE010493  AE010493  AE010493  AE000493  AE000493  AE000951  AE010493  AE0104	SGluGluGlyAsnProIleLysLeuHisPhePheIleGlyThrProPhe 919 	IGIYVAlArgTrpAlaSerProValGlyGlnValArgValAspValAlaThrGlyValLy 903	AsnAlaTyrAspLysGlyPheThrAsnAspThrLysIleGlyAlaGlyVa 883	eG1y	tLysaspLeuAlgLeuAlgleheGlyAspI1 865 ::::::::       :::::        cTTCCCGATGCCCGGTGCGAAAGACGCACGCACCGTCCGCCTGAGCCTGTTTGCCGACGC 2141	rGlyGlyGlnValLeuAlaValGlyThrAlaGluTyrAsnTyrGluPheMe 854         :::::	nSerIleArgGlyTyrAlaHisAspSerLeuSerProIleSerAspLysGlyTyrLeuTh 837    :::        	eTrpSerAspAsnPheAsnHisValProTyrArgLeuArgPhePheAlaGlyGlyAspGl 817 :::   :::    :::     :::       GCAGAACCAAAGAAATCCCCTTCTTTGAAAACTTCTACGGCGGCGGCCTGGG 1970		rSerPheGlyAspAsnAlaTyrGlySerAsnArgAlaHisGlnMetThrGly 790	rSerGlyLeuValSerAspAlaAsnMetAlaIleAlaArgAlaGlyIleSerGlyValTy 773 

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                               . No.:
                                                                                                                                                                                    311 LysTyrGluThrLysLysAsnLeuIleGlu---AsnAlaSerAlaGluHisGlyTyrPhe 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
                                       SerLeuIleTyrAspThrGlyThrGlnTyrArgPheAsp------GluValVal 365
                                                                                                   AspGlyArgTrpLeuAspArgSerValAspValIleLeuProAspAsnThrAlaAspVal 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                      9.12e-07
262.50
38.08%
22.59%
5.55%
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Gaps:

5192

5252

Length: Matches: Mismatches: Indels: Conservative:

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SLEYIGKLEKIYGYDIVKNYKVANLLSVRRITNKDVAFOK VEFYLENLKANVEGDIKNL
KDFSNNLISLKGDYDVKNGKVANNLSVRRITNKDVAFOK VEFYLENLKANVEGDIKNL
VSLSEKHLEKYYGAKDIGYILYGGIDVKGVAGKIKAVKGFATNEEKKLDDLAVDIEY
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FVDIANISKLDKEDLIRSLFYKLHFKMDHFNYFYFEIIKISGSTELTATNEEYYGNLI
LMPIDFVKYEKPILIDMDNFNIVPEVYGKLYIDLLNGKKGKYYTTGETELKEGYF
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RDNSRFGHNIGTTAGVGILLNTGGFFNOGNEDGMKFYFNMGQSF".
FWKANVRIIGTGKDVIKNOTMKVDSKVREYDVGLEVKVDD9KTIEIGVGTVPDKYRTD
PNKDYRKPNYHIGFKFRKRYRDFSEIFSF"
1 1691 c 1027 g 4209 t
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/gene="FN1912"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /transl_table=11
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4205	ECHAPAGATACAGATAGAGTATCTTGGGGATGG	4249	Db S
ı N	ATTTGAAAAATCAAATAAAAATTACACAGGTTTTGCATTAGATTTCTATGATCCTT	- 0	₽ ₽
639	ArgLeuSerGluAspLysLysGlyValLysLeuTyrAlaThrLysProLeuSerHisPro	620	Qy
4310	TTAGGTACTTTATCATTAAAAGATAGTAACTGGAGAGGTAAAAATCAACAATTTGGTTTC	4369	В
619		604	Qy
4370	ATTACAAGGTGGGTTGCTTATGGTTCTGAAACAGGA	4411	Db
2	spG vG nT eG vTenG vTrnG vSerAsnThrG vThrArgIenVa ThrIvsph	5 8 4	O <sub>V</sub>
4412	Î       CAGGAGATCCAGAAGGAAT	4471	용 5
44/2	GITGAFAACETAATIGAGAFTGGGAATATTCAAAAATGTTAAATATGAAGCAAGATC	571	2 5
70	uAlaAsnArgLysThrProAlaAspValTyrGlnSerLysLy	n on	γ <sub>0</sub>
4532	TAGACAGAGAAATAGAAATACAACCTGGAAAAATATTTA	4591	Db
555	ProAspGluSerGluAsnGluValIleAspLeuProGluArgThrA	539	δ
4592	AAACAAAAAGGTAATAGAAGAACACCTAATGATGTTTTGAAAACTAAAGACTATGTT	4651	Db
538	pAlaValSerAlaValAlaArgAlaI	527	Qγ
σ	:::            TATTGTAAGAAGAATTGAAGTTAAAAAA	4711	Db
526	uAlaIleAsnHisAspAspGlyValAsnArgSerI	511	Оy
4712	::::::::::::::::::::::::::::::::::::::	4771	рь
510	laLysAlaArgHisLeuTyrAspMetProAsp	496	γQ
4772	  AAATTTTAGGATTGTAT	4831	Db
495	\snLeuIleGlnAspLysLeuAs	485	Qγ
4832		4891	Db
484	ThrAspGlyIleLeuMetAspIleSerProIleGluPheSerAla	469	οy
4892	::::	4924	Db
468	ThrLeuGluProValIleGluThrValGlu	449	Qγ
4925	GCACAAGTAGCAAATGGAAAAATGGCTTTATCATTTGAA	4963	В
448	lnIleGlnAsnAspGlnValSerPheGluGlnSerSerSerSer	431	οy
4964	CAAAGAAGATTATTAGCGACTGGAAAATTTTCAGAAGTTAGACCAGAT	5011	DЬ
430	nMetValAsnThrGl	411	Qy
5012		5071	DЬ
410	euThrValAsnMetGlyGluAlaTyrAsnLeuGlnAlaValArgAlaLeu	394	γQ
5072		5131	Db
393	llLysArgGluLeuLe	383	Qγ
5132		5191	Db
382	1	366	Qy

NGU81959 LOCUS DEFINITION ACCESSION VERSION KEYNORDS SOURCE ORGANISI	9 34 SULT	Qy 88	Qy 87 Db 356	Qy 85 Db 362	Qy 83 Db 367	Qy 81 Db 371	Qy 79 Db 375	Qy 77 Db 379	Qy 75 Db 385	Qy 73 Db 391	Qy 71 Db 397	Qy 70 Db 402	Qy 69 Db 408	Qy 67 Db 414	Qy 66 Db 420
NGU81959  ON Neisseria gonorrhoeae outer membrane protein (omp85) gene, complete cds.  U81959  U81959.1 GI:1766041  Neisseria gonorrhoeae.  Neisseria gonorrhoeae  Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  Neisseria.  Neisseria.	LysGluGlyAsnProIleLysLeuHisPhePheIleGlyThrProPhe 919	ValArgTrpAlaSerProValGlyGlnValArgValAspValAlaThrGlyVal 902 	2 GlyPheThrAsnAspThrLysIleGlyAlaGlyValGly 884 	77 LeuArgLeuAlaValPheGlyAspIleGlyAsnAlaTyrAspLys 871 :::	7 ThrGlyGlyGlnValLeuAlaValGlyThrAlaGluTyrAsnTyrGluPheMetLysAsp 856	7 GlnSerIleArgGlyTyrAlaHisAspSerLeuSerProIleSerAspLysGlyTyrLeu 836	7 IleTrpSerAspAsnP	7 ASPASNALATYTGLYSERASNATGALAHISGLNMETThTGLYGLYILEGLNALAGLYTYT 796 	9 ASPALAASNMETALAILEALAATGALAGLYILESETGLYVALTYTSETPheGLY 776		9 GlnGluAlaLeuLeuAlaGlyValAlaValHisLysThrValAlaAspAsnLeuValAsn 738	00AlaProProGluThrTrpGlnAspLeuProValAspPheValAsnGlyLysProSer 718     :::::	5 LysLeuLysThrGln	6 SerileIleGlnAsnGlyGlyTrpAsnArgThrTyrSerLeuArgTyrArgLeuAsp 694 	0 ASNGLYPheASpLeuSerThrArgThrLeuGluHisGluIleSerArg 675 

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Best Local Similarity:
Query Match:
DB:
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ORIGIN
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MEDLINE
PUBMED
REFERENCE
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TITLE
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TITLE
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259 GTTATCGTATGCCCTACCATCGGCTCGCTCAACATCACCGGCGCCAAAATGCTGCAGAAC 318
                                                                                                                                                         199
                                                                                                                                                                                                   170 AlaArgLeuPheAsnAspGlyVal------
                                                                                                                                                                                                                                                                                          163 -----
                                                                                                                                                                                                                                                                                                                          150 GluValValValProProThrLeuGluProGluLysProGlyLeuIleLysArgLeuTyr 169
                                                                                                                                                                                                                                                                                                                                                                                                   106 ACCGAGCCGAGCACCGTATTCAACTACCTGCCCGTCAAAGTCGGCGACACCTACAAC--- 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 ThrProLeuSerLeuGluGluLeuPheAlaGlnGluSerThrGluMetGlyIleAsnPro 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
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                                                                                                                                    GCCACCGGTTTCTTTGACGACGTACGAGTCGAAACTGCGGACGGGCTGCTTCTGCTGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AsnAsp-----TyrIleProGluTyrGlnGlyGluGlnProAsnSer 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :::||||||:::
TCGCCTTTGGCATTTGCCGACTTCACCATCCAAGACATCCGTGTCGAAGGCTTGCAGCGT 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reschke,D.K., Manning,D.S. and Judd,R.C. Direct Submission
Submitted (11-DEC-1996) Division of Biological Sciences, University of Montana, Health Sciences 104, Missoula, MT 59812-1002, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Manning,D.S., Reschke,D.K. and Judd,R.C. Omp85 proteins of Neisseria gonorrhoeae and Neisseria meningitidis are similar to Haemophilus influenzae D-15-Ag and Pasteurella multocida Oma87 Microb. Pathog. 25 (1), 11-21 (1998) 98379445
                                                           ------AsnLysValProArgLeuLysAlaLysPheTyrGlnSer 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           636
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L. .2379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
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259.50
33.95%
20.89%
5.49%
                                                                                                                                                                                                                                                                  ------GACACACGGCAGTGCCATCAACAAGCCTGTAC 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                       ---- 177
                                                                                                                                    258
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TTTTGAT 12	74 TTGGGCTACTTCGACAACGTACAG	117	Db
rgSerIleLeuGlyArgIleSerAspAlaValSer	13 IleAsnHisAspAspGlyValAsnArgSerIleLeuGly	51	Qy
CCAAGCTGCAACGCTCC	:::	ب	ф
GTCGTGCGCCGCGAATTGCGCCAA 1	2 LeuTyrAspMetProAspAsp2		Q YQ
AsnLeuValAlaAlaLysAlaArgHis :::    :::	<pre>/ PreserAlaSerAsnLeuIleGlnAspLysLeuAs / PreserAsnLeuIleGlnAspLysLeuAs / PreserAsnLeuIleGlnAspLysLeu</pre>	<u>د</u> 4 د	<u> </u>
ACCGGGCAG	00 ACCGTCGATTTCGTCCTGCACATCGAACCGGGCAC		g ::
(Pro	ThrAspGlyIleLeuMetAspIleSerPro		Qy
::::::::::::::::::::::::::::::::::::::	61	9	ДD
rThrLeuGluProValIleGluThrValGlu	50 ThrGluProAlaG	4	Qy
CGCATGGGCTCGGCAGGCTACGCATACAGC 960	19	Db 91	_
SerArg 4	30 ProGluArgGluG	Qy 43	0
918	10 GTTT	Db 91	
Phe 4	10 LeuS	0у 41	_
GCC 9	50 CTGG	00	-
Ala 4	90 LeuG	Оу 39	_
GAA 84	817 GAAGGCGACCAACGAA	œ	_
	spProLysThrAs	Οу з'	_
_	766 AAAATCACCGTCCACGAAGGCGGACGTTTCCGCTGGGGC	Db 7:	_
Ile 3	IleTyrAs		_
AACCAACGAAGACAAAACCAGGCAGACCATC 7	706 GATTTCCGTATCCTCGATACCGACATCCAAACCAACGA	Db 7	
pValIleLeuProAspAsnThrAlaAspVal 3	30 AspGlyArgTrpLeuAspArgSerValAspValIleLe		
TCTACCAGAACAACGGCTACTTC 7	TGGAAAAAGTAACCGAC	Db 6	
nLeuIleGluAsnAlaSerAlaGluHisGlyTyrPhe 329	310 GlyLysTyrGluThrLysLysAsnLeuIleGluAsnAla	Qy 3	
TTGGACATGGCTGACGCGAAGCGACCGGTTCGACCGC 645	586 ATGTCGCTGACCGAAGGCGGCATTTGGACATGGCTGAC	Db 5	
pGluValProLeuLeuIleGlyAspValPheHisHis 309		Qу 2	
CAG 5	547 GGCAACCAAGTCTATTCCGACCGCAAACTGATGCGG	υı	
gGlyGluGlyAlaAspAsp 2	270 GlyGluProValTyrIleAspTyrArgAlaValGluVa	Qy 2	
54	490 ATCGACATCACGATTGACGAGGGCAAATCCGCCAAAAT	4	
26	250 IleAspLeuSerIleIleArgAsnSerIleGlyGluValAspValIleIleHisAspLeu	Qy 2	
4	430 GGCAAACTCAATATCCAAATCACGCCCAAAGTAACCAA		
AlaValGlyTyrTyrAsp 2	230 SerIleProArgLeuArgGlnThrAlaLeuValAlaAl	Qy 2	
	379 GCGACACTCAACCAGGCAGTCGCCGGCCTGAAAGAAGAATAT	Db 3	
22	210 AlaAsnIleLysAlaAlaLeuGluAspIleThrGlnGl	Qy	
ACGCCATCAAGAAAAACCTCGAATCGTTCGGGCTGGCGCAGTCGCAATACTTTAATCAG 378	319 GACGCCATCAAGAAAAACCTCGAATCGTTCGGGCTGGC	Db	
erAlaIleGlySerSerHisGlnLysThrGluProTyr 209	191 SerGinSerGlyGluThrSerAlaIleGlySerSe	VY	

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LysAspLeuArgLeuAlavalPheGlyAspIl 865	854 t	Qy
CTACGGCGGCAA	TΑ	DЪ
aValGlyThrAlaGluTyrAsnTyrGluPheM	lnValLeuAlaVa	Qy
AGCGGCACGCTCGGCCCGAAAGTGTATGACGA 2	:::	Db
disAspSerLeuSerProIleSerAspLysGlyTyrLeuTh 8	rIleArgGlyTyrAlaH	Qy
<pre>IPheAsnHisValProTyrArgLeuArgPhePheAlaGlyGlyAspG1 817 IPHITTER IPHITTER</pre>	797 eTrpSerAspAsnPheAsnHi	рь
 	60 CTTAAGCAAAACCTTC	Db
GlyIle		Qy
пататуг	yaspashataty	Db 4
ACCGGCGTAAATGCCGAAATCGCCCTGCCCGGCAGCAAACTGCAATA	4CTG	₽ B
SerAspAlaAsnMetAlaIleAlaArgAlaGlyIleSerGlyValT	lyLeuVal	Qy
TACTAC	A (	B 2
ACTGTCGGCTGGGGGGCGCAACAAGAC 17	່ ດ	₽ ₽
luAlaLeuLeuAlaGlyValAlaValHisLySThrValAl 733	9 nG	Qy
	: 23 CA	ф
AsnGlyLysProSerGl 71	spLeu	Qγ
AspLysLeuLysThrGlnAlaProProGluThrTr 705    :::::	691 TyrArgLeu-AspLysLeuLy	Db Qy
CGTA	16 TATAAAACCA	DЬ
SerIleIleGlnAsnGlyGlyTrpAsnArgThrTyrSerLeuAr	lulleSerArgSerIle	Qy
PACGGAAAAGCCTTCGACCCGCGCAAAGCATCGACCAGCGTCAAACAA 1515	1462GATATTTACGGAAAA	B 8
	651 Clackachuranh	
ProLeuSerHisProLeuAsnAspGlnLeuArgAlaThrLeuGlyTyr 650 :::           :::	631 TyrAlaThrLysProLeuSer ::: 1402 AACGGCTCGCTCTCCTTTACC	D Oy
ACCACGCTC 14	48 TTCGGTAC	Db .
/AlaGluLeuArgLeuSerGluAspLvsLvsGlvValLvsLeu 63	1 AspGlvTv	0
ThrArgLeuValThr	591 TrpGlySerAspThrGlyThr.	Оy
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lAlaSerAspLysProArgAspGlyGlnIleGlyLeuGly 59	ValPhe	Qy
	43 AACATGAGCCTG	da .
 AsnArqLysThrProAlaAspValTvrGlnSerLvsLvsValPro 57	53 ArgThrAlaLeu	Q
LeuProAspGluSerGlu       ::: ACGCCCGACAAA	533 AlavalalaargalaileLeu        1204 GCCGTCCCGCTTGCCGGTACG	Qу

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                                                                                                                                          163
                                                                                                                                                                                                                                                        46 TCGCCTTTGGCACTTGCCGACTTCACCATCCAAGACATCCGCGTCGAAGGCTTGCAGCGT
GluProTyrAlaAsnIleLysAlaAlaLeuGluAsp-----IleThrGlnGluSerAla 224
                                                                                                                                                         GluValValValProProThrLeuGluProGluLysProGlyLeuIleLysArgLeuTyr 169
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                                                     PheTyrGlnSerSerGlnSerGlyGluThrSerAlaIleGlySerSerHisGlnLysThr 206
                                                                                                           AlaArgLeuPheAsnAspGlyValAsnLysValPro-----ArgLeuLysAlaLys 186
                                                                                                                                                                                                                             AsnAsp-----
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Patent: WO 0138350-A 2 31-MAY-2001;
Chiron Spa (IT); Statens Institutt
Location/Qualifiers
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Neisseria meningitidis
Bacteria; Proteobacteria;
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_	524 LeuGlyArgileSerAspAlaValSerAlaValAlaArgAlaIleLeuProAspGluSer 543	Qy
)7	TTCGACAATGTCCAG 119	Db 1
	509ArgValLeuAlaIleAsnHisAspAspGlyValAsnArgSerIle 523	Qy
5	GTCGTCCGCCGTGAATTACGCCAAATGGAATCCGCACCTTACGACACCTCCAAGCTG 114	ш
_	AsnLeuValAlaAlaLysAlaArqHisLeuTyrAspMetProAspAsp	Oy
9	480	1 dd 1
	CARCCUSCINCCOMACUCISMANUCCAMANUCCSICUSAIIICSICUISCACAICUSAACUCUSUSCI	
	GluProValIleGluThrValGluLeuThrAspGlyIleLeuMetAspIleSerPro ::::   ::: ::::  ::: ::::  ::::	
10	940 TCGGCAGGCTACGCATACAGC	Db
0	rPheGluGlnSerSerSerSerArgThrGluProAlaGlnValAspGluSerThrLe	Qy
	919GAGATTCAGAACCGCATGGGC 939	DЬ
	421 AsnMetValAsnThrGluIleValPheProGluArgGluGlnIleGlnAsnAspGlnVal 440	Qy
_	883 TGCTACCAACGCCAGCAGATGACCGCCGTTTTGGGT	Вb
J	401 AlaTyrAsnLeuGlnAlaValArgAlaLeuSerAsnAspLeuIleAlaThrArgTyrPhe 420	Qy
	835GTCCCCAAAGCCGAACTGGAAAAACTGCTGACCATGAAGCCCGGCAAA 882	Db
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	TGGGGCAAAGTCTCCATCGAAGGCGACACCAACGAA	
	361 PheAspGluValValPhePheThrIleAspProLysThrAsnGlnLeuThrThrAspPro 380	Q Y
<b>~</b>	AACGAAGACAAAACCAAGCAGCAGCATCAAAATCACCGTCCACGAAGGCGGACGTTTCCGT 79	
S	rGlyThrGlnTyrAr	Qy VQ
	679 GACTTCTACCAAAATAACGGCTACTTCGATTTCCGTATCCTCGATACCGACATCCAAACC 738	Ф
J	321 AsnAlaSerAlaGluHisGlyTyrPheAspGlyArgTrpLeuAspArgSerValAspVal 340	Q <sub>y</sub>
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	290 LysAlaPheThrThrValAlaAspGluValProLeuLeuIleGlyAspVal 306	Oy
	547 GGCAACCAAGTCTATTCCGAACCGCAAACTGATGCGG	
		Qy
0.	490 ATCGACATCACGATTGACGAGGGCAAATCCGCCAAAATCACCGACATCGAATTTGAA 546	Db
	AspLeuSerIleIleArgAsnSerIleGlyGluValAspValIleIleHisA	Оy
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	237ThrAlaLeuValAlaAlaArgAlaValGlyTyrTyrAsp 249	Оy
	70 TTTAATCAGGCGACACTCAATCAGGCAGTCGCCGGCCTGAAAGAAGAATACCTCGGGCGC 42	
	225 MetAspLeuAsnGlySerIleDroArgLeuArgGln 236	O <sub>Y</sub>
	319 GACGCCATTAAGAAAAACCTCGAATCGTTCGGGCTGGCGCAGTCGCAATAC 369	Db

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809 LeuArgPhePheAlaGlyGlyAspGlnSerIleArgGlyTyrAlaHisAspSerLeuSer 
791GlyIleGlnAlaGlyTyrIleTrpSerAspAsnPheAsnHisValProTyrArg
785 AlaHisGlnMetThrGly
765 AlaArgAlaGlyIleSerGlyValTyrSerPheGlyAspAsnAlaTyrGlySerAsnArg
745 GlnArgTyrSerLeuGluValGlySerSerGlyLeuValSerAspAlaAsnMetAlaIle
731 ThrValAlaAspAsnLeuValAsnProMetArgGlyTyrArg
714 AsnGlyLysProSerGlnGluAlaLeuLeuAlaGlyValAlaValHisLys
697 LysThrGlnAlaProProGluThrTrpGlnAspLeuProValAspPheVal     :::     11111::: 1597 GCAGAACACCTGACCGTCAACACCTACAACAAGCGCCCAAACACTATGCCGACTTTATC
682 GlyTrpasnarg
662 PheAspLeuSerThrArgThrLeuGluHisGluIleSerArgSerIleIleGlnAsnGly
642 AspClnLeuArgAlaThrLeuGlyTyrGlnGlnCluValPheGlyHisSerThrAsnGly :::          :::    ::: 1435 ACGGCAGACGGGGTCAGCCTGGGCTACGATGTTTACGGAAAAGCCTTCGACCCG
622 SerGluAspLysLysGlyValLysLeuTyrAlaThrLysProLeuSerHisProLeuAsn
602 LysPheGluHisAsnLeuIleAsnArgAspGlyTyrGlnAlaGlyAlaGluLeuArgLeu
584 AspGlyGlnIleGlyLeuGlyTrpGlySerAspThrGlyThrArgLebValThr
1269
564 AspValTyrGlnSerLysLysValProLeuTyrValPheValAlaSerAspLysProAr
544 GluAsnGluValIleAspLeuProGluArgThrAlaLeuAlaAsnArgLysThrProAla :::      :::   1234GTCGATTTGAACATGAGTCTGACCGAACGTTCCACC
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1147	Db	187 PheTyrGlnSerSerGlySerGlyGluThrSerAlaIleGlySerSerHisGlnLysThr 206 :::           ::: :::	Qy Db
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1033	Db	GluValValValProProThrLeuGluProGluLysProGlyLeuIleLysArgLeuTyr	
480	مر م	106 ACCGAGCCGAGTACCGTATTCAACTACCTGCCCGTCAAAGTCGGCGACACCTACAAC 162	Db
9 4 5 L	2 2	136 AsnAspTyrIleProGluTyrGlnGlyGluGlnProAsnSer 149	Qy
940	) da	:::      :::    TCGCCTTTGGCACTTGCCGACTTCACCATCCAAGACATCCGCGTCGAAGGCCTTGCAGCGT	
441	· Qy	116	(
919	Db	014-168-0 (1-010) V NYTESAAT (1-000A)	- 00
421	Qy	5.48*	Query 1
883	Db	Conservative:	Percent
401	Qy	Scores: 2.29e-07 Length: 250 no Matches.	Alignment Pred. No. Score:
835	Db		OKIGIN
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361	Оу	Location/Qualifiers	FEATURES
739	DЪ	NAL Patent: WO 0138350-A 10 31-MAY-2001; Chiron Sba (IT) : Statens Institutt for Folkehelse (NO)	JOURNAL
341	Оу		AUTHORS
679	Db	Neisseria.	REFERE
321	Оу	NISM	ORGANISM
619	Db	DS . Neisseria go	KEYWORDS SOURCE
307	Qy	ON AX155447 AX155447.1 GI:14536772	ACCESSION VERSION
583	DЪ		AX155447 LOCUS DEFINITION
290	Qy	30	RESULT 30
547	Db	2356 ATCCAACGCTTCCAACTCGACCGCACGACGTTC 2391	Db 2:
270	Оу	908 ProIleLysLeuHisPhePheIleGlyThrProPhe 919	Qy
490	Db	296 CCTTTAGGCCCGATGAAATTCAGCTACGCCTACCCCGCTGAAGAAAAAACCGGAAGAACGAA 2355	Db 2:
250	Qy	890 ProValGlyGlnValArgValAspValAlaThrGlyValLysGluGluGlyAsn 907	Qy
430	Db	2236 AAATCCACCTTTACCAACGAATTGCGCTATTCCGCCGGCGCGCGC	Db 2:
237	Qy	871LysGlyPheThrAsnAspThrLysIleGlyAlaGlyValGlyValArgTrpAlaSer 889	Qy
370	Db	2176 AACAGCAGTTCCGCGACCGGCGGCAGGGTTCAAAACATTTACGGCGCCGGCAATACCCCAT 2235	Db 2:
225	Оу	870 870	Qy
319	Db	2116 GTCCGCCTGAGCCTGTTTGCCGACGCAGGCAGGCTGTGGGACGGCAAAACCTACGACGAC 2175	Db 2
207	Qy	857 LeuArgLeuAlaValPheGlyAspIleGlyAsnAlaTyrAsp	Qy

GGCTACTTCGACAACGTACAG	::::::::::::::::::::::::::::::::::::::	1147	Db
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GluArgGluGlnIleGlnAsnAspGlnVal 440	${\tt AsnMetValAsnThrGluIleValPheProGluArc}$	ت	Qy
TTGGGT 918	TGGTACGAACGCCAGCAGATGACCGCCGTTTTGGGT	883	Db
SerAsnAspLeuIleAlaThrArgTyrPhe 420	AlaTyrAsnLeuGlnAlaValArgAlaLeuSerAsr	401	Qy
GANANACTGCTGACCATGAAGCCCGGCAAA 882		835	Db
GluGlnLeuLeuThrValAsnMetGlyGlu 400	~	381	Оу
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lnLeuThr 	PheAspGluValVal	61	Оу
ATCACCGTCCACGAAGGCGGACGTTTCCGT 798	AACGAAGACAAAACCAAGCAGAC	739	Db
pValSerLeuIleTyrAspThrGlyThrGlnTyrArg 360	IleLeuProAspAsnThrAlaAs	341	Оу
TTCCGCATCCTCGATACCGACATCCAAACC 738	GACTTCTACCAGAACAACGGCTACTTCGATTTCCG	679	DЬ
rpLeuAspArgSerVal	AsnAlaSerAlaGluHisGlyTyrPheAspGlyAr	321	Qy
AAATTTGCCCAAGACATGGAAAAAGTAACC 678	CTGACACGAAGCAACCAATTCAACGAGCAGAAATTTC	619	Db
rLysLysAsnLeul	PheHisHisGlyLysTyr	307	Qy
ATTTGGAC	- i	583	Db
pGluValProLeuLeuIleGlyAspVal 306		290	Qy
ATGCGG 582		547	Db
Ę,	GlyGluProValTyrIleAspTyrArgAlaValGluValArgGlyGluGlyAlaAs	270	ОУ
GCCAAAATCACCGACATCGAATTTGAA 546	-	490	Db
_	IleAspLeuSerIleIleArgAsnSerIleGlyGluValAspValIleIleHisAsp	250	Qy
GTAACCAAACTCGCCCGCAACCGCGTCGAC 489		430	Db
rgAlaValGlyTyı	ThrAlaLeuValAl	237	Qy
AAGAA1	TTTAATCAGGC	370	Db
ln	MetAsp	225	Оу
		319	Db
GluAspIleThrGluSerAla 224	GluProTy	207	Qy

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856	ThrAlaGluTyrAsnTyrGluPheMetLysAsp	846
845 2055	ProfleSerAspLysGlyTyrLeuThrGlyGlyGlnValLeuAlaValGly [	829 2005
828 2004	LeuArgPhePheAlaGlyGlyAspGlnSerIleArgGlyTyrAlaHisAspSerLeuSer	809 1945
808 1944	GlyfleGlnAlaGlyTyrfleTrpSerAspAsnPheAsnHisValProTyrArg	791 1894
790 1893	BHISGINMETThrGly	785 1834
784 1833	erGlyValTyrSerPheGlyAspAsnAlaTyrGl     AACTGCAATACAACTGCAATAC	765 1798
764 1797	uValGlySerSerG	745 1774
744 1773	ThrValAlaAspAsnLeuValAsnProMetArgGlyTyrArg	731 1717
730 1716	AsnGlyLysProSerGlnGluAlaLeuLeuAlaGlyValAlaValHisLys	714 1657
713 1656	LysThrGlnAlaProProGluThrTrpGlnAspLeuProValAspPheVal	697 1597
696 1596	yrArgLeuAsp TGAATTTCGGT	682 1537
681 1536	> ≧	662 1489
661 1488	AspGlnLeuArgAlaThrLeuGlyTyrGlnGlnGluValPheGlyHisSerThrAsnGly :::	642 1435
641 1434	SerGluAspLysGlyValLysLeuTyrAlaThrLysProLeuSerHisProLeuAsn	62 <b>2</b> 1381
621 1380	LysPheGluHisAsnLeuIleAsnArgAspGlyTyrGlnAlaGlyAlaGluLeuArgLeu :::	602 1321
601 1320	euGlyTrpGlySerAspThrGlyThrArgLeuValT 	584 1270
1269	•	1269
583	yrGlnSerLysLysValProLeuTyrValPheValAlaSerAspLysProAr	564
563 1269		544 1234
543 1233	LeuGlyArgIleSerAspAlaValSerAlaValAlaArgAlaIleLeuProAspGluSer	52 <b>4</b> 1198

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US-09-914 QY 116 Db 46 QY 136 QY 136 QY 150 Db 163 QY 170 Db 163	Alignment Pred. No.: Score: Score: Percent Sin Best Local Query Match DB:	b 205 y 9 85 b 211 b 211 b 211 b 211 b 217 y 87 y 8
4-168-2 (1-919) x AX202489 (1-2394)  6 ThrProLeuSerLeuGluGluLeuPheAlaGlnGluSerThrGluMetGlyIleAsnPro 135	ment Scores:       2.29e-07       Length:       2394         NO.:       259.00       Matches:       191         ent Similarity:       33.48%       Conservative:       121         Local Similarity:       20.49%       Mismatches:       342         Match:       5.48%       Indels:       278         Gaps:       40	

523		Qy
1146	1090GTCGTCCGCCGTGAATTACGCCAAATGGAATCCGCACCTTACGACACCTCCAAGCTG	DЬ
508	Ins	Qy
1089	1033 CGGAAAATCTACGTCAACGAAATACACATCACCGGCAACAACAACAAAACCCGCGACGAA	дb
492	Leu	Qy
0	3 CAGCCGCTGCCGAACGCTGAAACCAAAACCGTCGATTTCGTCCTGCACATCGAACCGGG	Db .
7	61 G	QV
7	40 TCGGCAGGCTACGCATACAGC	Db .
5 (	41 SerPheGluGlnSerSerSerSerArgThrGluProAlaGlnValAs	Qy
w	19	pb .
►	421 AsnMetValAsnThrGluIleValPheProGluArgGluGlnIleGlnAsnAsnGlnVal	Qγ
420 918	401 AlaTyrAsnLeuGlnAlaValArgAlaLeuSerAsnAspLeuIleAlaThrArgTyrPhe	Qy Db
882	835GTCCCCAAAGCCGAACTGGAAAAACTGCTGACCATGAAGCCCGGCAAA	DЪ
400	381 AspLysLeuProValLysArgGluLeuLeuGluGlnLeuThrValAsnMetGlyGlu	Qy
834	799 TGGGGCAAAGTCTCCATCGAAGGCGACACCAACGAA	Db
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798	739 AACGAAGACAAAACCAAGCAGACCATCAAAATCACCGTCCACGAAGGCGGACGTTTCCGT	Db
360	341 IleLeuProAspAsnThrAlaAspValSerLeuIleTyrAspThrGlyThrGlnTyrArg	Qγ
738	679 GACTTCTACCAAAATAACGGCTACTTCGATTTCCGTATCCTCGATACCGACATCCAAACC	Db
340	321 AsnAlaSerAlaGluHisGlyTyrPheAspGlyArgTrpLeuAspArgSerValAspVal	Qγ
678	: : : AGCAACCAATTCAACGAGCAGAAATTTGCCCAAGATATGGAAAAAGTAA	Db
320	307PheHisHisGlyLysTyrGluThrLysLysAsnLeuIleGlu	Qγ
618	583CAAATGTCCCTGACCGAAGGCGGCATTTGGACATGG	Db
306	290 LysalaPheThrThrValAlaAspGluValProLeuLeuIleGlyAspVal	Оy
582	547 GGCAACCAAGTCTATTCCGACCGCAAACTGATGCGG	Db
289	270 GlyGluProValTyrIleAspTyrArgAlaValGluValArgGlyGluGlyAlaAspAsp	οy
546	::::::    490 ATCGACATCACGATTGACGAGGGCAAATCCGCCAAAATCACCGACATCGAATTTGAA	DЬ
269	250 IleAspLeuSerIleIleArgAsnSerIleGlyGluValAspValIleIleHisAspLeu	Oy
489		Db
249	237ThrAlaLeuValAlaAlaArgAlaValGlyTyrTyrAsp	Qy
429	CAG	рь
236		Qу
369	319 GACGCCATTAAGAAAAAACCTCGAATCGTTCGGGCTGGCGCAGTCGCAATAC	Db
224	FyrAlaAsnIleLysAlaAlaLeuGluAspIleThrC	Qy
μ,	:::	Db .
206	187 PheTyrGlnSerSerGlnSerGlyGluThrSerAlaIleGlySerSerHisGlnLysThr	Qy

euAlaValGly 845 :::::	ProIleSerAspLysGlyTyrLeuThrGlyGlyGlnValLeu  +	829	Qy
ACGAAAGCGGCACGCTCGGT 2004	GAAAACTTCTACGGCGGCGGGCCTGGGTTCGGTGCGCGGATACGAAAGC	1945	DЬ
AspSerLe	LeuArgPhePheAlaGlyGlyAsp	809	Qy
9 0	GAAGTCGGCATTGCGGGCGGCTAC	9	Db *
20 C	GlvTleGlnAlaGlvTvr	79	0
CCCCTGAGCAAAACCTTCACGCTGATGCTCGGCGGC 1893	AlaHisGlnMetThrGly           ACCCACAACCAAACCTGGTTCTTC	785 1834	Qу Дъ
TACTCCGCC 1	GCCCTGCCTGGCAGCAAACTGCAATAC	9	Db
ату	AlaArgAlaGlyIleSerGlyValTyrSerPheGlyA	76	Qy
CGGGCGTGAACGCCGAAATC 1797		1774	ф
)AlaAsnMe	GlnArgTyrSerLeuGluValGlySerSerGlyLeuValSe	745	Qy
GGCCGACGCGCGGCTAC 1773		1717	Db
snProMetArgGlyTyrArg 744	ThrValAlaAspAsnLeuValAsn	731	Qy
CAAAGGCTGGCTGTACAAAGGT 1716	AAGAAATACGGCAAAACCGACGGCACAGACGGCAGCTTCAAA	1657	Db
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ValAspPheVal 713	LysThrGlnAlaProProGluThrTrpGlnAspLeuPro	697	Qy
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IleIleGlnAs	PheAspLeuSerThrArgThrLeuGluHisGluIleSe	662	Qy
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roLeuSerH	SerGluAspLysLysGlyValLysLeuTyrAlaThrLys	622	Qy
GCAAGTCGGCCGCACTGCGCGCC 1380	TCCGCAGGCGTTTCCCAAGACAACCTGTTCGGTACGG	1321	DЪ
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TTGG1	GGTTCCCTGGATTTGAGCGCGGGTTGGG	1270	Db
ľhr/	AspGlyGlnIleGlyLeuGlyTrpGly	584	ОУ
1269		1269	Db
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CTGACCGAACGTTCCACC 1269	GTCGATTTGAACATGAGTCTGACC	1234	Db
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Ser 54	LeuGlyArgIleSerAspAlaValS	524	Qy
  ACAATGTCCAG 1197		1147	ДЬ

Oy 150 GluValValValProProThrLeuGluProGluLysProGlyLeuIleLysArgLeuTyr 169   Db 1033 CGGAAAATCTACGTCAACGAAAACGCTGTAC 198   Db 163		136 AsnAspTyrIleProGluTyrGlnGlyGluGlnProAsnSer 149 :::	Oy 441    III	Gaps: 40 Db 919	No.: 2.29e-07	P 655 a 758 c 586 g 395 t Qy 381	Location/Qualifiers Qy 361 1.2394 2.70rganism="Neisseria meningitidis" Db 799 2.7db_xref="taxon:487"	Outer membrane vesicle (omv) vaccine comprising N. meningitidis Qy 341 serogroup b outer membrane proteins Patent: WO 0152885-A 10 26-JUL-2001; Db 739 Chiron Spa (IT)	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Qy 321 Neisseria. Neisseria to 2394) 1 (bases 1 to 2394) 1 (bases 1 to 2394) Db 679	AX202497.1 GI:15392217  .  Nelsseria meningitidis.  M Neisseria meningitidis  M Neisseria meningitidis	2394 bp DNA linear PAT 30-AUG-2001 Qy 290 LysAlaPheThrThrVa WOO152885. Db 583	908 PROIIELYSLEUHISPNEPHEILGLYTHEPROPHE 919  956 ATCCAACGCTTCCAACTCCGGCACGTTC 2391  Db 547		237  11	2176 AACAGCAGTTCCGCGACCGGCAGGGTTCAAAACATTTACGGCGCCGGCAATACCCAT 2235  871!vsGlvDhoThrAsnAsnThrivsTloGlvDlaGlvDalGlvDalGlvDalGlvDalAscTTDAlasor 889	2116 GTCCGCCTGAGCCTGTTTGCCGAGGCAGGCAGGCGGGCAAAACCTACGACGAC 2175  B70  Db 319	2056 AAAGCCAACGTCTCCGGAGCTGCTCTCCCGATGCCCGGCGCGAAAGACGCGCGCACC 2115  857 LeuargLeualavalpheGlvAspileGlvAspalaTyrasp	Db 2005 CCGAAAGTCTATGACGAATACGGCGAAAAAATCAGCTACGGCGGCAACAAA 2055
493 AsnLeuValAlaAlaLysAlaArgHisLeuTyrAspMetProAspAsp 508 :::    :::     :::	480		uProAlaGlnValAspGluSerThrLeu     :::::   GAAATÇAGCGTA	ASHMELVALASHTHICHLILEVALFREEFOGLUAFIGG-LIGHTH-H-H-H-H-H-H-H-H-H-H-H-H-H-H-H-H-H-H	401 AlaTyrAsnLeuGlnAlaValArgAlaLeuSerAsnAspLeuIleAlaThrArgTyrPhe 420	ASPLYSLeuProValLySArgGluLeuLeuGluGlnLeuLeuThrValAsnMetGlyGlu 400     :::       :::         :::       :::	361 PheAspGluValValPhePheThrIleAspProLysThrAsnGlnLeuThrThrAspPro 380 ::: ::    :::   :::	IleLeuProAspAsnThrAlaAspValSerLeuIleTyrAspThrGlyThrGlnTyrArg 360 :::	ASNALASERALAGIUHISGIYTYRPheASPGIYARGTIPLeUASPARGSERVALASPVAL 340 ::: GACTTCTACCAGAACAACGGCTACTTCGATTTCCGCATCCTCGATACCGGACATCCAAACC 738	PheHisHisGlyLysTyrGluThrLysLysAsnLeuIleGlu 320	LysalaPheThrThrValalaAspGluValProLeuLeuIleGlyAspVal 306	GlyGluProValTyrIleAspTyrargAlaValGluValArgGlyGluGlyAlaAspAsp 289	IleAspLeuSerIleIleArgAsnSerIleGlyGluValAspValIleIleHisAspLeu 269        :::::	GCCAAACTCAATATCCAAATCACGCCCAAAGTAACCAAACTCGCCGGCAACCGCGTCGAC 489	225 MetAspLeuAsnGlySerlleProArgLeuArgGln	GluProTyrAlaAsnIleLysAlaAlaLeuGluAspIleThrGlnGluSerAla 224 :::	187 PheTyrGinSerGerGinSerGlyGluThrSerAlaIleGlySerSerHisGlnLysThr 206 :::     :::	

36066	GCGG	194	В
AlaGlyGlyAspGlnSerIleArgGlyTyrAlaHisAsp	^laG]	808	Qy
:::   ::: 	   GAAGTCGGCATTGCGG	189	дь
eAsnHisValProTyrArg 8	:	791	Q
	ACCCAC	1834	DЬ
NMetThrGly 790	Si	78	γo
GGCAGCAAACTGCAATACTACTCCGCC 1833	GCCCTGCCCGGC	1798	Вb
IleSerGlyV	AlaArgAlaGlyIleSerG	765	Qy
CTGACGGGCGTGAACGCCGAAATC 1797	4	1774	B
SerLeuGluValGlySerSerGlyLeuValSe	GlnArgTyrSer	745	Qy
TGGGGGCGCAACAAAACCGACAGCGCGTTATGGCCGACGCGCGCG	ACCGTCGGCT	1717	Db
- S	- }	73:	Qy
SGCAAAAACCGACGGCACAGACGGCAGCTTCAAAGGCTGGCT	7 AAGAAATACGGCAAAACCG	165	В
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AlaProProGluThrTrpGlnAspLeuProValAspPheVal 713		697	Qy
		1537	망
ArgThrTyrSerLeuArgTyrArgLeuAspLysLeu 696	2 GlyTrpAsnArg	683	Qy
CGCAAAGCATCGACCATCAAACAATATAAAACCACCACGGCAGGC 1536	9 CGCAAAGCATCGACCAGCA	1489	В
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1269	1	1269	Дb
GlnSerLysLysValProLeuTyrValPheValAlaSerAspLysProArg 583	AspValTyrGlnSe	564	Q
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ValIleAspLeuProGlu	GluAsnGluVa	544	Qy
		1198	Db
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AAAGAGCGCGTCGAGCTTTTGGGCTACTTCGACAACGTACAG 1197	CAACGCTCC	1147	В
g	1	509	Qy
GTCGTGCGCCGCGAATTGCGCCAAATGGAATCCGCGCCTTACGACACCTCCAAGCTG 1146	;	1090	Db

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	ATURES	FEA.
Direct://. Direct/o.c.  Direct:// Submission Submitted (17-MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA	TITLE JOURNAL	u
Tettelin.H., Saunders,N.J., Heldelberg,J., Jeffries,A.C., Nelson,K.E., Elsen,J.A., Ketchum,K.A., Hood,D.W., Peden,J.F., Dodson,R.J., Nelson,W.C., Gwinn,M.L., DeBoy,R., Peterson,J.D., Hickey,E.K., Haft,D.H., Salzberg,S.L., White,O., Fleischmann,R.D. Dougherty,B.A., Mason,T., Ciecko,A., Parksey,D.S., Blair,E., Cittone,H., Clark,E.B., Cotton,M.D., Utterback,T.R., Khouri,H., Qin,H., Vamathevan,J., Gill,J., Scarlato,V., Masignani,V., Qin,H., Grandi,G., Sun,L., Smith,H.O., Fraser,C.M., Moxon,E.R.	AUTHORS	Ą
Science 287 (5459), 1809-1815 (2000) 20175755 10710307 2 (bases 1 to 13538)		J( Mi 1 REF1
l (bases 1 to 13538)  I (bases 1 to 13538)  Tettelin, H., Saunders, N.J., Heidelberg, J., Jeffries, A.C., Nelson, K.E., Elsen, J.A., Ketchum, K.A., Hood, D.W., Peden, J.F., Dodson, R.J., Nelson, W.C., Gwinn, M.L., DeBoy, R., Peterson, J.D., Hickey, E.K., Haft, D.H., Salzberg, S.L., White, O., Fleischmann, R.D. Dougherty, B.A., Mason, T., Ciecko, A., Parksey, D.S., Blair, E., Cittone, H., Clark, E.B., Cotton, M.D., Utterback, T.R., Khouri, H., Qin, H., Vamathevan, J., Gill, J., Scarlato, V., Masignani, V., Pizza, M., Grandi, G., Sun, L., Smith, H.O., Fraser, C.M., Moxon, E.R., Rappuoli, R. and Venter, J.C.  Complete genome sequence of Neisseria meningitidis serogroup B strain MCS8	REFERENCE AUTHORS TITLE	REF AI
AE002375 AE002098 AE002375.1 GI:7225394  Neisseria meningitidis MC58. Neisseria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.		ACCI VER: KEYI SOUI
E002375 . 13538 bp DNA linear BCT 25-MAY-2000 Weisseria meningitidis serogroup B strain MC58 section 17 of 206 of	T 33 375/c ITION	RESUL AE002 LOCUS DEFIN
TOIleLysLeuHisPhePheIleGlyThrProPhe 919 	908 ProI 2356 ATCC	Qу
ProValGlyGlnValArgValAspValAlaThrGlyValLysGluGluGlyAsn 907    :::    :::::     	890 Pr 11 2296 CC	Оy
LysGlyPheThrAsnAspThrLysIleGlyAlaGlyValGlyValArgTrpAlaSer 889	871 2236 A	Qу
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870	870	Qy
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ProlleSerAspLysGlyTyrLeuThrGlyGlyGlnValLeuAlaValGly	829 Pro 111 2005 CCG	Оy

gene

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CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"similar to GB:L02948 SP:P29011 PID:145703 GB:U00096 PID:1651591 percent identity: 76.98; identified by sequence similarity; putative"
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Glimmer2; putative"
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                                                                                                                                                                                                                                                                                                                       AGNTHKSTFTNELRYSAGGAYTWLSPLGPMKFSYAYPLKKKPEDEIQRFQFQLGTTF"
                                                                                                                                                                                                                                                                                                  complement(8645. .9985)
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                                                                     /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(6195. .8588)
/gene="NMB0182"
                                                                                                    codon_start=1
                                                                                                                                                                                                        'gene="NMB0183"
                                                                                                                                                                                                                                                                          /gene="NMB0183"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similar to GP:2460281 percent identity: 99.87; identified by sequence similarity; putative"
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/gene="NMB0182"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="mtrltrafaaalIGLCCTAGAHADTFQKIGFINTERIYLESKOARKIQKTLDSEFSARQDELQKLQREGLDLERQLAEGKLRNAKKAQAEEKWRGLVAAFRK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to GB:M34854
identity: 46.88; identified
putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAF40637.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /transl_table=11
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by sequence similarity;
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Percent Similarity:
Best Local Similarity:
Query Match:
DB: US-09-914-168-2 (1-919) x AE002375 (1-13538) Alignment Scores: Pred. No.: Score: 8543 TCGCCTTTGGCACTTGCCGACTTCACCATCCAAGACATCCGCGTCGAAGGCTTGCAGCGT 8484 116 ThrProLeuSerLeuGluGluLeuPheAlaGlnGluSerThrGluMetGlyIleAsnPro 135 TTTAATCAGGCGACACTCAATCAGGCAGTCGCCGGCCTGAAAGAAGAATACCTCGGGCGC MetAsp------LeuAsnGlySerIleProArgLeuArgGln-------GACGCC-----ATTAAGAAAAACCTCGAATCGTTCGGGCTGGCGCAGTCGCAATAC GTTATCGAACGCCCCACCATCGGCTCGCTCAACATCACCGGCGCAAAAATGCTGCAAAAC GluValValValProProThrLeuGluProGluLysProGlyLeuIleLysArgLeuTyr 169 ACCGAGCCGAGTACCGTATTCAACTACCTGCCCGTCAAAGTCGGCGACACCTACAAC---AsnAsp-----TyrIleProGluTyrGlnGlyGluGlnProAsnSer 149 GluProTyrAlaAsnIleLysAlaAlaLeuGluAsp-----IleThrGlnGluSerAla PheTyrGlnSerSerGlnSerGlyGluThrSerAlaIleGlySerSerHisGlnLysThr 206 AlaargLeuPheAsnAspGlyValAsnLysValPro-----ArgLeuLysAlaLys 186 ------GACACACGGCAGTGCCATCAACAAAGCCTGTAC GCCACCGGTTTCTTTGACGACGTACGCGTCGAAACTGCGGACGGGCAGCTCCTGCTGACC -----ThrAlaLeuValAlaAlaArgAlaValGlyTyrTyrAsp /translation="MHTLLAFIFAILILVSLHEFGHYIVARLCGVKVVRFSVGFGKPFFTKRRGDTEWCLAPIFLGGYVKMVDFREGEVSEADLDYAFDKOHDAKRIAIVAAGPLTNLALAVLLYGLSFSFGVTELRPYVGTVEPDTIAARAGFQSGDKIQSVKGTPVADWGSAQTEIVLNLEAGKVAVUCVOTASGAQTVETIDAAGTPEAGKIAKNOGYIGLMPFKITTVAGCVEKGSPAEKAGLKFGDRLTAADGKPIASWOBWANLTRQSPCKKITLNYERAGQTHTADIRPDTVEQSDHTLIGRYGLRPQPDRAWDAQIRRSYRPSVVRAFGMGWEKTVSHSWT TLREFGKLISGNASVSHISGBLTIADIAGQSAELGLQSYLEFLALVSISLGVLNLLPV
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Matches:
Conservative:
Mismatches:
Indels: .11204) Gaps: 249 8160 8220 8427 8331 8391 236 224

G1y 681      GGC 7053	662 PheAspLeuSerThrArgThrLeuGluHisGluIleSerArgSerIleIledinAsnGly	Фу	
ly 661 CG 7101	642 AspGlnLeuArgAlaThrLeuGlyTyrGlnGlnGlnValPheGlyHisSerThrAsnGly :::          :::   :::    7154 ACGGCAGGGGGTCAGCCTGGGCTACGATGTTTACGGAAAAGCCTTCGACCCG	Qy Db	
sn 641 TC 7155	622 SerGluAspLysLysGlyValLysLeuTyrAlaThrLysProLeuSerHisProLeuAsn	Qy	
eu 621 CC 7209	602 LysPheGluHisAsnLeuIleAsnArgAspGlyTyrGlnAlaGlyAlaGluLeuArgLeu	Оу	
hr 601 TG 7269	584 AspGlyGlnIleGlyLeuGlyTrpGlySerAspThrGlyThrArgLeuValThr	Qy Db	
7320	7320	Db	
cn ·	564	Qy	·
la 563 7320	544 GluAsnGluVallleAspLeuProGluArgThrAlaLeuAlaAsnArgLysThrProAla :::       :::	Qy Db	
er 543 7356	524 LeuGIYAT9IIeSerAspAlaValSerAlaValAlaArgAlaIieLeuProAspGluSer	Db Qy	
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TG 7443	7499GTCGTCCGCCGTGAATTACGCCAAATGGAATCCGCACCTTACGACACCTCCAAGCTG	Db	
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	461 GluProValIleGluThrValGluLeuThrAspGlvTleLeuMetAs	0	
eu 460 :: TA 7617	441 SerPheGluGlnSerSerSerSerArgThrGluProAlaGlnValAspGluSerThrLeu	Db Oy	
GC 7650	7670GAGATTCAGAACCGCATGGGC	Db	
al 440	421 AsnMetValAsnThrGluIleValPheProGluArgGluGlnIleGlnAsnAspGlnVz	Qy	
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	7754GTCCCCAAAGCCGAACTGGAAAAACTGCTGAACCATGAAGCCCGGCAAA	Db	•
	381	O <sub>V</sub>	
ro 380 7755	361 PheAspGluvalValPhePheThrIleAspProLysThrAsnGlnLeuThrThrAspPro ::::::   ::::   :::: 7790 TGGGGGAAAGTCTCCATGAAGGCGACACCAACGA	Db	
GT 7791	7850 AACGAAGACAAAACCAAGCAGACCATCAAAATCACCGTCCACGAAGGCGGACGTTTCCGT	Db	
rg 360	341 IleLeuProAspAsnThrAlaAspValSerLeuIleTyrAspThrGlyThrGlnTyrArg	Qy	
CC 7851	7910 GACTICTACCAAAATAACGGCTACTICGATITCCGTATCCTCGATACCGACATCCAAACC	Db	

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321

AsnalaSeralaGluHisGlyTyrPheAspGlyArgTrpLeuAspArgSerValAspVal 340

CTGACACGAAGCAACCAATTCAACGAGCAGAAATTTGCCCCAAGATATGGAAAAAAGTAACC

--PheHisHisGlyLysTyrGluThrLysLysAsnLeuIleGlu

8006

290

LysAlaPheThrThrValAlaAspGluValProLeuLeuIleGlyAspVal------

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7971

306

8042

GGCAACCAAGTCTATTCCGACCGCAAACTGATGCGG-----

8007

289 8043 269 8100

ATCGACATCACGATTGACGAGGGCAAATCCGCCAAAATCACCGACATCGAATTTGAA----

270

8099

8159

GGCAAACTCAATATCCAAATCACGCCCAAAGTAACCAAACTCGCCCGCAACCGCGTCGAC

IleAspLeuSerIleIleArgAsnSerIleGlyGluValAspValIleIleHisAspLeu

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                                                                                                                                                   ProlleLysLeuHisPhePheIleGlyThrProPhe 919
                                                                                                                                                                                                     ProvalGlyGlnValArgValAspValAlaThrGlyValLySGlu-----GluGlyAsn
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                                                                                                                                                                                                                                                                                      AACAGCAGTTCCGCGACCGGCGGCAGGGTTCAAAACATTTACGGCGCCGGCAATACCCAT
                                                                                                                                                                                                                                                                                                                                          GTCCGCCTGAGCCTGTTTGCCGACGCAGGCAGCGTGTGGGACGGCAAAACCTACGACGAC
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                                                                                                                                                                             CCTTTAGGCCCGATGAAATTCAGCTACGCCTACCCGCTGAAGAAAAAACCGGAAGACGAA
                                                                                                                                                                                                                                                                                                                                                                                                                          ThrAlaGluTyrAsnTyrGluPheMet-----
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                      misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (30-MAR-2000) Submitted on behalf of the Neisseria sequencing team, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: parkhill@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Details of N. meningitidis sequencing at the Sanger Centre available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Parkhill, J., Achtman, M., James, K.D., Bentley, S.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Parkhill, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 404 (6777), 502-506 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.sanger.ac.uk/Projects/N_meningitidis/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="NMA0002, nuoL, NADH dehydrogenase I chain L, len: 674 aa; similar to many e.g. NUOL_RHOCA NADH dehydrogenase I chain L (EC 1.6.5.3) (700 aa). Contains Pfam match to entry PF00361 oxidored_q1, NADH-Ubiquinone/plastoquinone (complex I), various chains, and to entry PF00662
                                                                                                                                                                    YFKRPSATFANLKAFLINRVGDEGFLLGIGLVLAYFGGSLRYQDVFAYLPNVQNATIQ
LFPGVEWSLITVTCLLLFVGAMGKSAQFPLHVWLPDSMEGPTPISALIHAATMVTAGL
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HIYTIGYMHDEKVGYQRFESYISLETFSMLMLIMSNNFIQLFFGWEAVGLVSYLLIGF
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/db_xref="GI:7378780"
                                                                                                                                                                                                                                                                                                                                                                                                                               oxidored\_q\hat{1}\_N, NADH-Ubiquinone oxidoreductase chain 5 N-terminus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(414. .2438)
/gene="nuoL"
complement(414. .2438)
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/note="NNA"
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complement/^^
                      NGIVNGSARLVGAVAAQVRKVQTGFIYTYAAAMVFGVLVLLGMTFWGLFR
1035. .1044
                                                                                                        LIGNLSLIGTPFFSGFYSKDSIIEAAKYSTLPGSGFAYFAVLASVFVTAFYAFRQYFM
VFHGEEKWRSLPEHHSDGHGEEHHGLGKNDNPHESPLVVTLPLILLAVPSVIIGYIAI
                                                                                                                                                ALGASAYSVAMFHVMTHAFFKALLFLAAGSAIIGMHHDQDMRHMGNLKKYMPITWLTM
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                                                                                    EPMLYGDFFKDV1FVNADAHPTMH1MKEEFHGALAMVSHSLHSPVLYLA1AGVLSAWL
                                                                                                                                                                                                                                                                                                                                                                                     /transl_table=11
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/EC_number="1.6.5.3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="SPTREMBL:Q9JX93"
/translation="MSNTQTIRSADFTTSRAWGALDIANMNGTTVRLHWTDQPYKWHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
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DNA uptake sequence:
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                                                                                                                                                                                                                          note-"NMA0005, nuoK, NADH dehydrogenase I chain K, len: 101 aa; simlar to many e.g. NUOK_RHOCA NADH dehydrogenase I chain K (EC 1.6.5.3) (102 aa), fasta scores; E(): 1.1e-24; 65.0% identity in 100 aa overlap. Contains Pfammatch to entry PF00420 oxidored_q2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(2833..2837)
complement(2952..3527)
/gene="NMA0004"
complement(2952..3527)
/gene="NMA0004"
                                                                                                    /product="NADH dehydrogenase
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/db_xref="GI:7378783"
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/gene="nuoK"
/EC_number="1.6.5.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-*NHA004, unknown, len: 191 aa; similar to hypothetical proteins e.g. Y977_HAEIN HI0977 (191 aa), fasta scores; E(): 0; 80.5% identity in 190 aa overlap, and to proteins involved in cell cycle e.g. TR:054679 (EMBL.AF036487) Lactococcus lactis plasmid pNZ4000 putative mobilization protein (200 aa), fasta scores; E(): 0, 55.1% identity in 167 aa overlap, and FIC_ECOLI cell filamentation protein FIC (200 aa), fasta scores; E(): 0.093, 29.4% identity in 126 aa overlap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(2487. .2828)
/gene="NMA0003"
complement(2487. .2828)
/gene="NMA0003"
/note="NMA0003, unknown, 1
                                                                                                                                                                                                         NADH-ubiquinone/plastoquinone oxidoreductase chain 4L"
                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="nuoK"
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                                                                            'db_xref="SPTREMBL:Q9JQU9"
                                                                                                                                                                                           /codon_start-1
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MNIAHPFLEGNGRSTRIWLDLVLKKNLKKVVNWQNVSKTLYLQAMERSPVNDLELRFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label-DUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Core DNA uptake sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref~"SPTREMBL:Q9JQR9"
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/transl_table=11
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Eaadkil570ebkTqtgftelil5gggvhalkysmeyivlokpmcdlfteeqlavark
Rlervgfvspk*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="hypothetical protein NMA0003"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Pfam match to entry Pr00662 oxidored_q1_N, NADH-Ubiquinone oxidoreductase (complex I), chain N-terminus, score 77.20, E-value 3.5e-19"
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DB:
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CDS

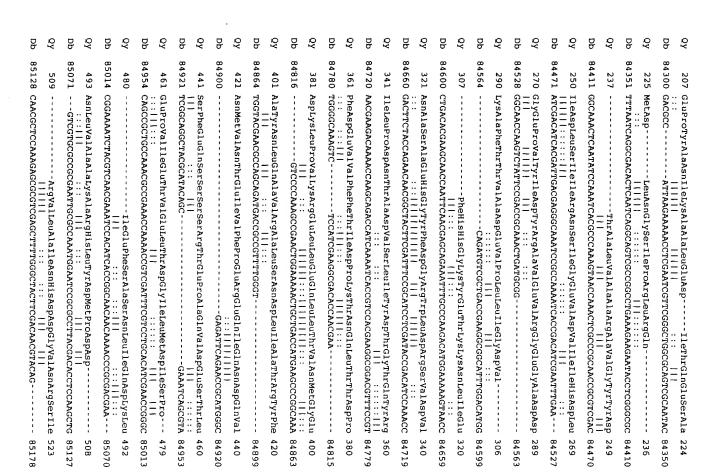
CDS gene

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US-09-914-168-2 (1-919) x NMA1Z2491 (1-340806)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
84240 GTTATCGAACGCCCCACCATCGGCTCGCTCAACATCACCGGCGCAAAAATGCTGCAAAAC 84299
                                                                                                                                                                                                                                                                                                     84087 ACCGAGCCGAGTACCGTATTCAACTACCTGCCCGTCAAAGTCGGCGACACCTACAAC---
                                               187 PheTyrGlnSerSerGlnSerGlyGluThrSerAlaIleGlySerSerHisGlnLysThr 206
                                                                                                                                                                                                                                                                                                                                                                     136 AsnAsp---
                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 ThrProLeuSerLeuGluGluLeuPheAlaGlnGluSerThrGluMetGlyIleAsnPro 135
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                                                                                                                                              AlaArgLeuPheAsnAspGlyValAsnLysValPro
                                                                                                                                                                                                                                   GluValValProProThrLeuGluProGluLysProGlyLeuTleLysArgLeuTyr 169
                                                                                                                                                                                                                                                                                                                                                                                                    TCGCCTTTGGCACTTGCCCACCTTCACCATCCAAGACATCCGCGTCGAAGGCTTGCAGCGT 84086
                                                                                                 GCCACCGGTTTCTTTGACGACGTACGCGTCGAAACTGCGGGACGGGCAGCTCCTGCTGACC 84239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"Pfam match to entry PF00499 oxidored_q3, NADH-ubiquinone/plastoquinone oxidoreductase chain score 77.90, E-value 2e-19" complement(4570, .5277)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(3874. .3879)
/gene="nuoJ"
complement(4034. .4525)
/gene="nuoJ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(4570. .5277)
/gene="NMA0007"
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NADH-ubiquinone/plastoquinone oxidoreductase chain 6"
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/gene="nuoJ"
complement(3863..4534)
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259.00
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Tue May

6 09:37:16 2003



584 AspGlyGlnIleGlyLeuGlyTrpGlySerAspThrGlyThrArgLeuValThr

US-09-914 OY 116 Db 180761 OY 136 Db 180701	Alignment Sco Pred. No.: Score: Percent Simil Best Local S: Query Match: DB:	BASE COUNT	FEATURES Sour	SOURCE ORGANISM REFERENCE	RESULT 36 AX043922/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS	Oy 908	Db 86277	Оу 890	Qy 871 Db 86217	Db 86157	Оу 870	Oy 857 Db 86097	Db 86037
-168-2 (1-919) x AX043922 (1-349980)  ThrProLeuSerLeuGluGuLeuPheAlaGlnGluSerThrGluMetGlyIleAsnPro 135 :::      :::    TCGCCTTTGGCACTTGCCACTTCACCATCCAAGACATCCGCGTCGAAGGCTTGCAGCGT 180702  ASnAspTyrIleProGluTyrGlnGlyGluGlnProAsnSer 149 :::	t'Scores: 0.000164 Length: 349980 .: 259.00 Matches: 191 Similarity: 33.48% Conservative: 121 al Similarity: 20.49% Mismatches: 342 atch: 5.48% Indels: 278 Gaps: 40	/organism related mentily truth /organism related mentily truth / organism related mentily truth / organism related mentily truth / organism related mentily for the following related mentiles and the following related mentiles are related mentiles and seen related mentiles and seen related mentiles are related mentiles and seen		Neisseria meningitidis.  Neisseria meningitidis  Bacteria; Proteobacteria; beta subdivision; Nei  Neisseria.  1 (bases 1 to 349980)	AX043922 349980 bp DNA linear PAT 24-NOV-2000 N Sequence 1 from Patent WO0066791. AX043922 AX043922.1 GI:11342850	ProlleLysLeuHisPhePheIleGlyThrProPhe 919 :::         :::	CCTTTAGGCCCGATGAAATTCAGCTACGCCTACCCGCTGAAGAAAAAACCGGAAGACGAA 86336	ProvalGlyGlnValArgValAspValAlaThrGlyValLysGluGluGlyAsn 907	LysGlyPheThrAsnAspThrLysIleGlyAlaGlyValGlyValArgTrpAlaSer 889	AACAGCAGTTCCGCGACCGGCGGCAGGGTTCAAAACATTTACGGCGCCGGCAATACCCCAT 86216	870	LeuArgLeuAlaValPheGlyAspIleGlyAsnAlaTyrAsp	

492	Araba er Alaser Asa Leu IleGln AspLysLeu	480	Qγ
179775	CAGCCGCTGCCGAACGCTGAAACCAAAACCGTCGATTTCGTCCTGCACATCGAACCGGGC	179834	Db
479	luProValIleGluThrValGluLeuThrAspGlyIleLeuMetAspIleS	461	Qy
460 179835	SerPheGluGlnSerSerSerArgThrGluProAlaGlnValAspGluSerThrLeu	441 179867	Qy Db
179868	GAGATTCAGAACCGCATGGGC	179888	Db
440	lnIleGlnAs	421	Qy
179889	ATATYTASTLEUGITALAVALAIGALBLEUSETASTASTLEULIEALBITTAIGTYTPHE	179924	Db 42
179925		7 0	Db C3
380 179 <b>97</b> 3	easpGluValValPhePhePhrIleAspProLysThrAsnGlnLeuThrThrAspP 	361 180008	B 84
360 180009	IleLeuProAspAsnThrAlaAspValSerLeuIleTyrAspThrGlyThrGlnTyrArg ::: :!         :::::   AACGAAGACAAAACCAAGCAGACCATCAAAATCACCGTCCACGAAGGCGGACGTTTCCGT	341 180068	Оy
340 180069	ASHALASERALAGIUHISGIYTYRPheASPGIYARGTTRLEUASPARGSERVALASPVal::: :::	321 180128	Db Qy
320 180129	PheHisHisGlyLysTyrGluThrLysLysAsnLeuIleGlu	307 180188	D Qy
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289 180225	GlyGluProValTyrIleAspTyrArgAlaValGluValArgGlyGluGlyAlaAspAsp	270 180260	Qу
269 180261	IleAspLeuSerIleIleArgAsnSerIleGlyGluValAspValIleIleHisAspLeu	250 180317	рь
249 180318		237 180377	Оу
236 180378	MetAspLeuAsnGlySerIleProArgLeuArgGln	225 180437	Оу
224 180438	GluProTyrAlaAsnIleLysAlaAlaLeuGluAspIleThrGlnGluSerAla:::	207 180488	Дb
206 180489	PheTyrGlnSerSerGlnSerGlyGluThrSerAlaIleGlySerSerHisGlnLysThr:::	187 180548	Qy Db
186 180549	AlaArgLeuPheAsnAspGlyValAsnLysValProArgLeuLysAlaLys	170 180608	Db Qy
180609	GIUVAIVAIVAIPTOPTOTRI LEUGIUPTOGIULYSPTOGIYLEUITELYSAIGLEUTYI ::: ::	180644	Db 49

·	DS	FEATURES	E &	JOURNAL REFERENCE	REFERENCE AUTHORS TITLE	SOURCE	ACCESSION VERSION KEYWORDS	RESULT 37 AF461795 LOCUS DEFINITION	Db 178451 /	Qy 908 I	Qy 890 I Db 178511 (	Db 178571 /	178631	Qу 870	Qy 857 I Db 178691 (	Qy 846 : Db 178751 /	Qy 829 I Db 178802 (	Db 178862 (	178913
note code from from from from from from from from	/or /db 53.	ourg D-79104, Germany	,K., Scha Institut	Unpublished 2 (bases 1 to 6444)	l (bases 1 to 6444)  Zimmermann,R., Augustin,K., Schaal,K. and Sander,A.  Cloning, nucleotide sequencing, and expression of a hemin-binding	~ (D (D (D	5	6444 bp DNA linear nenselae Omp89 (omp89), LyxD (lyxD), F	ATCCAACGCTTCCAACTCGGCACGACGTTC 178416	ProIleLysLeuHisPhePheIleGlyThrProPhe 919	ProValGlyGlnValArgValAspValAiaThrGlyValLysGluGluGlyAsn 907    :::    ::::::	AAATCCACCTTTACCAACGAATTGCGCTATTCCGCCGGCGCGCGC	ACAGCAGTTCCGCCGACCGGCGGCAGGGTTCAAAACATTTACGGCGCCCGGCAATACCCCAT 17	870	LeuArgLeuAlaValPheGlyAspIleGlyAsnAlaTyrAsp	ThrAlaGluTyrAsnTyrGluPheMet	ProlleSerAspLysGlyTyrLeuThrGlyGlyGlnValLeuAlaValGly	LEUAL PHEFHEALTGLYGLYASPOLITSELLEATGCLYTYLIAH ISASPSELLEGGET 828	CGGCAGAACCAAAGAAATCCCCTTCTTT 17

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influenzae bacterial surface antigen AG15"
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/bound_moiety⇔"Fur"
1335. .3731
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Percent Similarity:
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                                                                                                                                                                     AspLeuGlyGluProValTyrIleAspTyrArgAlaValGluValArgGlyGluGlyAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGAGGGTTATTGCCCCAACAACAGCCTTTGTATCAATTGCTATGGTTGAAGAAGTGCAA 1445
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TTTGGGAGTAGCCGTTTACGTGATGTGATTTCAACAAAGCCTTCAGGAATACTTTCGTTA 1991
                                                                                                                                                                                                                                                                                                       AspIleAspLeuSerIleIleArgAsnSerIleGlyGluValAspVal----IleIleHis
                                                                                                                                                                                                                                                                                                                                                                   GCTGATGTTAATGTGATTCGTGAA-------GCTTATAAAAACTGTTGGTCGTAAT 1811
                                                                                                                                                                                                                                                                                                                                                                                                                            GlySerTleProArgLeuArgGlnThrAlaLeuValAlaAlaArgAlaValGlyTyrTyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AATAAATCTCTTAAAGATCCTGATCTTAAACGGTTTATTTCTTTAAAACCCAATGAGCCC 1742
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                                                                                                                        AATATTGTTGAAGGTCGCAGGACAAAGATTAGCAATATCACTTTTAAGGGGAATCACGCT
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                                                            ·AspAspLysAlaPheThrThrValAlaAspGluValPro··-
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DEADALLYKYEHCELSIVELARLVKILKAAEICNIVLAGGVKRRPLLKQ"
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VRVGHHAFIGGVSALVGDLIPYGTAVGVQAKLAGLNIIGMKRAGLERKDIHALRHAVA
MLFDHSKPFKERVSDVASFYPASQSVVDVVNFIKEKGKRFYCTPKFEGDRIKENKD"
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[leLeuProAspAsnT SATGAAGCGCGTAATG PheAspGluValValF ATTGGTGATGTT	SerAl	IleGly
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ANGCGCGTAATGCTTATGAAAT  ANGCGCGTAATGCTTATGAAAT  ANGCGCGTAATGCTTATGAAAT  ANGCGCGTAATGCTTATGAAAT  ANGCGCGTAATGCTTATGAAAT  ANGCGCGTAATGCTTATGAAAT  ANGCGCGTAATGTTT	SGLYLY TGGTTA	LPheHi:  :::  TATAG
IleLeuProAspAsnThrAlaAspvalians [] GATGAAGCGCGTAATTGAATTGAATTGAATTGAAGCGCGTAATGAATTGAATTGAATTGAATTGAAGCGCGTAATGGTTATTGAAATTGAATTGAAATTGAAATTGAAATTGAAAGTTGAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTTGAAAAATTGAAAATTGAAAATTGAAAAATTTGAAAAATTTGAAAAATTTGAAAAATTTGAAAAATTTGAAAAATTTGAAAAATTTGAAAAATTTGAAAAATTTGAAAAATTTGAAAAATTTGAAAAATTTGAAAAAA	TGCAG	sHisGl TGAGGA
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RESULT 38  AF021245  AF021245  LOCUS  DEFINITION  Complete cds.  ACCESSION  AF021245  AF021245	Db 3506 ATTATTTGCGGATGTTGCAACGCTTTGCATGTTGCTTGCT	810 ArgPhe-PheAlaGlyGlyAspGlnSerI	Db 3249	0 A 1 3 V 3 V 3 V 3 V 3 V 3 V 3 V 3 V 3 V 3	Db 2889 CGACAGACGGTGGATCACTTCGGTTTGCGGTACCATTAATGACAGTTATCTGCTAAT 2  648 LeuGlyTyrGingingluvalpheglyHisSerThrAsnglyPheAsp (
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                                                                            GluValValValProProThrLeuGluProGluLysProGlyLeuIleLysArgLeuTyr
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Submitted (27-AUG-1997) Division of Biological Sciences, University
of Montana. HS 104, Missoula, MT 59812-1002, USA
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Manning,D.S., Reschke,D.K. and Judd,R.C.
Cmp85 proteins of Neisseria gonorrhoeae and Neisseria meningitidis
are similar to Haemophilus influenzae D-15-Ag and Pasteurella
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Manning, D.S., Reschk
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VDFVLHIEPGRKIYVNEIHITGINKTROEVVRRELRQMESAPYDTSKLQRSKERVELL
GYFDNVQFDAVPLAGTPDKVDLMSLTERSTGSLDLSAGMVQDTGLVMSAGVSQDNLF
GTGKSAALRASRSKTTLMGSLSFTDPYETADGYSLDLSGYDYYGKAFDPRKASTSIKQYKT
TTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHYADFIKYYGKTDGTDGSFK
GMLYKGTYGMGRRKTDSALMPTRGYLTGVNAEIALPGSKLQYYSATHNQTWFFELSKT
FTLMLGGEVGLAGGYGRYKEIPFFENYFGGLGSVRGYESGTLGFKVYBEYGRKISYG
GNKKANVSAELLFPMPGAKDARTVRLSFADAGSVWDCKTYDDNSSSATGGRVQNIYG
GNKKANVSAELLFPMPGAKDARTVRLSFADAGSVWDCKTYDDNSSSATGGRVQNIYG
AGNTHKSTFTNELFYSAGGAVTWLSPLGPMKFRYAYPLKKKPEDEIQRFQFQLGTTF"
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RVDIDITIDEGKSAKITDIEFEGNQVYSDRKLMRQMSLTEGGIWTWLTRSNQFNEQKF
AQDMEKVTDFYQNNGYFDFRILDTDIQTNEDKTKQTIKITVHEGGRFRWGKVSIEGDT
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/translation-"MKLKQIASALMMLGISPLAFADFQLLLTVIERPTIGSLNITGAK
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Location/Qualifiers
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/strain="HH"
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/transl_table-11
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AsnLeuValAlaAlaLysAlaArgHisLeuTyrAspMetProAspAsp---
                                                          CGGAAAATCTACGTCAACGAAATCCACATCACCGGCAACAACAAAAACCCGGGGAA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlyGluProValTyrIleAspTyrArgAlaValGluValArgGlyGluGlyAlaAspAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GluProTyrAlaAsnIleLysAlaAlaLeuGluAsp-----IleThrGlnGluSerAla ::: ||||
                                                                                                                                      CAGCCGCTGCCAAACGCCGAAACCAAAACCGTCGATTTCGTCCTGCACATCGAACCGGGC
                                                                                                                                                                          GluProValIleGluThrValGluLeuThrAspGlyIleLeuMetAspIleSerPro---
                                                                                                                                                                                                                                                      SerPheGluGlnSerSerSerArgThrGluProAlaGlnValAspGluSerThrLeu
                                                                                                                                                                                                                                                                                                                                                                          TGGTACGAACGCCAGCAGATGACCGCCGTTTTGGGT---------
                                                                                                                                                                                                                                                                                                                                                                                                            AlaTyrAsnLeuGlnAlaValArgAlaLeuSerAsnAspLeuIleAlaThrArgTyrPhe 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AspLysLeuProValLysArgGluLeuLeuGluGlnLeuLeuThrValAsnMetGlyGlu 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PheAspGluValValPhePheThrIleAspProLysThrAsnGlnLeuThrThrAspPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IleLeuProAspAsnThrAlaAspValSerLeuIleTyrAspThrGlyThrGlnTyrArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGACACGAAGCAACCAATTCAACGAGCAGAAATTTGCCCCAAGACATGGAAAAAGTAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----PheHisHisGlyLysTyrGluThrLysLysAsnLeuIleGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LysalaPheThrThrValAlaAspGluValProLeuLleuIleGlyAspVal------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGCAACCAAGTCTATTCCGACCGCAAACTGATGCGG--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATCGACATCACGATTGACGAGGGCAAATCCGCCAAAATCACCGACATCGAATTTGAA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IleAspLeuSerIleIleArgAsnSerIleGlyGluValAspValIleIleHisAspLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCAAACTCAATATCCAAATCACGCCCAAAGTAACCAAACTCGCCCGCAACCGCGTCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTTAATCAGGCGACACTCAATCAGGCAGTCGCCGGCCTGAAAGAAGAATACCTCGGGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MetAsp-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PheTyrGlnSerSerGlnSerGlyGluThrSerAlaIleGlySerSerHisGlnLysThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCGGCAGGCTACGCATACAGC-------GAAATCAGCGTA
                                                                                                                                                                                                                                                                                                                                  AsnMetValAsnThrGluIleValPheProGluArgGluGlnIleGlnAsnAspGlnVal 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGGGCAAAGTC----TCCATCGAAGGCGACACCAACGAA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AACGAAGACAAAACCAAGCAGACCATCAAAATCACCGTCCACGAAGGCGGACGTTTCCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AsnAlaSerAlaGluHisGlyTyrPheAspGlyArgTrpLeuAspArgSerValAspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTTATCGAACGCCCCACCATCGGCTCGCTCAACATCACCGGCGCAAAAATGCTGCAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                     -GTCCCCAAAGCCGAACTGGAAAAACTGCTGACCATGAAGCCCGGCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -LeuAsnGlySerIleProArgLeuArgGln------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTAAGAAAAACCTCGAATCGTTCGGGCTGGCGCAGTCGCAATAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -ThrAlaLeuValAlaAlaArgAlaValGlyTyrTyrAsp
                                                                                              IleGluPheSerAlaSerAsnLeuIleGlnAspLysLeu
                                                                                                                                                                                                                                                                                            :::|||||||||
----GAGATTCAGAACCGCATGGGC
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1032

972 460 882

834 380 798 360 738 340 678 320 306 582 289 546 269 489 249 429

1945 GAAAACTTCTACGGCGGGCGGGCTGGGTTCGGTGCGCGGATACGAAAGCGGCACGCTCGGT 2004	Db
hePheAlaGlyGlyAspGlnSerIleArgGlyTyrAlaHisAsp	Qy
AAGTCGGCATTGCGGGCGGCTAC	DЬ
<pre>ileGlnAlaGlyTyrIleTrpSerAspAsnPheAsnHisValProTy</pre>	Qy
TAAGCAAAACCTTCACGCTGATGCTCGG	ДЪ
	Qy
CCCTGCCCGGCAGCAAACTGCAATA	Db
rSerPhe 	Qy
1774CTGACGGGCGTGAACGCCGAAATC 1797	В
745 GlnArgTyrSerLeuGluValGlySerSerGlyLeuValSerAspAlaAsnMetAlaIle 764	Qy
TCGGCTGGGGGCGCAACAAAACCGACAGCGCGTTATGGCCGACGCGCGCTA	DЬ
731 ThrVal	Qy
1657 AAGAAATACGGCAAAACCGACGGCACAGACGGCAGCTTCAAAAGGCTGGCT	DЬ
ysProSerGlnGluAla	Qy
NACAAAGCGCCCAAACACTATGCCGACTTTAT	Db
roValAspPhe	Qy
ATGAGCGTGCCTGTTACCGAATACGAC	ДЬ
ThrTyrSerLeuArgTy	Qy
1489 CGCAAAGCATCGACCAGCATCAAACAATATAAAACCACCACGGCAGGC 1536	뫄
${\tt ArgThrLeuGluHisGluIleSerArgSerIleIleGlnAsnG}$	Qy
1435 ACGGCAGACGGGGTCAGCCTGGGCTACGATGTTTACGGAAAAGCCTTCGACCCG 1488	DЬ
lyTyrGlnGlnGluValPheGlyHisSerT	Qy
1381 TCACGAAGCAAAACCACGCTCAACGGCTCGCTGTCGTTTACCGACCCGTACTTC 1434	Db
rGluAspLysLysGlyValLysLeu	Qy
1321 TCCGCAGGCGTTTCCCAAGACAACCTGTTCGGTACGGGCAAGTCGGCCGCCCTGCGCCCC 1380	Db
602 LysPheGluHisAsnLeuIleAsnArgAspGlyTyrGlnAlaGlyAlaGluLeuArgLeu 621	Qy
GCTCGCTCGACTTGAGCGCGGGCTGGGTACAGGATACCGGCCTGGT	Db
lyLeuGlyTrpGlySerAspThrGlyThrArc	Qy
1269 1269	DЬ
564 AspValTyrGlnSerLysLysValProLeuTyrValPheValAlaSerAspLysProArg 583	Qy
1234GTCGATTTGAACATGAGCCTGACCGAACGTTCCACC 1269	рь
euProGlu	Qy
1198TTTGATGCCGTCCCGCTTGCCGCACACCCGACAAA 1233	Db
aArgAlaIleLeuProAspGluS	Qy
1147 CAACGCTCCAAAGAGCGCGCGCGCACTTTTGGGCTACTTCGACAACGTACAG 1197	DЬ
509ArgValLeuAlaIleAsnHisAspAspGlyValAsnArgSerIle 523	Qy
1090GTCGTGCGCCGCGAATTGCGCCAAATGGAATCCGCGCCCTTACGACACCTCCAAGCTG 1146	Db

	REFERENCE AUTHORS TITLE JOURNAL COMMENT	ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL	Db 2356 / RESULT 39 ACO10535/c LOCUS DEFINITION	N	Qy 871 Db 2236	85 211 87	Qy 846 Db 2056	Qy 829 Db 2005
* NOTE: This record contains 76 individual  * sequencing reads that have not been assembled into  * contigs. Runs of N are used to separate the reads  * and the order in which they appear is completely  * arbitrary. Low-pass sequence sampling is useful for  * identifying clones that may be gene-rich and allows  * overlap relationships among clones to be deduced.  * However, it should not be assumed that this clone  * will be sequenced to completion. In the event that  * the record is updated, the accession number will  * be preserved.  944: contig of 944 bp in length  935 1570: contig of 626 bp in length  * 1571 2381: contig of 811 bp in length  gap of unknown length  gap of unknown length  gap of unknown length  # 1571 2381: contig of 811 bp in length	Di Di Di Di Di Di Di Di Di Di Di Di Di D	ACO10535 ACO10535 ACO10535 HTG; HTGS; HTG sapid Homo sapid Eukaryota Eukaryota Mammalia; 1 (bases DOI joint Sequencinn Unpublisho	ATCO AC AC SZ	ProvalGlyGlnValArgValAspValAlaThrGlyV    :::    :::::     ::::  CCTTTAGGCCCGATGAAATTCAGGTACGCCTACCCGC	- AACAGCAGTTCCGCGACCGCGCAGGGTTCAAAACATTTACGGCGCCGCGAATACCCAT 2235LysGlyPheThrAsnAspThrLysIleGlyAlaGlyValGlyValArgTrpAlaSer 889LysGlyPheThrAsnAspThrLysIleGlyAlaGlyValGlyValArgTrpAlaSer 889	LeuArgLeuAlaValPheGlyAspIleGlyAsnAlaTyrAsp	ThralaGluTyrAsnTyrGluPheMet	ProIleSerAspLysGlyTyrLeuThrGlyGlyGlnValLeuAlaValGly

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34186:		33208:	31997:	30889:	29673:	28664:	78786:	2/034:	3 (	26033:	25438:	24389:	23354:	)   	22693:	22614:	22233:	21427:	20329:	20255:	19464:	18784:	18676:	17522:	16482:	16346:	15050:	14676:	11979:	11815:	T0379:	10006	9359:	8141:	7386:	5969:	1 (	5020:	4621:	3510:
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78 bp in	own len								own len	unknown length of 595 bp in length	049 bp			unknown length	own length 9 bp in le	of 381 bp in	~		4 bp in le	of 791 bp in length	of 680 bp in	08 bp i	g of 1154 bp in length funknown length	040 bp	of 136 bp in	of 1296 bp in unknown length	of 374 bp in unknown leng	of 2697 bp in unknown length	of 164 bp in unknown leng	y of 889 bp in le f unknown length	own length	own length	own lengt) 218 bp in	of 755 bp in lea	117 bp in	own leng	i ie	mown length	of 1111 bp in	17 bp in
n length	. ⊊.	bp in length	in length	bp in length length	bp in length length	<u>-</u>	length	op in length length	length	gth n lengt	bp in length	ín length	p in tengtn length	gth	gth length	p in length	n lengt	bp in length	in length	n lengt ath	n length ath	p in lengt	in leng qth	in leng	n length ath	in length ath	ń length ath	ín length ath	p in length length	n length gth	dry Tu Tendru	gth	gth in length	n length	in length ath	n length gth	gth	gth n length	gth in length	n length
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722 25358	y 703 GluThrTrpGlnAspLeuProValAspPheValAsnGlyLysProSerGlnGluAlaLeu	d Vo
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639 25679	y 620 ArgLeuSerGluAspLysLysGlyValLysLeuTyrAlaThrLysProLeuSerHisPro :::	Ωу
619 25718	y 600 ValThrLysPheGluHisAsnLeuIleAsnArgAspGlyTyrGlnAlaGlyAlaGluLeu	Дb
599 25736	y 580 AspLysProArgAspGlyGlnIleGlyLeuGlyTrpGlySerAspThrGlyThrArgLeu :::	Db dq
579 25790	y 562 ProAlaAspValTyrGlnSerLysLysValProLeuTyrValPheValAlaSer	Db Qy
561 25850	y 542 GluSerGluAsnGluValIleAspLeuProGluArgThrAlaLeuAlaAsnArgLysThr	9d V0
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517 26015	y 501 HisLeuTyrAspMetProAspAspArgValLeuAlaTleAsnHisAspAsp	Qу
	S-09-914-168-2 (1-919) x ACO10535 (1-181233)	US
	Alignment Scores: 0.00049 Length: 181233 Score: 245.50 Matchbes: 130 Percent Similarity: 37.00% Conservative: 55 Best Local Similarity: 26.00% Mismatches: 180 Query Match: 2.19% Indels: 136 Gaps: 21	All Pre Sco Pel Bes Que DB
	Source 1181233 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="16" /clone="RP11-273P15" BASE COUNT 45888 a 45036 c 44713 g 45408 t 188 others	BAS

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Allves, L. M.C., do Amaral, A.M., Bertolini, M.C., do Amaral, A.M., Bertolini, M.C., 2.A., Camarotte, G., Cannavan, F., Cardozo, J., Capina, L.P., Cicarelli, R.M.B., Couttnho, L.L., Clapina, L.P., Cicarelli, R.M.B., Couttnho, L.L., Clapina, L.P., Cicarelli, R.M.B., Couttnho, L.L., Clapina, L.P., Cicarelli, R.M.B., Couttnho, L.L., C.C., Ferro, M.I.T., Formighieri, E.F., Franco, M.C., C.C., Ferro, M.I.T., Formighieri, E.F., Franco, M.C., C.C., Ferro, M.I.T., Formighieri, E.F., Franco, M.C., G.C., Matchado, M.A., M.S., M.N., Martins, E.C., Meidanis, J.S., B.N., Martinez-Rossi, N.M., Martins, E.C., Meidanis, J.A.B.N., Martinez-Rossi, N.M., Martins, E.C., Meidanis, J.A.B.N., Moon, D.H., Moreira, L.M., Novo, M.T.M., Oliveira, M.C., Oliveira, V.R., Pereira, Jr., H.A., Sena, J.A.D., Silva, C., de Souza, R.F., Spinola, J.A.F., Tandade Truffi, D., Tsai, S.M., White, F.F., Setubal, J.C. and	bacteria; Proteobacteria; gamma subdivision; xanthomonas group; Xanthomonas.  1 (bases 1 to 10029)  da Silva A C R . Ferro J A . Reinach F C . Farah C S . Furlan L R .	AE012236.1 GI:21112424  Xanthomonas campestris pv. campestris str. ATCC 33913.  Xanthomonas campestris pv. campestris str. ATCC 33913.		CGGATAAAGACGAACACGGGTTACAGTTTTACATCG	LysGluGluGlyAsnProIleLysLeuHisPhePhe	lyAlaGlyValArgTrpAlaSerProValGlyGlnValArgValAspValAlaT 900	laValPheGlyAspIleGlyAsnAlaTyrAspLySGlyPheThrAsnAspThrLySIleG 880	InValLeuAlaValGlyThrAlaGluTyrAsnTyrGluPheMetLysAspLeuĀrgLeuA 860 	rgGlyTyrAlaHisAspSerLeuSerProIleSerAspLysGlyTyrLeuThrGlyGlyG 840 	SPASNPheAsnHisValProTyrArgLeuArgPhePheAlaGlyGlyAspGlnSerIleA 820 ::::   :::	GCACACTGTACGATCGCCATCGTTTTGTTACACGCGGCACGCTGGGCTGGATTGAAACCG 25080	CACCCACCGGGGGTTAAACCGATTTCCCCGTTTTACAGGCGCAGAACGGCTGGATCC 25	rAsnArgAlaHisGlnMetThrGlyGly]	GGGAGGGTACGCCCCTCTTTGTGTGTGGGGCATACACGTGGGGTCCACCAACTATTGA 25	galadivTleserdivValTvrserDhedivAspAspAlaTvr 780	TyrArgGlnArgTyrSerLeuGluValGlySerSerGlyLeuValSerAspAlaAsn-Me 762	AGT	LeuAlaGlyValAlaValHisLysThrValAlaAspAsnLeuValAsnProMetArgGly 742

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (28-NOV-2001) Departmento de Bioquimica, Universidade Sao Paulo, Av. Prof. Lineu Prestes 748, Sao Paulo, SP 05508-900,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12024217
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ALLEYTSDA TINTLSNVGYAFAKVNPIPTPNREDETVAVNLQVVPGPRVSVRRILYKG
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VDSNQITTFPGTTPQAIVDYIQAIGTDTFKAVRTEGWARDTRNDFFMPTRGWYQRVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(2525. .3871)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LKKEDNDETERLOFTFGGQF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RPVTATGLPFYENFYAGGTNSVRGFEDNTLGPRSEAINGFNRGQPLGGSLKTVGSVEM
YFPKLFDSPSARISAFFDFGNVYSDVDAFKANELRASTGVALLWRAPVGPISISYAFP
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/gene-"oma"
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located using Blastx/Glimmer/Genemark"
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33913"
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                                                                                                                                                                                                                                                                                                                                                                                                                782 SerAsnArgAlaHisGlnMetThrGlyGlyIleGlnAlaGlyTyrIleTrpSerAspAsn 801
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                707 AspLeuProValAspPheValAsn-----GlyLysProSerGlnGluAlaLeuLeuAla 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   848 GTCTCGGCGATGATCGGCGTCGATAGCAATCAGATCACTACCTTCCCGGGTACGACGCCG 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 ATCGAGCGTCTGCAGTTCACCTTCGGCCGCCAGTTT 75
                                                                                              890 ProValGlyClnValArgValAspValAlaThrGlyValLysGluGluGlyAsnPro---
                                                                                                                                                 230
                                                                                                                                                                                                                                                                                                                                                                               410 TTCGAAGACAACACGCTGGGACCGCGCTCGGAGGCGATCAACGGATTCAACCGTGGTCAG 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                488 ACCACGCGTCACCGCCACCGGC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       548 TTGGGCTATGGCGACAGCTACGGCAAGGACAGTTCTGGCGTAATCACCAACGCCGACGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              608 TATCAGATTTCGAACTACTGGCCGATCATTCCTGCGATTGTTCTCAATACGCGGTTTGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    687 TyrSerLeuArgTyrArgLeuAspLysLeuLysThrGlnAlaProProGluThrTrpGln 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           908 AACAGCACGAATGGGTCGGCACAGGTGGTGTTCGGCGTGCCGATCACCGAGAACGATACT
                                                                                                                                                 GATGCTTTCAAGGCCAATGAGCTGCGTGCCCTCAACCGGTGTCGCACTCCTGTGGCGCGCCC 171
                                                                                                                                                                                    AspLysGlyPheThrAsnAspThrLysIleGlyAlaGlyValGlyValArgTrpAlaSer 889
                                                                                                                                                                                                                                                       Asp······LeuArgLeuAlaValPheGlyAspIleGlyAsnAlaTyr····--
                                                                                                                                                                                                                            GACAGCCCGTCGGCGCGCATCTCGGCGTTCTTCGACTTCGGCAACGTTTACAGCGACGTG 231
                                 ---IleLysLeuHisPhePheIleGlyThrProPhe 919
                                                                      CCGGTCGGCCCGATTTCGATCAGCTATGCGTTCCCGCTGAAGAAGAAGAAGAACAACGACGAA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                462
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Search completed: May 6, 2003, 01:32:46 Job time: 5790 secs

Result No.

fragment

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-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XOAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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1: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*

2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*

3: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*

4: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*

6: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*

6: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*

6: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*

7: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*

9: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*

9: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*

10: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*

11: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*

12: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*

13: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*

14: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*

15: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*

16: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*

17: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*

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23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*

24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*

24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*

24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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RESULT 1 AAA50536 BASB081 gene; inflammation; diagnosis; ds. CDS Moraxella Moraxella catarrhalis BASB081 gene coding region. 05-DEC-2000 AAA50536; AAA50536 standard; catarrhalis. (first entry) therapy; antibacterial; antiinflammatory; waccine; infection; otitis media; Location/Qualifiers 1..2670 DNA; 2760 BP pneumonia; sinusițis;

ALIGNMENTS

Drosophila

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Query Match:
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                                                                                                                                                                                                                                                                                                               The present sequence is that of the coding region of the BASB081 cgene from Moraxella catarrhalis MC2931 (ATCC 43617). A translation of the sequence is given in AAY95987. The present sequence shows 2C 99.9% identity to a BASB081 sequence (see AAA50537) obtained by PCR 2C amplification of plasmid DNA. The invention provides BASB081 pCR 2C polypeptides, polynucleotides, expression vectors, host cells, and 2C a process for producing a BASB081 polypeptide. Also provided are 2C vaccine compositions comprising a BASB081 polypeptide or 2C polynucleotide, and optionally at least 1 other M. catarrhalis 2C antigen. A method for diagnosing a M. catarrhalis infection 2C involves identifying a BASB081 polypeptide, or an antibody that is 2C immunospecific for it, in a sample. A therapeutic composition 2C immunospecific for it, in a sample. A therapeutic composition 2C infections be a bacterial infection, e.g. otitis media in infants 2C and children, pneumonia in elderlies, sinusitis, nosocomial 2C infections and invasive diseases, chronic otitis media with hearing 2C constituted speech learning, upper respiratory tract infection, and 2C infiammarion of the middle ear, auditive nerve damage, 2C infiammarion of the middle ear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New BASB081 polypeptides from Moraxella catarrhalis and polynucleotides encoding the polypeptides used for treating infections, or as a vaccine for preventing infections, especially those caused by M. catarrhalis -
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                    AsnAlaSerAlaGluHisGlyTyrPheAspGlyArgTrpLeuAspArgSerValAspVal
                                                                                                               LeuLeuIleGlyAspValPheHisHisGlyLysTyrGluThrLysLysAsnLeuIleGlu
                                                                                                                                                                       AATGCCAGTGCTGAACATGGATATTTTGATGGGCGTTGGCTGGATCGTTCAGTTGATGTA
                                                                                                         CAAGAGTCAGCGATGGATTTGAATGGCTCTATCCCACGCCTAAGGCAAACTGCTTTGGTG
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The present invention relates to a Moraxella catarrhalis genomic librar comprising of a combination of 41 nucleic acid molecules (see AAF28514-AAF2854). The library has a number of uses described in the specification e.g. is useful for aidentifying diagnostic and therapeuti compositions. M. catarrhalis (Branhamella catarrhalis) is a large aerobic, gram-negative diplococcus, normally found among the bacterial flora of human upper airways. M. catarrhalis is known to cause acute, localised infections such as otitis media, sinusitis and bronchopulmona.

genomic library

therapeutic

and

life-threatening, systemic

a, sinusitis and bronchopulmonary diseases including endocarditis

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                                                                                                                                                                                                                                                                                                                                                                                         AsnPheAsnHisValProTyrArgLeuArgPhePheAlaGlyGlyAspGlnSerIleArg
                                                                                                                                                                                                                                                                                                                                                                                                                    GGCAGCAATCGTGCCCATCAGATGACTGGTGGCATACAAGCAGGATACATTTGGTCGGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTTTTGATTTATCCACACGCACCCTAGAGCATGAGATTAGCCGCAGTATTATCCAAAAT
                                                                                                                                                              standard; DNA;
                                                                                                        catarrhalis BASB081 mature protein coding
                                                     catarrhalis
                                                                                                                           (first
                                                                              therapy;
                                                                              infection; otitis media;
therapy; antibacterial; i
                Location/Qualifiers replace(1003,G)
/*tag= a
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         "corresponds
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                                                                              antiinflammatory;
         base 1093
         of.
                                                                                        sinusitis;
                                                                                                        region
                                                                               vaccine;
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The present sequence is that of DNA encoding BASB081 mature protein CC (see AAY95988) of Moraxella catarrhalis Mc2931 (ATCC 43617). It was Cobtained by sequencing PCR-amplified DNA from a BASB081 expression CC plasmid. The sequence shows 99.9% identity to a mature BASB081 CC coding sequence (see AAA50537) obtained from M. catarrhalis ATCC 43617. CC The invention provides BASB081 polypeptides, polynucleotides, CC expression vectors, host cells, and a process for producing a BASB081 CC polypeptide. Also provided are vaccine compositions comprising a CC EAASB081 polypeptide. As provided are vaccine compositions comprising a M. CC catarrhalis infection involves identifying a BASB081 polypeptide, or CC catarrhalis infection involves identifying a BASB081 polypeptide, or CC catarrhalis infection useful in treating M. catarrhalis diseases in humans comprises an antibody directed against a BASB081 protein. CC infants and children, pneumonia in elderlies, sinusitis media in CC infections and invasive diseases, chronic otitis media with hearing CC infections and invasive diseases, chronic otitis media with hearing CC delayed speech learning, upper respiratory tract infection, and cc inflammation of the middle ear, auditive nerve damage, CC delayed speech learning, upper respiratory tract infection, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New BASB081 polypeptides from Moraxella catarrhalis and polynucleotiencoding the polypeptides used for treating infections, or as a vacc for preventing infections, especially those caused by M. catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 8; Page 60-61; 97pp; English.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB;
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DB; AAY95988.
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  вP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polynucleotides
or as a vaccine
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δÃ 밁 QY В δÃ Ър Š Вр δÃ Percent Similarity: Best Local Similari US-09-914-168-2 Score: Alignment Pred. No.: Match: 111 181 121 91 71 61 51 GATCAATCGCCGATATCTCGTATCGGTGAGCAATCACCCCCTTTGGGTTTGGATATGTCG AspGlnSerProIleSerArgIleGlyGluGlnSerProProLeuGlyLeuAspMetSer Similarity:  $(1-919) \times AAA50537$ 4581.00 100.00% 99.89% 96.91% 21 (1-2670)Length:
Matches:
Conservative: Mismatches: Indels: Gaps: 000H

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240

180 90 120 70 60 50

130

300

В

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490	spGlyIleLeuMetAspIleSerProIleGluPheSerAlaSerAsnLeuIleGlnAsp	4	9
·ω	GAACCAGCACAAGTTGATGAAGCACACTTGAACCTGTCATTGAAACCGTTGAGCTAACG	1261	DЬ
470	<pre>luProAlaGlnValAspGluSerThrLeuGluProValIleGluThrValGluLeuThr</pre>	451	Qy
1260	GAGGGTGAACAGATCCAAAACGACCAAGTGAGCTTTGAGCAGTCTTCAAGTAGCCGTACT	1201	Db
450	luArgGluGlnIleGlnAsnAspGlnValSerPheGluGlnSerSerSerSerArgTh	431	Qy
i	TCAAATGATTGATTGCCACACGGTATTTTAATATGGTGAATACCGAGATTGTCTTTCCA	1141	DЬ
430	erAsnAspLeuIleAlaThrArqTyrPheAsnMetValAsnThrGluIleValPhePro	411	Ογ
1140	GAGCAGTTACTCACCGTTAACATGGGAGAGGCTTACAATTTACAGGCGGTGCGTGC	1081	В
410	luGlnLeuLeuThrValAsnMetGlyGluAlaTyrAsnLeuGlnAlaValArgAlaLeu	391	Qγ
1080	AATTGACAACCGATCCAGATAAGCTGCCAGTTAAACGAGAATTACTT	1021	Вþ
390	roLysThrAsnGlnLeuThrThrAspProAspLysLeuProValLysArgGluLeuLeu		9
1020	CAGGTACGCAGTATCGCTTTGATGAGGTC	961	DЬ
370	eulleTyrAspThrGlyThrGlnTyrArgPheAspGluValValPhePheThrIleAsp		Qy
	CGTTCAGTTGATGTAATTTTGCCAGATAATACCGCTGATGTCAGC		DЬ
350	lyArgTrpLeuAspArgSerValAspValIleLeuProAspAsnThrAlaAspValSer	331	γQ
900	AAAAAAATCTCATCGAAAATGCCAGTGCTGAACATGGATATTTTGAT	841	DЬ
330	ysTyrGluThrLysLysAsnLeuIleGluAsnAlaSerAlaGluHisGlyTyrPheAsp		Qy
840	GCATTTACTACCGTGGCGGATGAGGTGCCATTGCTGATCGGCGATGTCTTTCATCACGGC	781	DЬ
310	AlaPheThrThrValAlaAspGluValProLeuLeuIleGlyAspValPheHisHisGly	9	Q
780	GAACCTGTTTATATTGATTATCGAGCGGTGGAGGTACGAGGTGAAGGTGCTGATGATAAA	721	Db
290	GluProValTyrIleAspTyrArgAlaValGluValArgGlyGluGlyAlaAspAspLys	7	Qy
	AGCATCGGAGAGGTGGATGTCATCATCATGATTTAGGT	661	В
270	AspLeuSerIleIleArgAspSerIleGlyGluValAspValIleIleHisAspLeuGly	251	δ
660	GCTTTGGTGGCAGCGCGTGCTGTCGGTTATTATGATATT	601	Db
250	leProArgLeuArgGlnThrAlaLeuValAlaAlaArgAlaValGlyTyrTyrAspIl	231	9
600		541	Db
230	${\tt nIleLysAlaAlaLeuGluAspIleThrGlnGluSerAlaMetAspLeuAsnGlySet}$	211	Qy
540	TCGCAATCAGGCGAAACCAGTGCGATTGGGTCATCGCATCAAAAAACAGAGCCTTATGCA	481	рь
	SerGlnSerGlyGluThrSerAlaIleGlySerSerHisGlnLysThrGluProTyrAl	191	Qy
480	CGCCTATTTAATGATGGTGTCAATAAGGTGCCTAGGCTTAAGGCAAAATTTTATCAATCA	42	DЬ
190	gLeuPheAsnAspGlyValAsnLysValProArgLeuLysAlaLysPheTyrGlnSe	17:	Οy
420	GTGGTTGTTACCACCGACATTAGAACCTGAAAAACCAGGTTTGATCAAGCGTCTTTATGCA		B 3
			? ;
٧.	ATGGGAATGAATGATTATTATTATTATTATTATTATTATT	30.	밁
150	MetGlyIleAsnProAsnAspTyrIleProGluTyrGlnGlyGluGlnProAsnSerGl	131	Qγ

870	${\tt TyrGluPheMetLysAspLeuArgLeuAlaValPheGlyAspIleGlyAsnAlaTyrAsp}$	851	Qу	
2460	TCAGATAAGGGTTATCTGACAGGCGGTCAAGTATTGGCGGTTGGTACAGCTGAATATAAT	2401	Дb	
850	erAspLysGlyTyrLeuThrGlyGlyGlnValLeuAlaValGlyThrAlaGluTyrAs	831	Qy	
4		2341	Db .	
بر د	ePheAlaGlvGlvAspGlnSerIleArgGlvTvrAlaHisAspSerIeuSerProTl	11	0	
iii i	GCATACAAGCAGGATACATTTGGTCGGATAATTTTAATCATGTGCCATATCGTTTGCGT		Db ?	
٠ د	VIleGlnAlaGlvTvrTleTrpSerAspAspPheAspH:sValDroTvrArofenAr	791	٥	
2280		_	Db	
90	ValTyrSerPheGlyAspAsnAlaTyrGlySerAsnArgAlaHisGlnMetThrGl	771	γQ	
2220	GTTGGCTCAAGCGGTTTGGTATCGGATGCTAATATGGCTATTGCTCGAGCTGGTATTAGT	2161	Db	
	alGlySerSerGlyLeuValSerAspAlaAsnMetAlaIleAlaArgAlaGlyIleSe	751	Qy	
	ACGGTTGCAGATAATTTGGTTAATCCGATGCGTGGCTATCGTCAGCGATATTCTTTAGAG	2101	Db	
750	rValAlaAspAsnLeuValAsnProMetArgGlyTyrArgGlnArgTyrSerLeuGl	731	Qy	
2100	GATTTTGTCAATGGTAAGCCAAGACCCAAGAGGCGTTATTGGCAGGTGTTGCTGTGCATAAA	2041	Db	
730	spPheValAsnGlyLysProSerGlnGluAlaLeuLeuAlaGlyValAlaValHisLy	711	Qy	
2040	TATCGTCTTGATAAGCTTAAAACCCAAGCACCCCCTGAAACATGGCAGGATTTACCAGTG	1981	DЪ	
710	yrArgLeuAspLysLeuLysThrGlnAlaProProGluThrTrpGlnAspLeuProVa	691	Qy	
1980	CATGAGATTAGCCGCAGTATTATCCAAAATGGTGGCTGGAATCGTACTTATTCATTGCGT	1921	рь	
690	isGluIleSerArgSerIleIleGlnAsnGlyGlyTrpAsnArgThrTyrSerLeuAr	671	Оу	
1920	CAACAAGAAGTTTTTGGTCACTCTACCAATGGTTTTGATTTATCCACACGCACCCTAGAG	1861	Db	
670	lnGlnGluValPheGlyHisSerThrAsnGlyPheAspLeuSerThrArgThrLeuGl	651	Qy	
	TATGCCACCAACCGCTTAGCCACCCTCTAAATGATCAGCTAAGAGCAACTTTGGGTTAT	1801	Db	
650	yralaThrLysProLeuSerHisProLeuAsnAspGlnLeuArgAlaThrLeuGlyTy	631	Qy	
	GATGGCTATCAAGCAGGCGCTGAGCTAAGACTGTCTGAGGATAAAAAAAGGGGTCAAGTTA	1741	Дb	
630	spGlyTyrGlnAlaGlyAlaGluLeuArgLeuSerGluAspLysLysGlyValLysLe	611	Qy	
1740	TGGGGATCGGACACAGGTACCCGCCTAGTCACAAAATTTGAGCATAATTTGATTAATCGT	1681	Db :	
5 6	rnG] VSprAsp@hrG]V@hrArqI puVa d@hrI vabhoG];;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;	л О	0	
יס כ	GTGCCGCTATATGTCTTTGTGGCGAGTGATAAACCCCGAGATGGTTCAAATTGGTTTTTGGGC	1621	당 2	
0	alProLeuTyrValPheValAlaSerAspLysProArgAspGlvGlnIleGlvLeuGl	571	VQ	
6		1561	Db	
570	roGluargThrAlaLeuAlaAsnArgLysThrProAlaAspValTyrGlnSerLysLy	551	Qy	
	GTATCTGCCGTTGCACGTGCTATTTTACCTGATGAATCTGAAAATGAGGTAATAGATTTG		DЪ	
550	alSerAlaValAlaArgAlaIleLeuProAspGluSerGluAsnGluValIleAspLe		Qy	
	CTTGCCATCAATCATGATGATGATGACCTAAATCGCTCTATTTTGGGCAGAATCAGCGATGCC	1441	DЬ	
530	euAlaIleAsnHisAspAspGlyValAsnArgSerIleLeuGlyArgIleSerAspA	511	Qy	
1440	AGCTAAATTTGGTGGCTGCCAAGGCTCGCCATTTATATGACATGCCTGATGATAGGGTG	1381	Db	
510	ysLeuAsnLeuValAlaAlaLysAlaArgHisLeuTyrAspMetProAspAspArgV	491	Qy	

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                                                                                                                  of Pseudomonas putida KT2440. The invention also describes (1) recombinant expression vector containing (I); (2) prokaryotic or eukaryotic cells transformed or transfected with (I) or the vector
                                                                                                                                                    Claim 1a;
                                                                                                                                                                                                                                                                                                                   microbial
                                                                                                                                      This invention describes novel DNA sequences (I) for specific detection
                                                                                                                                                                 related
                                                                                                                                                                                                                                                                           01-FEB-2001
                                                                                                                                                                                                                                                                                                                         Transgenic plant;
                                                                                                                                                                                                                                                                                                                                                   16-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                              AAF61044 standard; DNA;
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                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                 (QUIA-)
(GBFB )
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                                                                                                                                                                                                                                                              27-JUL-1999;
                                                                                                                                                                                                                                                                                                     Pseudomonas putida
                                                                                                                                                                               New DNA sequences specific
                                                                                                                                                                                                          (MEDI-)
                                                                                                                                                                                                                                    (TIGR-)
                                                                                                                                                                                                                                                 27-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                  AAF61044;
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                                                                                                                                                                                                                 TIGR INST GENOMIC RES.
QUIAGEN GMBH.
GES BIOTECHNOLOGISCHE FORSCHUNG P
DKFZ DEUT KREBSFORSCHUNGSZENTRUM
                                                                                                                                                                                                          MEDIZINISCHE
                                                                                                                                                    Page 94; 158pp; German.
                                                                                                                                                                                                                                                                                                                   production
                                                                                                                                                                                                                                                                                                                                      KT2440-associated
                                                                                                                                                                       engineering
                                                                                                                                                                                                                                                                                                                                                   (first
                                                                                                                                                                                                                                                              99DE-1035088
                                                                                                                                                                                                                                                                                                                        detection;
                                                                                                                                                                                                                                                                                                                                                   entry)
                                                                                                                                                                                                          HOCHSCHULE HANNOVER
                                                                                                                                                                                                                                                                                                                  tection; probe; amplification; vaccine
strain; biological remediation; ds.
                                                                                                                                                                                                                                                                                                                                                                              1374
                                                                                                                                                                        host,
   other
                                                                                                                                                                               for Pseudomonas
                                                                                                                                                                                                                                                                                                                                      DNA ORF06604
                                                                                                                                                                                                                                                                                                                                                                              ВP
                                                                                                                                                                        allow detection
                                                                                                                                                                                                                                                                                                                                                                                                                      919
  (specifically
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                                                                                                                                                                       KT2440, useful as presence of other
  the
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LysValProLeuTyrValPheValAlaSerAspLysProArgAspGlyGlnIleGlyLeu
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US-09-914-168-2 (1-919)
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Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 related pathogen P. aeruginosa). Compared with other 'safe' bacteria, has greater catabolic activity and better survival in, and adaptation the rhizosphere and soil
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                                                                        LeuProGluArgThrAlaLeuAlaAsnArgLysThrProAlaAspValTyrGlnSerLys
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                                             - ATTCGCCTGCACTTTTCCATGGGG
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                                               US-09-914-168-2 (1-919)
                                                                                    Query Match:
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Best Local Similarity:
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                                                                                                                                                                                                       The present sequence is that of the coding region of the BASB067 gene of Haemophilus influenzae strain Rd KW20. It encodes a 578-amino acid surface expressed protein (see AAY95820) that is recognised by the immune system. The invention relates to recognised by the immune system. The invention relates to polypeptides and polynucleotides, for use especially in therapeutic and prophylactic vaccines. It also relates to methods for using such polypeptides and polynucleotides, for the prevention and treatment of microbial diseases, in the prevention and diseases associated with microbial infections, and assays for detecting expression or activity of BASB067 plypeptides or polynucleotides. A polynucleotide having at least 85% identity to the present sequence can be used in the recombinant production of BASB067 immunogenic polypeptides in transformed host cells, and
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of
in
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                                                                                                                                                                         Sequence 1737 BP; 517 A;
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antibacterial;
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217
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                        243
                                                                                                                                                                                                vaccine compositions
CGTGTGTTTGGTTATTATGAATCTTCCGTGCGTTTTGAACGAAAACAGCGTCAAGGCAAA
                     ArgAlaValGlyTyrTyrAspIleAspLeuSerIleIleArgAsnSer---IleGlyGlu
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67..1734
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1..66
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1..1737
                                                                       4.6e-26
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20.49%
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                                                                                                                                                                                                                                                                                                                                                                                                                      polynucleotide from Haemophilus influenzae treating H. influenzae infections -
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142
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276
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638	0 ArgLeuSerGluAspLysLysGlyValLysLeuTyrAlaThrLysProLeuSerHis	620	Qy
906	CAAATAGGCTGGACAAA	847	В
619	ValThrLysPheGluHisAsnLeuIleAsnArgAspGlyTyrGlnAlaGlyAlaGluLe	600	Qy
846	CGTAAAAAAAAATGCGATGGAACTCGGTGTGGGCTTTTCTACTGATGGCGGCGTTCACGGA	787	DЪ
599	) AspLysProArgAspGlyGlnIleGlyLeuGlyTrpGlySerAspThrGlyThrArgLeu	580	Оу
786	5CATAAAAGCAAAACTGTGGATGTGGAGATTATTCTTTATCCA	745	Db
579	) LysThrProAlaAspValTyrGlnSerLysLysValProLeuTyrValPheValAlaSer	560	Qy
744		744	Db
559	$) \   \textbf{ProAspGluSerGluAsnGluValIleAspLeuProGluArgThrAlaLeuAlaAsnArg}$	540	Qy
744		74.	DЬ
539	) As n Arg Ser I le Leu Gly Arg I le Ser Asp Ala Val Ser Ala Val Ala Arg Ala I le Leu	520	Qy
744		74.	рь
519	$) \   {\tt ArgHisLeuTyrAspMetProAspAspArgValLeuAlaIleAsnHisAspAspGlyVal}$	500	Qy
744	TTAGTTCAGCCTAATGTTAAT	72,	Db
499	) IleGluPheSerAlaSerAsnLeuIleGlnAspLysLeuAsnLeuValAlaAlaLysAla	480	Qy
723		723	Db
479	) LeuGluProValIleGluThrValGluLeuThrAspGlyIleLeuMetAspIleSerPro	460	Qy
723		723	DЬ
459	$) \ \ Val Ser {\tt PheGluGlnSerSerSerSerArgThrGluProAlaGlnValAspGluSerThr}$	440	Qy
723	TTTAGCTCAGTA····························	1	망
439	PheAsnMetValAsnThrGluIleValPheProGluArgGluGlnIleGlnAsnAspGln	420	Qy
	<pre>:::     ::: ::: ::::::::::::::::::::::</pre>	Ġ	DЬ
419	) GluAlaTyrAsnLeuGlnAlaValArgAlaLeuSerAsnAspLeuIleAlaThrArgTyr	0	Qy
5		9	DЬ
399	ProAspLysLeuProValLysArgGluLeuLeuGluGlnLeuLeuThrValAsnMetGl	380	Qy
594		574	Db
379		360	Qy
573		514	DЬ
359	VallleLeuProAspAsnThrAlaAspValSerLeuIleTyrAspThrGlyThrGlnTy	340	Qy
513		454	Db
339	GluAsnAlaSerAlaGluHisGlyTyrPheAspGlyArgTrpLeuAspArgSerValA	320	Qy
453	CCGAAAGATGGCGTTTTGGTTGAGCACCAAACTTACGATGATTACAAAACA	397	Db
319	ProLeuLeuIleGlyAspValPheHisHisGlyLysTyrGluThrLysLysAsnLeuIl	300	Qy
396	GTGCAAATTGAGGGGG	w c	당 5
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OULT 6 50270 AAA50270 standard; DNA; 1731 BP.  AAA50270;  07-NOV-2000 (first entry) Haemophilus influenza non-typeable strain 289 BASB067 gene.	84 GlyValArgTrpAlaSerProValGlyGlnValArgValAspValAlaThrGlyValLys 90	824 HisAspSerLeuSerProIleSerAspLysGlyTyrLeuThrGlyGlyGlnValLeuAla 843 ::: :::::::::::::::::::::::::::::::::	4 IleAlaArgAlaGlyIleSerGlyValTyrSerPheGlyAspAsnAlaTyrGlySerAsn 78 :::   2 AAAGTGCAAGCATCTAGCGCGTGGGTTCGTACTATGCAGAAAAT	719 GInGluAlaLeuLeuAlaGlyValAlaValHisLySThrValAlaAspAsnLeuValAsn 738  1135	679 GlnAsnGlyGlyTrpAsnArgThrTyrSerLeuArgTyrArgLeuAspLysLeuLysThr 698	

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                                                                                                                                                                                                                                                                                                        Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                    Sequence 1731 BP; 509 A; 322 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Page 80; 87pp; English.
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280 ValGluValArgGlyGluGlyAlaAspAspLysAlaPheThrThrValAlaAspGluVal 299
                                                                         262 ValAspValIleIleHisAspLeu-----GlyGluProValTyrIleAspTyrArgAla 279
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                                                                                                                                      243 ArgAlaValGlyTyrTyrAspIleAspLeuSerIleIleArgAsnSer---IleGlyGlu 261
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                                             CGCGATTTATTGATTGCTCATGTTACACCAGGCGAGCCAACAAAAATTGCGGGGACTGAT 330
                                                                                                          CGTCTCTTTCCTTATTATCAATCTTCCCTGCGTTTTGAACGAAAACAGCGTCAAGGCAAA 270
                                                                                                                                                                                                                                                                                                                                                                      vaccine
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ProLeuAsnAspGlnLeuArgAlaThrLeuGlyTyrGlnGlnGluValPheGlyHisSer 6	GAATGCCACTGCTTAAAAAT 9	ArgLeuSerGluAspLysGlyValLysLeuTyrAlaThrLysProLeuSerHis 6	AAATTGGCTGGACAAAACCTTGGATTAATAGCCGTGGACATAGTTTGCGTTCAAATCTT	ω ⊏		AspLysProArgAspGlyGlnIleGlyLeuGlyTrpGlySerAspThrGlyThrArgLeu 5		LysThrProAlaAspValTyrGlnSerLysLysValProLeuTyrValPheValAlaSer 5	7	${\tt ProAspGluSerGluAsnGluValIleAspLeuProGluArgThrAlaLeuAlaAsnArg~5}$	7	AsnArgSerIleLeuGlyArgIleSerAspAlaValSerAlaValAlaArgAlaIleLeu 5	7	HisLeuTyrAspMe	:::    GTTAAT	) LysLeuAsnLeu		LeuMetAspIleSerPro	7	ValSerPheGluGlnSerSerSerSerArgThrGluProAlaGlnValAspGluSerThr 4	TTTAGCTCAGTA7	.ValAsnThrGluIleValPheProGluArgGluGlnIleGlnAsnAspGln			GACGATTATCTCAATAATATTCTTAACATCAAATCTGGC		•		ATCAGCCCTGAAACCCATCAAGCATGGTGGCGAATGTTATTTGATAGTGGTGTCCGTTAT	VallleLeuProAspAsnThrAlaAspValSerLeuIleTyrAspThrGlyThrGlnTyr	TCACGCTTGGCATTAAATCGTGGGTATTTTGATGGGAACTTTAAAATTTCACGTTTAGAA	GluAsnalaSerAlaGluHisGlyTyrPheAspGlyArgTrpLeuAspArgSerValAsp	CCAAAAGAAGGCGTTTTGGTTGAACACCCAAACTTACGATGATTACAAAACAGCGATT	ProLeuLeuIleGlyAspValPheHisHisGlyLysTyrGluThrLysLysAsnLeuIle	GTGCAAATTGAGGGGGAAGCCGCACAAGATGAAAATTTTGATGCGCTACGTAAAAACTTG
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WO200175067-A2
                                                     Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                  DNA encoding
                                                                                                                                  13-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for identifying expressed genes. (1) is useful in gene therapy techniques (II). (II) is useful in gene therapy techniques (II). (II) is useful in gene therapy techniques (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at first, wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for instance of the polynucleotides.
                                                                                                                                           2094
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23-AUG-2000;
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                               AspGluValProLeuLeuIleGlyAspValPheHisHisGlyLysTyrGluThrLysLys
                                                                     GATCAGGGCATTGACCTGCGCAACGAT----
                                                                                                      TyrArgAlaValGluValArgGlyGluGlyAlaAspAspLysAlaPheThrThrValAla
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AsnLeuIleGluAsnAlaSerAlaGluHisGlyTyrPheAspGlyArgTrpLeuAspArg

### IleGlnAspLysLeuAsnLeuValAlaLaLysAlaArgHisLeuTyrAspMetl ### ::::::::::::::::::::::::::::::::::	IleGlnAspLysLeuAsnLeuValAalaLysAlaArgHisLeuTyrAspMetProAs  IleGATCGCGAAAAACACCACTATCCCGACCAAGCACGACGAGGTGTTCCTACCGCTGAAAACACCACTATCCCGACCAAGCACAAGCACGAGGTGTTCCTACCGCTGAAAACAACCACTATCCCATGTGCTGCAGGTGTTCCTACCGCTGAAACG  AspArgValLeuAlaIleAsnHisAspAspGlyValAsnArgSerIleLeuGlyAr
auAsnLeuValAlaAlaLysAlaArgHisLeuTyrAspMet ::: RCACCACTATCCCGACCAAGCACAGCCAGGTGTTCTCTACC !!: !!	auAsnLeuValAlaAlaLysAlaArgHisLeuTyrAspMetProl ::::::::::::::::::::::::::::::::::::
LaAlaLySAlaArgHisLeuTyrAspMet	LaAlaLysAlaArgHisLeuTyrAspMetProJ
gHisleuTyrAspMet CCAGGTGTTCTCTACC lAsnArgSerIleLeu click cli	gHisLeuTyraspMetProJ CCAGGTGTTCTCTACCGCTG LASnArgSerIleLeuGlyJ GCTGCAGGGTGAACGTAAAA AGCCCGGTGC JThralaLeuAlaAsnArg1 GTATATATATACGACCCLeuTyrValPheValJ CAACTTCCACTGGGTGGCCC CAACTTCCACTGGGTGGCCC CAACTTCCACTGGGTGGCCC CAACTTCCACTGGGTGGCCC CAACTTCCACTGGGTGGCCC CAACTTCCACTGGGTGGCCC CAACTTCCACTGGGTGGCCC CAACTTCCACTGGGTGGCCC CAACTTCCACTGGGTGGCCC CAACTTCCACTGGGTGGCCC CAACTTCCACTGGGTGGCCC CAACTTCCACTGGGTGGCCCT CCCAGAAATTATGAGGG GGLUHis
	roll CTG CTG AAG AAG CCCC CCCC CCCC CCCC CCC

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07; antibacterial; anti-inflammatory; vaccine; ss;	philus influenzae strain BASB207 upstream nucleotide seq	1 (	155 standard: DNA; 944 BP.		CGGT 249	13		luGlyAsnProIleLysLeuHisPhePhe	GGTCGGGCCAATCAAACTCG	eGlyAlaGlyValGlyValArgTrpAla-SerProValGlyGlnValArgVal	TGGGGCGCGGTGTTTGTCGATAGTGGCGAAGCGGTAAGCGATATTCGCCGCAGCGACTTT 364	ArgLeuAlaValPheGlyAspIleGlyAsnAlaTyrAspLysGlyPheThrAsnAspThr 877	GGGCCTCGAAGTTGAT	GlyGlyGlnValLeuAlaValGlyThrAlaGluTyrAsnTyrGluPheMetLysAspLeu 857	AGTATTCGTGGCTACAAATACAAATCTATCGCTCCGAAATACGCCAACGGTGACCTGAAA 484	leArgGlyTyrAlaHisAspSerLeuSerProIleSerAspLysGlyTyrI	GAAACCGGTGATTTCGACAAAGTACCGCCGGATCTGCGTTTCTTCGCCGGGGGGGG	rAspAsnPheAsnHisValProTyrArgLeuArgPhePheAlaGlyGlyAsp	CGCCATCGTTTTGTTACACGCGCACGCTGGGCTGG	lnMetThrGlyGlyIleGlnAlaGlyTyr	::: :::	erAspAlaAsnMetAlaIleAlaArgAlaGlyIleSerGlyValTyrSerPheGly	GGCGACTCGCAACGCTACTCTATCGACTACTCCAACACGGC	roMetArgGlyTyrAr	7	LeuAlaGlyValAlaValHisLysThrValAlaAspAsnLeuV		eValAsnGlyLysProSe		PASnArgThrTyrSerLeuArgTyrArgLe	GCCTTCCAGAACCCCCGACATCACACG 895	ThrargThrLeuGluHisGluIleSerArgSerIleIleGlnAsn 680	ATGT	GlnGlnGluValPheGlyHisSerThrAsnGl	AGGCAGTTGGGTTGGCACGGCCTGCGTTATCATCGACGCTGCTGATCACCTTCATCTGCAT 982

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                                                                                                                                                                                                                                                                                                                                                                                                                                      influenzae, including pneumonia, exacerbation of chronic bronchitis, sinusitis and otitis media; as immunogens to produce antibodies immunospecific for such polypeptides and polynucleotides, These may also be used in diagnosing the stage of infection and type of infection the pathogen has attained. The polynucleotides may be further used in genetic immunisation, as components of polynucleotide arrays useful for diagnostic and prognostic purposes, in the discovery and development of antibacterial compounds, and to interfere with the initial physical interaction between a pathogen and a eukaryotic host responsible for sequelae of infection. Compositions comprising the sequences of the invention are useful in the preparation of a medicament for generating an immune response in an animal. The present sequence represents the upstream DNA sequence of the Haemophilus influenzae BASB207 cDNA of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASB207 protein. The proteins of the invention may have antibacterial or anti-inflammatory activity and may be used to create a vaccine. The BASB207 polypeptides and polynucleotides are useful as vaccines against bacterial infections particularly those caused by non-typeable H. activities and polynucleotides are useful as vaccines against bacterial infections particularly those caused by non-typeable H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention relates to the cDNA and protein BASB207 protein. The proteins of the invention
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otitis media; infect:
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                                                                                                                                                   AsnLeuIleAsnArgAspGlyTyrGlnAlaGlyAlaGluLeuArgLeuSerGluAspLys
             GATTTTGCCGTCGGTTGGGAA----
                                                                                                  LysGlyValLys---LeuTyrAlaThrLysProLeuSerHisProLeuAsnAspGlnLeu
                                                                                                                                                                                                                     GlnIleGlyLeuGlyTrpGlySerAspThrGlyThrArgLeuValThrLysPheGluHis
                                         ArgAlaThrLeuGlyTyrGlnGlnGluValPheGlyHisSerThrAsnGlyPheAspLeu
                                                                      CAAACTCTAGAGGCAACTTATCGAATGCCACTGCTTAAAAATCCATTAAATTATTACTAT
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ion; immunisation; antibacterial.
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Query Match:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence represents a DNA encoding a Neisseria meningitidis serogroup A 85 kba antigenic protein. Neisseria meningitidis colonises the pharynx, causing meningitis and, occasionally, septicaemia in the absence of meningitis. This antigenic protein is useful in the manufacture of a medicament for treating or preventing infection due to Neisseria bacteria, such as meningitis and septicaemia. It is also useful as a diagnostic reagent for detecting the presence of Neisseria bacteria or antibodies raised against Neisseria, and as a reagent for raising the antibodies. The Neisserial nucleotide sequences can be expressed in a variety of different expression systems, for example, mammalian cells, baculoviruses, plants, bacteria and yeast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 6; Fig 2; 92pp; English.
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ATACGGCGAAAAAATCAGCTACGGCGGCAACAAAAAAAGCCAACGTCTCCGCCGAGCTGCT
                         rGlyGlyGlnValLeuAlaValGly-----ThrAlaGluTyrAsnTyrGluPheMe
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                                                                                     Composition for treating or preventing infection to, detecting, raising antibodies against Neisserial bacteria, comprises an N. meningitidis serogroup B outer membrane preparation and an immun
                                                                                                                                                                                                                                                                                                                               CDS
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                                                            Disclosure; Page
                                                                                                                                                       Pizza
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09-MAR-2000;
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vaccine; ss.
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specification describes a composition, comprising a Neisseria meningitidis scrogroup B outer membrane preparation and an immunogenic component. The immunogenic component is protein disclosed in W099/57280 W099/36544, W099/24578, W099/66791, W097/28273, W096/29412, W095/03413

The present sequence encodes a Neisseria gonorrheae protein.

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Query Match:
DB:
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        350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               136 AsnAsp------TyrTleProGluTyrGlnGlyGluGlnProAsnSer 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 ThrProLeuSerLeuGluGluLeuPheAlaGlnGluSerThrGluMetGlyIleAsnPro 135
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Ser \texttt{LeuIleTyrAspThrGlyThrGlnTyrArgPheAspGluValValPhePheThrIle}
                                                                                                   CAGAAATTCGCCCAAGACATGGAAAAAGTAACCGACTTCTACCAGAACAACGGCTACTTC
                               GATTTCCCTATCCTCGATACCGACATCCAAACCAACGAAGACAAAAACCAGGCAGACCATC
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                                                                                                                                                                                                                                                                                                                                       IleAspLeuSerIleIleArgAsnSerIleGlyGluValAspValIleIleHisAspLeu 269
                                                                 AspGlyArgTrpLeuAspArgSerValAspValIleLeuProAspAsnThrAlaAspVal 349
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                                                                                                                                                                                                                                                                                                       ATCGACATCACGATTGACGAGGGCAAATCCGCCAAAATCACCGACATCGAATTTGAA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GluProTyrAlaAsnIleLysAlaAlaLeuGluAsp-----IleThrGlnGluSerAla 224
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JLeu-AspLysLeuLysThrGlnAlaProProGluThrTr 705	TyrArgLe	691	Qy
AACCACCACCGCGGCGGCGCGTAAGGATGGG-TATCCCCGT 1562	TATAAAACCA	1516	Db
SerArgSerIleIleGlnAsnGlyGlyTrpAsnArgThrTyrs	isG	671	Qy
GATATTTACGGAAAAGCCTTCGACCCGCGCAAAGCATCGACCAGCGTCAAACAA 1515		62	Db 5
3 1	GlnGlnG		0
<pre>YrAlaThrLysProLeuSerHisProLeuAsnAspGlnLeuArgAlaThrLeuGlyTyr 650 YrAlaThrLysProLeuSerHisProLeuAspAglnLeuArgAlaThrLeuGlyTyr 650 ACGGCTCGCTGTCGTTTACCGACCCGTACTTCACGGCAGACGGGGTCAGCCTGGGCTAC 1461</pre>	TyrAlaT	631 1402	Дb
TACGGGCAAGTCGGCCCCTCGCGCGAAGCAAAACCACGCTC 1401	1	48	Db
pGlyTyrGlnAlaGlyAlaGluLeuArgLeuSerGluAspLysLysGlyValLysLeu 630	AspGlyT	611	Qy
AGGATACCGGCTTGGTCATGTCCGCCGGCGTATCGCAGGACA	GGGTT	1294	рb
SerAspThrGlyThrArgLeuVal	TrpGlyS	591	Qy
	1	1270	Db
rValPheValAlaSerAspLysProArgAspGlyGlnIleGlyLeuGly 5	LeuTyrV	573	Qy
ATGAGCCTGACCGAACGCTCCACC1269	AACATGA	1243	Дb
AlaLeuAlaAsnArgLysThrProAlaAspValTyrG	ArgThrA	553	Qy
CCCGCTTGCCGGTACGCCCGACAAAGTCGATTTG 1242	GCCGTCC	1204	Db
laArgAlaIleLeuProAspGluSerGluAsnGluV	AlavalA	533	Qy
TTGGGCTACTTCGACAACGTACAG17TGAT 1203	TTGGGCT	1174	Db
nHisAspAspGlyValAsnArgSerIleLeuGlyArgIleSerAspAlåValSer 532	IleAsnH	513	Qy
ATGGAATCCGCGCCTTACGACACCTCCAAGCTGCAACGCTCCAAAGAGCGCGTCGAGCTT 1173	ATGGAAT	1114	Db
	LeuTyrAs	502	Qy
ATCACCGGCAACAAAAACCCGGGACGAAGTCGTGCGCGCGCAATTGCGCCAA 1113	ATCACCG	1060	Дb
\snLeuIleGlnAspLysLeuAsn	PheSerA	482	Qy
CGTCGATTTCGTCCTGCACATCGAACCGGGCCGGAAAATCTACGTCAACGAAATCCAC 1059	ACCGTCG	1000	Db
pGlyIleLeuMetAspIleSerPro	ThrAspo	470	Qy
	-	961	Дb
roAlaGlnValAspGluSerThrLeuG	ThrGluP	450	Оy
GAGATTCAGAACCGCATGGGCTCGGCAGGCTACGCATACAGC 960	1	919	Db
gGluGlnIleGlnAsnAspGlnValSerPheGl	ProGluAr	430	Qy
rGGGT 918	GTTTTGGG	910	Db
erAsnAspLeuIleAlaThrArgTyrPheAsnMetValAsnThrGluIleValPhe 429	LeuSerAs	410	Qy
CTGGAAAAACTGCTGACCATGAAGCCCGGCAAATGGTACGAACGCCAGCAGATGACCGCC 909	CTGGAA	850	Дb
luGlnLeuLeuThrValAsnMetGlyGluAlaTyrAsnLeuGlnAlaValArgAla 409	LeuGlu	390	Qy
GTCCCCAAGGCCGAA 84	GAAGGC	817	Db
pProAspLysLeuProValLysArgGluLeu 38	AspPro	370	γо
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                                                                                                                                                                                             sGlu----
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                                                                                                                                                                                                                                     lGlyValArgTrpAlaSerProValGlyGlnValArgValAspValAlaThrGlyValLy
                                                                                                                                                                                                                                                                                                       AGGCAGCGTGTGGGACGGCAGAACCTATACCGCCGCCGAAAACGGTAACAACAAATCGGT
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                                                               outer membrane
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                                                                                                                                                                                           -GluGlyAsnProIleLysLeuHisPhePheIleGlyThrProPhe 919
                                                                                                                                                                                                                                                                                -AsnAlaTyrAspLysGlyPheThrAsnAspThrLysIleGlyAlaGlyVa
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                                                                                                                               DNA;
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                                                                                                                               2505
                                                              protein (omp)
                                                                                                                               ΒP
                                                                                                                                                                                                                                                                                                                                                                    -LysaspLeuArgLeuAlaValPheGlyAspIl
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AlaArgLeuPheAsnAspGlyVal--
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US-09-914-168-2 (1-919) x AAA15155 (1-2505)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neisseria species. The proteins, antibodies and polynucleotide sequences of the present invention may also be used in the scream development of chemical compounds such as drugs or vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hybridisation complexes. Antigens and antibodies specific omp proteins also provide diagnostic, therapeutic and prophylactic compositions for the treatment or prevention of the infections described above. The antibodies are useful for inducing a protective immune response in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated outer membrane protein 85 of Neisseria gonorrhoeae meningitidis useful for vaccine, therapeutic and diagnostic compositions for gonococcal or meningococcal infections -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 6; Fig 2; 98pp; English.
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                                                                GluValValValProProThrLeuGluProGluLysProGlyLeuIleLysArgLeuTyr
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512		LeuTyrAspMe :::	502	Q
1172	GTCGTGCGCCGCGAATTGCG	CCGGCA	1119	рь
501	AsnLeuIleGlnAspLysLeuAsnLeuValAlaAla 	rAlas	482	04
1118	ATTTCGTCCTGCACATCGAACCGGGCAGAAAAATCTACGTCAACGAAATCCAC	ACCGTCGATTT	1059	Db S
, c	OF COMPANY TO A DESCRIPTION OF THE PROPERTY OF	2	170	2 5
6.0	aGlnValAspGluSerThrLeuGluProValIleGluThrValGlu	hrGluProA	450	, 0
1019	-GAGATTCAGAACCGCATGGGCTCGGCAGGCTACGCATACA		978	DЬ
449	<pre>luGlnIleGlnAsnAspGlnValSerPheGluGlnSerSerSerArg :::         </pre>	ProGluArgG	430	Qy
977		GTTTTGGGT	969	DЬ
429	${\tt ipLeuIleAlaThrArgTyrPheAsnMetValAsnThrGluIleValPhe}$		410	Qy
968	AACTGCTGACCATGAAGCCCGGCAAATGGTACGAACGCCAGCAGATGACCGCC	CTGGAAAAAC	909	Db
409	snMetGlyGluAlaTyrAsnLeuGlnAla	LuG	390	Оу
908	CAACGAAGTCCCCAAGGCCGAA	GAAGGCGACACCAAC	876	В
389	LysThrAsnGlnLeuThrThrAspProAspLysLeuProValLysArgGluLeu	Pro	370	Qy
875	CACGAAGGCGACGTTTCCGCTGGGGCAAAGTGTCGATT	AAAATCACCGTCC	825	Ф
369	pThrGlyThrGlnTyrArgPheAspGluValValPhePhe	SerLeuIleTyrAs	350	Qy
349 824	rgTrpLeuAspArgSerValAspValIleLeuProAspAsnThrAlaAspVal 	AspGlyArgT	330 765	B 8
764	CATGGAAAAAGTAACCGACTTCTACCAGAACAA	CAGAAATTCGC	705	рь
329	aSerAlaGlu	GlyLysTyrG	310	Qy
704	CGAAGGCGGCATTTGGACATGGCTGACACGAAGCGACCGGTTCGACCGC	ATGTCGCTGAC	645	Db
309	heThrThrValAlaAspGluValProLeuLeuTleGlyAspValPheHisHis	LysalaPheT	290	Qy
644	AACCAAGTCTATTCCGACCGCAAACTGATGCGGCAG	유=	606	Db
289	ProValTyrIleAspTyrArgAlaValGluValArgGlyGluGlyAlaAspAsp	GlyGluProv	270	Оу
605	GATTGACGAGGGCAAATCCGCCAAAATCACCGACATCGAATTTGAA	ATCGACATCACGATTG	549	Db
269	leArgAsnSerIleGlyGluValAspValIleIleHis	IleAspLeuS	250	Qy
548	 AGTAACCAAACTCGCCCGCAACCG	GGCAAACTCA	489	Db
249	gLeuArgGlnThrAlaLeuValAlaAlaArgA	SerIleProAr	230	Qy
488	AACCAGGCAGTCGCCGGCCTGAAAGAAGAATATCTCGGGCGC	GCGACACTCA	438	Db
229	sAlaAlaLeuGluAspIleThr	AlaAsnIleLy	210	Qy
437	AAGAAAAACCTCGAATCGTTCGGGCTGGCGCAGTCGCAATACTTTAATCAG	GACGCCATCA	378	DЬ
209	erSerH	SerGlnSe	191	Qy
377	ATGCCCTACCATCGGCTCGCCTCAACATCACCGGCGCCAAAATGCTGCAGAAC	GTTATCGTAT	318	Дb
190	AsnLysValProArgLeuLysAlaLysPheTyrGlnSer		178	Оу
317			258	Db

CCGGCTACGAAAGCGGCACGCTCGGCCCGAAAGTGT	Db
AlaHisAspSerLeuSerProIleSerAspL	Qу
1977GGCAGAACCAAAGAAATCCCCTTCTTTGAAAACTTCTACGGCGGCGTGGG 2029	DЪ
JLeuArgPhePh	Qy
	Db
791GlyIleGlnAlaGlyTyrI1 797	Qy
1883 CTACTCCGCCACCAACCAAACCTGGTTCTTCCC 1918	Db
SerPheGlyAspAsnAlaTyrGlySerAsnArgAlaHis	Qy
1833CTGACCGGCGTAAATGCCGAAATCGCCCTGCCCGGCAGCAAACTGCAATA 1882	Db
753 rSerGlyLeuValSerAspAlaAsnMetAlaIleAlaArgAlaGlyIleSerGlyValTy 773	Qy
1802 CGACAGCGCCTTATGGCCGACGCGGCGAC 1832	фd
733 aAspAsnLeuValAsnProMetArgGlyTyrArgGlnArgTyrSerLeuGluValGlySe 753	Qy
1742 AGACGGCAGCTTCAAAGGCCTGCTGTACAAAGGCACTGTCGGCTGGGGGGCGCAACAAGAC 1801	ДĎ
719 nGluAlaLeuLeuAlaGlyValAlaValHisLysThrValAl 733	Qy
NAACGCTATGCCGACTTTATCAAACAATAC	Db
1	Qy
1622 TACCGAATACGACCGCGTCAATTTCGGGCTGGCGGCGGAACACCCTGACCGTCAACACCTA 1681	Дb
yrArgLeu-AspLysLeuLysThrGlnAlaProProGlu	Qy
75 TATAAAACCACCACCGCCGGCGGCGGCGTAAGGATGGG-TATCCCCG	DЪ
isGluIleSerArgSerIleIleGlnAsnGlyGlyTrpAsnArgThrTyr	Qy
1521GATATTTACGGAAAAGCCTTCGACCCGCGCAAAGCATCGACCAGCGTCAAACAA 1574	Дb
erThrAsnGlyPhe	Qy
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ysProLeuSerHisProLeuAsnAspGlnL	Οу
1407 TTCGGTACGGGCAAGTCGGCCCGCGCGCGCCCTCGCGGAAGCAAAACCACGCTC 1460	Db
aGluLeuArgLeuSerGluAspLysLysGl	Qy
1353 TGGGTTCAGGATACCGGCTTGGTCATGTCCGCCGGCGTATCGCAGGACAACCTG 1406	Db
pGlySerAspThrGlyThrArgLeuValThrLysPheGluHisAsnI	Qy
GCG	дb
G1	Qy
1302 AACATGAGCCTGACCGAACGTTCCACC 1328	Дb
LeuAlaAsnArgLysThrProAlaAspValTyrGlnSerLysLysValPro 5	Qy .
1263 GCCGTCCCGCTTGCCGGTACGCCCGACAAA	Db
ValAlaArgAlaIleLeuProAspGluSerGluAsnGluVa	Qy
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AsnHisAspAsp(	Qy
1173 ATGGAATCCGCGCCTTACGACACCTCCAAGCTGCAACGCTCCAAAGAGCGCGTCGAGCTT 1232	Дb

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel 85 kDa antigen from Neisseria meningitidis and Neisseria gonorrhoeae, useful in the manufacture of a medicament for treating and preventing Neisserial bacteria infection \cdot
                                                                                                                                 2320
                                                                                             2260
                                                                                                                                                           B antigen; pharynx; meningitis; septicaemia; mammalian cell; infection; baculovirus; yeast; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                             "Mature N. meningitidis serogroup B antigen"
                                                                                                               883
                                                                                                                                                  903
                                                    2081 ATACGGCGAAAAATCAGCTACGGCGCAACAAAAAAGCCAACGTCTCCGCCGAGCTGCT
                                                                                             2201 AGGCAGCGTGTGGGACGCAGAACCTATACCGCCGCAGAAACGGTAACAACAAATCGGT
                                                                                                               ------AsnAlaTyrAspLysGlyPheThrAsnAspThrLysIleGlyAlaGlyVa
       -ThrAlaGluTyrAsnTyrGluPheMe
                                         -- LysAspLeuArgLeuAlaValPheGlyAspIl
                                                                                                                                                 883 1GlyValArgTrpAlaSerProValGlyGlnValArgValAspValAlaThrGlyValLy
                                                                                                                                                                                     sGlu-----GluGlyAsnProlleLysLeuHisPhePheIleGlyThrProPhe 919
                                                                                                                                                                                                                                                                                                                                                                                   B antigen"
                                                                                                                                                                                                Neisseria meningitidis serogroup B antigenic protein DNA
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STATENS INST FOLKEHELSE
       rGlyGlyGlnValLeuAlaValGly
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64..2391
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                                                                                                                                                                                                                                                                                                                                       Neisseria meningitidis.
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P-PSDB; AAU03957.
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The sequence represents a DNA encoding a Neisseria meningitidis serogroup B 85 kba antigenic protein. Neisseria meningitidis colonises the pharynx, causing meningitis and, occasionally, septicaemia in the absence of meningitis. This antigenic protein is useful in the manufacture of a medicament for treating or preventing infection due to Neisseria bacteria, such as meningitis and septicaemia. It is also useful as a diagnostic reagent for detecting the presence of Neisseria bacteria or antibodies raised against Neisseria, and as a reagent for raising the antibodies. The Neisserial nucleotide sequences can be expressed in a variety of different expression systems, for example, mammalian cells, bacteria and yeast.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 319 GACGCC-----ATTAAGAAAAACCTCGAATCGTTCGGCCTGGCGCAGTCGCAATAC 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IleAspLeuSerIleIleArgAsnSerIleGlyGluValAspValIleIleHisAspLeu 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------PheHisHisGlyLysTyrGluThrLysLysAsnLeuIleGlu 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 ThrProLeuSerLeuGluGluLeuPheAlaGluGluSerThrGluMetGlyIleAsnPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46 TCGCCTTTGGCACTTGCCGACTTCACCATCCCAAGACATCCGCGTCGAAGGCTTGCAGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106 ACCGAGCCGAGTACCGTATTCAACTACCTGCCCGTCAAAGTCGGCGACACCTACAAC---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP; 657 A; 743 C; 583 G; 411 T; 0 other
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342
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: 679 G	::: GACTICTACCAAAATAACGGCTACTTCGATTTCCGTATCCTCGATACCGACATCCAAACC 738	qa
341	IleLeuProAspAsnThrAlaAspValSerLeuIleTyrAspThrGlyThrGlnTyrArg 360 ::: :::    aAGGAAGACAAAAGCAGGAGCATCAAAATCACCGTCCACGAAGGGGGACGTTTCCGT 798	qq ———
361	PheAspGluValValPhePheThrIleAspProLysThrAsnGlnLeuThrThrAspPro 380 ::: :::    :::    :::    ::: TGGGGCAAAGTCTCCATCGAAGGCGACACCAACGAA 834	0 Oy
381 835	AspLysLeuProValLysArgGluLeuLeuGluGlnLeuLeuThrValAsnMetGlyGlu 400	da
401	AlaTyrAsnLeuGlnAlaValArgAlaLeuSerAsnAspLeuIleAlaThrArgTyrPhe 420 	ζ Q
421	GluGlnIleGlnAsnAspGlnVal 44 :::           GAGATTCAGAACGCATGGGC 93	ζο qα
441		νο 
461 973	GlubrovalileGluThrValGluLeuThrAspGlyIleLeuMetAspIleSerPro 479 :::   ::	δλ 
480		до 90
493	AsnLeuValAlaAlaLysAlaArgHisLeuTyrAspMetProAspAsp 508 :::	da d
509		QY Db
524	LeuGlyArgIleSerAspAlaValSerAlaValAlaArgAlaIleLeuProAspGluSer 543	oy da
544	GluAsnGluValileAspLeuProGluArgThrAlaLeuAlaAsnArgLysThrProAla 563 :::	Qy
564	AspValTyrGlnSerLysLysValProLeuTyrValPheValAlaSerAspLysProArg 583	П
1269	1269	ad
584	AspGlyGlnIleGlyLeuGlyTrpGlySerAspThrGlyThrArgLeuValThr 601	άα
602	LysPheGluHisAsnLeuIleAsnArgAspGlyTyrGlnAlaGlyAlaGluLeuArgLeu 621 :::           TCGGAGGGGTTTCCCAAGACAACCTGTTCGGTACGGGCAAGTCGGCCGCACTGCGCGC 1380	QY QO
622	SerGluAspLysLysGlyValLysLeuTyrAlaThrLysProLeuSerHisProLeuAsn 641	QV Db
642	AspGlnLeuArgAlaThrLeuGlyTyrGlnGlnGluValPheGlyHisSerThrAsnGly 661	RE AA XX
662	PheAspLeuSerThrArgThrLeuGluHisGluIleSerArgSerIleIleGlnAsnGly 681	AC XX DT

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1537 GCAGGCATCCGCATGAGCGTGCCTGTTACCGAATACGACGCGTGAATTTCGCTTTGGTG 1596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2176 AACAGCAGTTCCGCGACCGGCGGCGGGTTCAAAACATTTACGGCGCCGGCAATACCCAT 2235
                                               682 GlyTrpAsnArg------ThrTyrSerLeuArgTyrArgLeuAspLysLeu 696
                                                                                                                                                  697 LysThrGlnAlaProProGluThrTrpGlnAspLeuPro-----ValAspPheVal 713
                                                                                                                                                                                                                                                    714 Asn.....GlyLys---ProSerGlnGluAlaLeuLeuAlaGlyValAlaValHisLys 730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        745 GlnArgTyrSerLeuGluValGlySerSerGlyLeuValSerAspAlaAsnMetAlaIle 764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           765 AlaArgAlaGlyIleSerGlyValTyrSerPheGlyAspAsnAlaTyrGlySerAsnArg 784
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973 CAGCCGCTGCCAAACGCCGAAACCAAAACCGTCGATTTCGTCCTGCACATCGAACCGGGC 1032
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  GluvalvalvalproProThrLeuGluProGluLysProGlyLeuIleLysArgLeuTyr 169
                                                                                         AlaArgLeuPheAsnAspGlyValAsnLysValPro------ArgLeuLysAlaLys 186
                                                                                                                                                                                                                                                                                                                319 GACGCC-----ATTAAGAAAAACCTCGAATCGTTCGGGCTGGCGCAGTCGCAATAC 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 PheaspGluValValPhePheThrlleAspProLysThrAsnGlnLeuThrThrAspPro 380
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                                            --GACACACGGCAGTGCCATCATCAAAAGCCTGTAC
                                                                                                                                 GCCACCGGTTTCTTTGACGACGTACGCGTCGAAACTGCGGACGGGCAGCTCCTGCTGACC
                                                                                                                                                                             PheTyrGlnSerSarGlnSerGlyGluThrSerAlaIleGlySerSerHisGlnLysThr
                                                                                                                                                                                                                          GTTATCGAACGCCCCACCATCGGCTCGCTCAACATCACCGGCGCAAAAATGCTGCAAAAC
                                                                                                                                                                                                                                                                      GluProTyrAlaAsnIleLysAlaAlaLeuGluAsp----IleThrGlnGluSerAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----ThrAlaLeuValAlaAlaArgAlaValGlyTyrTyrAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              430 GGCAAACTCAATATCCAAATCACGCCCAAAGTAACCAAACTCGCCGCAACCGCGTCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IleAspLeuSerIleIleArgAsnSerIleGlyGluValAspValIleIleHisAspLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATCGACATCACGATTGACGAGGGCAAATCCGCCAAAATCACCGACATCGAATTTGAA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        290 LysAlaPheThrThrValAlaAspGluValProLeuLeuIleGlyAspVal-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -------CAGATGTCGCTGACCGAAGGCGGCATTTGGACATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AACGAAGACAAAACCAAGCAGACCATCAAAATCACCGTCCACGAAGGCGGACGTTTCCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               381 AspLysLeuProValLysArgGluLeuLeuGluGlnLeuLeuThrValAsnMetGlyGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -- GAGATTCAGAACCGCATGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            883 TGGTACGAACGCCAGCAGATGACCGCCGTTTTGGGT--------
                                                                                                                                                                                                                                                                                                                                                             MetAsp-----LeuAsnGlySerIleProArgLeuArgGln----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  799 TGGGGCAAAGTC-----TCCATCGAAGGCGACACCAACGAA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                940 TCGGCAGGCTACGCATACAGC------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence represents a DNA encoding a Neisseria gonorrhoeae 85 kDa antiganic protein. N. gonorrhoeae is closely related to N. meningitidis, which colonises the pharynx, causing meningitis and, occasionally, septicaemia in the absence of meningitis. This antigenic protein is useful in the manufacture of a medicament for treating or preventing infection due to Neisseria bacteria, such as meningitis and septicaemia. It is also useful as a diagnostic reagent for detecting the presence of Neisseria bacteria or antibodies raised against Neisseria, and as a reagent for raising the antibodies. The Neisserial nucleotide sequences can be expressed in a variety of different expression systems, for example, mammalian cells, baculoviruses, plants, bacteria and yeast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel 85 kDa antigen from Neisseria meningitidis and Neisseria gonorrhoeae, useful in the manufacture of a medicament for treating and preventing Neisserial bacteria infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ThrProLeuSerLeuGluGluLeuPheAlaGlnGluSerThrGluMetGlyIleAsnPro 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :::||||||| :::||| :::
TCGCCTTTGGCACTTCACCATCCAGACATCCGCGTCGAAGGCTTGCAGCGT 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein; pharynx; meningitis; septicaemia; mammalian cell;
infection; baculovirus; yeast; ds; Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                          /*tag= c
/product= "Mature N. gonorrhoeae antigen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2394 BP; 655 A; 758 C; 586 G; 395 T; 0 other
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191
121
342
278
40
                                                                                                                                                                                                                                               gonorrhoeae antigen
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Matches:
Conservative:
Mismatches:
Indels:
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                       gonorrhoeae antigenic protein DNA
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                                                                                                                                                                             Location/Qualifiers
1..2394
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(STAT-) STATENS INST FOLKEHELSE
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/product= "N.
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259.00
33.48%
20.49%
5.48%
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2000GB-0005698
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/*tag= b
64..2391
/*tag= c
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                                                                                                                                 gonorrhoeae.
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Best Local Similarity:
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                                                                                                                                                                                                                                                                      sig_peptide
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                                                               Antigenic
bacterial
                     Neisseria
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2005 846 846 857 2005 857 2116 870 871 2236 871 871 871 871 871 871 871 871 871 871	1033 CGGAAAATCTACGTCAACGAAATCCACATCACGGCAACAACAAAACCGGGAACGAA 493 ASnLeuvalalaalaiysalaargHisLeuTyraspMetProAspAsp	1089 508 1146	1894 809 1945
Cursandiuvaliserlaphiavalserlandiahseghialiteauprokapdiuser 543   09   2056	9ArgvalLeuAlaIleAsnHisAspAspGlyvalAsnArgSerIl	523 1197	2005
Second control of the control of t	LeuGlyArgIleSerAs	543 1233	846 2056
Aspvalycolnserystystolproducyrotalphevalabsersplysprokery 583   09   871	GluAsnGluValIleAs	563	
Aspelydinilediyleu	AspvalTyrGlnSerLy	583	870
AspellyGlnIIeGlyLeu	:		2176 AA
Decode	4 AspGlyGlnIleGlyLeuGlyTrpGlySerAspThrGlyThrArgLeuValTh 	601 1320	2236 AA
	2 LysPheGluHisAsnLeuIleAsnArgAspClyTyrGlnAlaGlyAlaGluLeuArgLe	621	
	TCCGCAGGCGTTTCCCA	1380	806
### ##################################	SerGluAspLysLysGl       CACGAAGCAAA	641 1434	2356
	rteuGlyTyrGlnG :           :CTGGGCTAC	661 1488	SULT 14 442128 AAH42128 standard; DNA; 2394
GlyTrpAsnArgThrTyrSerLeuArgTyrArgLeuAspLysLeu 696  GlyTrpAsnArgThrTyrSerLeuArgTyrArgLeuAspLysLeu 696  KW	gThrLeuGluHisGlulleSerArgSerIlelleGlnAs ::::::::::::::::::::::::::::::::::::	681 1536	AAH42128; 17-SEP-2001 (first
LysThrGlnalaProProGluThTTrpGlnaspLeuProvalAspPheVal 713  LysThrGlnalaProProGluThTTrpGlnaspLeuPro	GlyTrpAsnArg	696	
	ccaeccaiccecaieae LysThrGlnAlaProPr	713	
		1656	Key
Thrval		730	sia nentide
### MOZGUEGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1 Thrval	744	mat_peptide 642391
AlaArgalaGlyIleSerGlyValTyrSerPheGlyAspAsnAlaTyrGlySerAsnArg 1797  AlaArgalaGlyIleSerGlyValTyrSerPheGlyAspAsnAlaTyrGlySerAsnArg 784		1//3 764	WO200152885 26-JUL-2001
Name		1797	17-JAN-2001;
-y	SerPheGlyAspAsnAlaTyrG	784	17-JAN-2000; 09-MAR-2000;
XXGlylleGlnAlaGlyTyrlleTrpSerAspAsnPheAsnHisValProTyrArg 808   OR		790	(CHIR-) CHIRON SPA. Pizza M, Rappuoli R,
	}	808	

TCCCGATGCCCGGCGCGAAAGACGCGCGCGCC 2115 AlaThrGlyValLysGlu-----GluGlyAsn 907 ||| :::|||::: || :::|||::: STTCAAAACATTTACGGCGGCGGCAATACCCAT 2235 ----GGCAGAACCAAAGAAATCCCCTTCTTT 1944 31yGlyGlnValLeuAlaValGly------ 845 ....-LysAsp 856 870 ne protein; Neisserial infection; ¥ eria serogroup B protein" ia serogroup B protein. hrProPhe 919 SIS Ξ. us-09-914-168-2.rng

The present sequence encodes a Neisseria serogroup B protein. The protein is used to produce the compositions of the invention. The specification describes a composition, comprising a Neisseria meningitidis serogroup B outer membrane preparation and an immunogenic component. The immunogenic component is protein disclosed in WO99/57280, WO99/3613, WO99/36813, WO99/36813, WO99/36813, WO99/56813, WO99/56813, WO99/5883, WO99/56813, WO99/5883, WO99/56813, WO99/56 Composition for treating or preventing infection to, detecting, or for raising antibodies against Neisserial bacteria, comprises an N. meningitidis serogroup B outer membrane preparation and an immunogenic Disclosure; Page 58-59; 83pp; English also be used as a vaccine. component 

583 G; 411 T; 0 other; ς; Sequence 2394 BP; 657 A; 743

369 116 ThrProLeuSerLeuGluGluLeuPheAlaGlnGluSerThrGluMetGlyIleAsnPro 135 136 AsnAsp------TyrIleProGluTyrGlnGlyGluGlnProAsnSer 149 GluvalvalvalProProThrLeuGluProGluLysProGlyLeuIleLysArgLeuTyr 169 AlaArgLeuPheAsnAspGlyValAsnLysValPro-----ArgLeuLysAlaLys 186 259 GTTATCGAACGCCCCACCATCGGCTCGCTCAACATCACCGGCGCGAAAATGCTGCAAAAC 318 224 429 ------ThrAlaLeuValAlaAlaArgAlaValGlyTyrTyrAsp 249 GGCAAACTCAATATCCAAATCACGCCCAAAGTAACCAAACTCGCCCGCAACCGCGTCGAC 489 IleAspLeuSerIleIleArgAsnSerIleGlyGluValAspValIleIleHisAspLeu 269 546 GlyGluProValTyrIleAspTyrArgAlaValGluValArgGlyGluGlyAlaAspAsp 289 582 -----GACACACACGCCAGCCATCAAAAGCCTGTAC 198 ATCGACATCACGATTGACGAGGGCAAATCCGCCAAAATCACCGACATCGAATTTGAA---:::|||||||:::||| :::
TCGCCTTTGGCACTTCACCATCCAAGACATCCGCGTCGAAGGCTTGCAGGT GCCACCGGTTTCTTTGACGACGTACGCGTCGAAACTGCGGACGGGCAGCTCCTGCTGACC 319 GACGCC-----ATTAAGAAAAACCTCGAATCGTTCGGGCTGGCGCAGTCGCAATAC PheTyrGlnSerSerGlnSerGlyGluThrSerAlaIleGlySerSerHisGlnLysThr GluProTyrAlaAsnIleLysAlaAlaLeuGluAsp-----IleThrGlnGluSerAla Metasp-----LeuAsnGlySerIleProArgLeuArgGln------Length:
Matches:
Conservative:
Mismatches:
Indels: 547 GGCAACCAAGTCTATTCCGACCGCAAACTGATGCGG---Gaps: US-09-914-168-2 (1-919) x AAH42128 (1-2394) 2.06e-11 259.00 33.48% 20.49% 5.48% Best Local Similarity: Percent Similarity Alignment Scores: Query Match: .. Q 46 106 150 170 199 207 225 430 270 187 237 163 Score Pred. qq QQ QQ g ò g δ g ò Dp δy Pp ò q ò οy ò g δ

δý	290	GluvalProLeuLeuIleGlyAspval 3	90
qq	583	G G	18
οy	307		20
QQ	619	CTGACACGAAGCAACCAATTCAACGAGCAGAAATTTGCCCCAAGATATGGAAAAAGTAACC 67	7.8
Qy	321	1 3	3.8
3 3	0 0		9
S G	34.1 739	34 Ilebeurioaspasninialaaspvalseileulleiyiraspiniciyiniciniyriig soo 	0 86
δy	361	PheAspGluValValPhePheThrIleAspProLysThrAsnGlnLeuThrThrAspPro 36	80
qq	199	::: :::    :::    :::    :::	34
δÿ	381	AspLysLeuProValLysArgGluLeuLeuGluGluGlnLeuLeuThrValAsnMetGlyGlu 4(	00
QQ	835		82
Qy	401	AlaTyrAsnLeuGlnAlaValArgAlaLeuSerAsnAspLeuIleAlaThrArgTyrPhe 4	20
QQ	883	TGGTACGAACGCCAGAAGACGCCCGTTTTGGGT9	118
ΟY	421	AsnMetValAsnThrGluIleValPheProGluArgGluGlnIleGlnAsnAspGlnVal 4	40
qq	919	-:	39
δy	441	SerPheGluGlnSerSerSerArgThrGluProAlaGlnValAspGluSerThrLeu 40	09
qq	940	TCGGCAGGCTACGCATACAGCGAAATCAGCGTA 9	172
Qy	461	GluProValIleGluThrValGluLeuThrAspGlyIleLeuMetAspIleSerPro 4	179
Dp	973	CAGCCGCTGCCGAACGCTGAAACCGTCGATTTCGTCCTGCACATCGAACCGGGC 10	032
Qy	480		92
qq	1033	CGGAAAATCTACGTCAACGAAATACACATCACCGGCAACAAAAAACCGGCGACGAA 1	1089
ΟŊ	493	AsnLeuValAlaAlaLysAlaArgHisLeuTyrAspMetProAspAsp5	809
qq	1090	GTCGTCCGCCGTGAATTACGCCAAATCCGCACCTTACGACCTCCAAGCTG 1	1146
Qy	509	2	523
qq	1147	CAACGTTCCAAAGAGGGGGCGTCGAGGCTTTGGGCTACTTCGACAATGTCCAG1	1197
Qy	524	r 5	543
qq	1198	$\vdash$	123
ΟŸ	544	S	563
qq	1234	1	126
Οy	564	5	583
qq	1269	$\vdash$	126
δy	584	9	501
QQ	1270		132
Qγ	602	LysPheGluHisAsnLeuIleAsnArgAspGlyTyrGlnAlaGlyAlaGluLeuArgLeu 6	621
Db	1321		138

Tue May

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1435 ACGCCAGACGGGTCAGCCTGGCTAC----GATGTTTACGGAAAAGCCTTCGACCC 1488
                                                                                                                                                                                   1489 CGCAAAGCATCGACCAGCATCAAACAATATAAAACCACCACGGCA------GGC 1536
                                                                                                                                                                                                                                                                  1537 GCAGGCATCCGCATGAGCGTGCCTGTTACCGAATACGACCGCGTGAATTTCGGTTTGGTG 1596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2056 AAAGCCAACGTCTCCGCCGAGCTGCTCTTCCCGATGCCCGGCGCGAAAGACGCGCGCACC 2115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----CTGACGGCGTGAAATC 1797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1834 ACCCACAACCAAACCTGGTTCTTCCCCCTGAGCAAAACCTTCACGCTGATGCTCGGCGGC 1893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2296 CCTTTAGGCCCGATGAAATTCAGCTACGCCTACCCGCTGAAGAAAAACCGGAAGACGAA 2355
                                                                                                                                                                                                                             682 GlyTrpAsnArg------ThrTyrSerLeuArgTyrArgLeuAspLysLeu 696
SerGluAspLysLysGlyValLysLeuTyrAlaThrLysProLeuSerHisProLeuAsn 641
                                                                                                                                                   PheAspLeuSerThrArgThrLeuGluHisGluIleSerArgSerIleIleGlnAsnGly 681
                                                                                                                                                                                                                                                                                                      697 LysThrGlnAlaProProGluThrTrpGlnAspLeuPro-----ValAspPheVal 713
                                                                                                                                                                                                                                                                                                                                                                                Asn-----GlyLys---ProSerGlnGluAlaLeuLeuAlaGlyValAlaValHisLys 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ThrVal------AlaAspAsnLeuValAsnProMetArgGlyTyrArg 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 745 GlnArgTyrSerLeuGluValGlySerSerGlyLeuValSerAspAlaAsnMetAlaIle 764
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                                     1381 TCCAGGAGCAAA-----ACCACGCTTAACGGCTCGCTGTCGTTTACTGACCCGTACTTC
                                                                         AspGlnLeuArgAlaThrLeuGlyTyrGlnGlnGluValPheGlyHisSerThrAsnGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           765 AlaArgAlaGlyIleSerGlyValTyrSerPheGlyAspAsnAlaTyrGlySerAsnArg
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Sequence 2394 BP; 655 A; 758 C; 586 G; 395 T; 0 other;

also be used as a vaccine.

2394 191 121 342 278 40

Conservative: Mismatches: Indels: Gaps:

2.06e-11 259.00 33.48% 20.49% 5.48%

Percent Similarity:
Best Local Similarity:
Query Match:
DB:

Alignment Scores:

Length: Matches:

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Composition for treating or preventing infection to, detecting, or for raising antibodies against Neisserial bacteria, comprises an N. meningitidis serogroup B outer membrane preparation and an immunogenic
                                                                                                             Serogroup A protein; outer membrane protein; Neisserial infection; vaccine; ss.
                                                                                                                                                                                 "Neisseria serogroup A protein"
                                                                                            Nucleotide sequence of a Neisseria serogroup A protein.
2356 ATCCAACGCTTCCAATTCCAACTCGGCACGACGTTC 2391
                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 70-71; 83pp; English.
                                                                                                                                                       Location/Qualifiers
1..2394
                                                                                                                                                                                                                                                                                                                                 Giuliani M;
                                          BP.
                                         AAH42130 standard; DNA; 2394
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2000GB-0005699
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64..2391
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                                                                                                                                      Neisseria meningitidis.
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                                                                                                                                                                                                                                                                                                               (CHIR-) CHIRON SPA.
                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAB84746.
                                                                                                                                                                                                                                  WO200152885-A1
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                                                                           17-SEP-2001
                                                                                                                                                                                          sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                     component
                                                          AAH42130;
                        RESULT 15
                                 AAH421
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0S-09	-914-	168-2 (1-919) x AAH42130 (1-2394)	
Οy	116	ThrProLeuSerLeuGluGluLeuPheAlaGlnGluSerThrGluMetGlyIleAsnPro 135	
Db	46	:::      :::    ::: TCGCCTTTGCCACTTCACCATCCAAGACATCCGCGTCGAAGGCTTGCAGCGT 105	
Qy Dp	136 #	AsnAspTyrIleProGluTyrGlnGlyGluGlnProAsnSer 149 	
0y			
QQ			
oy B	170 /	AlaArgLeuPheAsnaSpGlyValAsnLysValPtroTArgLeuLysAlaLys 186	
δy	187	PheTyrGlnSerSerGlnSerGlyGluThrSerAlalleGlySerSerHisGlnLysThr 206	
Q Q	259 (	::: GTTATCGAACGCCCCACCATCGGCTCGCTCACGGCGCGAAAATGCTGCAAAAC 318	
٥y	207	GluProTyrAlaAsnIleLysAlaAlaLeuGluAspIleThrGlnGluSerAla 224	
QQ	319 (	GACGCCATTAAGAAAACCTCGAATCGTTCGGCTGGCGCAGTCGCAATAC 369	
οy		MetaspLeuasnGlySerIleProargLeuargGln	
qq	370	TTTAATCAGGCGACACTCAATCAGGCAGTCGCCGGCCTGAAAGAAGAATACCTCGGGCGC 429	
Qy	237	ThrAlaLeuValAlaAlaArgAlGlyTyrTyrAsp 249	
Dp	430	GGCAAACTCAATATCCAAATCACGCCCAAAGTAACCAAACTCGCCCGCAACCGCGTCGAC 489	
Qy Db	250	IleaspLeuSerIleIleArgAsnSerIleGlyGluValAspValIIeIleHisAspLeu 269	
ΛO	270 (	GlyGluProValTyrIleAspTyrArqAlaValGluValArqGlyGluGlyAlaAspAsp 289	
. q		- 58	
ΟÝ	290 1	LysAlaPheThrThrValAlaAspGluValProLeuLeuIleGlyAspVal 306	
QQ	583	.:::::	
Qy	307		
QQ	619 (	CTGACACGAAGCAACTCAACGAGCAGAAATTTGCCCAAGACATGGAAAAAGTAACC 678	
Qy	321	AsnalaSeralaGluHisGlyTyrPheAspGlyArgTrpLeuAspArgSerValAspVal 340	
qq	649	GACTICTACCAGAACACGGCTACTICGATITCCGCATCCTCGATACCGACATCCAAACC 738	
Οy	П	g 36 	
g G	739	aacgaagacaaaaccaagaccatcaaaatcaccetccacgaaggcggacgttccgt 798	
٥y	361	PheAspGluValValPhePheThrIleAspProLysThrAsnGlnLeuThrAspPro 380	
qq	799	GGGCAAAGTCTCCATCGAAGGCGAC	
٥y	381	AspLysLeuProValLysArgGluLeuLeuGluGlnLeuLeuThrValAsnMetGlyGlu 400	
Dp	835	GTCCCCAAAGCCGAACTGGAAAAACTGCTGACGTGAAGCCCGGCAAA 882	
οy		AlaTyrAsnLeuGlnAlaValArgAlaLeuSerAsnAspLeuIleAlaThrArgTyrPhe 420     :::    ::	
QQ	883	TGGTACGAACGCCAGCAGATGACCGCCGTTTTGGGT	
٥y	421	AsnMetValAsnThrGluIleValPheProGluArgGluGlnIleGlnAsnAspGlnVal 440	

QQ	919	GAGATICAGAACCGCATGGGC 939
QY	441	erPheGluGlnSerSerSerArgThrGluProAlaGlnValAspGluSerThrLe
g	940	TCGGCAGGCTACGCATACAGCTCGGCAGGCTACGCGTA 972
δy	461	GluProVallleGluThrValGluLeuThrAspGlyIleLeuMetAspIleSerPro 479
QQ	973	CAGCCGCTGCCAAACGCCAAAACGGTCGATTTCGTCCTGCACATCGAACGGGC 1032
δλ	480	Š.
ΟD	1033	CGGAAAAATCTACGTCAACGAAATCCACATCACCGGCAACAACAAAAACCCGCGGCGAGAA 1089
δλ	493	ψ.
qq	1090	GTCGTGCGCCGCGAATTGCGCCAAATGGAATCCGCGCCTTACGACACCTCCAAGCTG 1146
ΟŊ	509	rgSerIle 523
QQ	1147	cgrcgagctttgggctacttcgacaacgi
Οy	524	erAspAlaValSerAlaValAlaArgAlaIleLeuProAspGluS
qq	1198	
ΟŊ	544	GluAsnGluValIleAspLeuProGluArgThrAlaLeuAlaAsnArgLysThrProAla 563
qq	1234	CGATITGAACAIGAG
δy	564	AspValTyrGlnSerLysLysValProLeuTyrValPheValAlaSerAspLysProArg 583
Dp	1269	1269
δy	584	AspGlyGlnIleGlyLeuGlyTrpGlySerAspThrGlyThrArgLeuValThr 601
qq	1270	GGCTCGCTCGCTTGAGGGGGGGGGTACAGGATACCGGCCTGGTCATG 1320
Øγ	602	LysPheGluHisAsnLeuIleAsnArgAspGlyTyrGlnAlaGlyAlaGluLeuArgLeu 621
qq	1321	
Qy	622	SerGluAspLysLysGlyValLysLeuTyrAlaThrLysProLeuSerHisProLeuAsn 641
q	1381	TCACGAAGCAAAACCACGCTCACGCTCGTCGTTTACCGACCGTACTTC 1434
Qy	642	AspGlnLeuArgAlaThrLeuGlyTyrGlnGlnGluValPheGlyHisSerThrAsnGly 661
QQ	1435	ACGCCAGACGGGGTCAGCCTGGGCTACGATGTTTACGGAAAAGCCTTCGACCC 1488
Qy	662	PheAspLeuSerThrArgThrLeuGluHisGluIleSerArgSerIleIleGlnAsnGly 681
QQ	1489	CCAGCATCAAACAATATAAAACCACCACGGCA
οy	682	GlyTrpAsnArgThrTyrSerLeuArgTyrArgLeuAspLysLeu 696
qq	1537	TGAGCGTGCCTGTT
οy	697	LysThrGlnAlaProProGluThrTrpGlnAspLeuProValAspPheVal 713
qq	1597	CAAAGCGCCCAAACACTATG
QY	714	AsnGlyLysProSerGlnGluAlaLeuLeuAlaGlyValAlaValHisLys 730
qq	1657	AAGAAATACGGCAAAACCGACGGCACAGAGGCTCTCAAAGGCTGGCT
Qy	731	ThrvalAlaAspAsnLeuValAsnProMetArgGlyTyrArg 744
qq	1717	ACCGTCGGCGGGGGCGCAACAAACCGACAGCGCGTTATGGCCGACGCGCGGCTAC 1773
Qy	745	GlnArgTyrSerLeuGluValGlySerSerGlyLeuValSerAspAlaAsnMetAlaIle 764
qq	1774	

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                                                                         1834 ACCCACAACCAAACCTGGTTCTTCCCCTTAAGCAAAACCTTCACGCTGATGCTCGGCGGC 1893
                                                                                                                  2005 CCG-----AAAGTGTATGACGAATACGGCGAAAAATCAGCTACGGCGACAAA 2055
                                                                                                                                                                                                                                                                                    2115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neisseria meningitidis; Neisseria gonorrheae; genome; immunogenic; antigen; vaccine; diagnosis; infection; antibacterial; identification; Meningococcus B; MenB; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2235 AACAGCAGTTCCGCGACCGGCGGCAGGGTTCAAAACATTTACGGCGCCGGCAATACCCAT 2235
AlaArgAlaGlyIleSerGlyValTyrSerPheGlyAspAsnAlaTyrGlySerAsnArg 784
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProValGlyGlnValArgValAspValAlaThrGlyValLysGlu...-GluGlyAsn 907
                                                                                                                                                                      -----GlyIleGlnAlaGlyTyrIleTrpSerAspAsnPheAsnHisValProTyrArg
                                                                                                                                                    LeuArgPhePheAlaGlyGlyAspGlnSerIleArgGlyTyrAlaHisAspSerLeuSer
                                                                                                                                                                                                                                                             ---LysAsp
                                                                                                                                                                                                                                                                                                                                                                                                             ---LysGlyPheThrAsnAspThrLysIleGlyAlaGlyValGlyValArgTrpAlaSer
                                                                                                                                                                                                         ProlleSerAspLysGlyTyrLeuThrGlyGlyGlnValLeuAlaValGly-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N. meningitidis partial DNA sequence gnm_26 SEQ ID NO:26.
                                                                                                                                                                                                                                                                                                            LeuArgLeuAlaValPheGlyAspIleGlyAsnAlaTyrAsp----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2356 ATCCAACGCTTCCAATTCCAACTCGGCACGACGTTC 2391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                908 ProlleLysLeuHisPhePheIleGlyThrProPhe
                         GCCCTGCCCGGCAGCAACTGCAATAC-----
                                                                                                                                                                                                                                                         846 ThrAlaGluTyrAsnTyrGluPheMet----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard; DNA; 52253 BP
                                                 785 AlaHisGlnMetThrGly----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neisseria meningitidis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200022430-A2.
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The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. AAA81453 to AAA82414

represent specifically claimed Neisseria meningitidis genomic DNA sequences; AAA81360 to AAA81360 to AAA81560 to AAA81550 to AAA81254 to AAA81259 and AAA81360 to AAA8131 represent PCR primers used in the Sequences; AAA81354 to AAA81351 represent PCR primers used in the AAA81452 represent Neisseria meningitidis DNA sequences; and AAA8132 to AAA81452 represent Neisseria meningitidis DNA sequences; and AAA8132 to AAA81452 represent Neisseria meningitidis DNA sequences; and AAA8132 to AAA81452 represent Neisseria meningitidis DNA sequences; and AAA8132 to AAA81452 represent Neisseria meningitidis DNA sequences; and antibodies sequences, which are all used in the manufacture of a composition. The nucleic acid sequences, protein sequences, and antibodies against them, can be used as a medicament (or in the manufacture of a medicament) for treating, preventing or diagnosing infection due to medicament) for treating, preventing or diagnosing infection due to Neisserial bacteria. For example, some of the identification due to proteins conformed be components of vaccines against Meningococcus B; against all serotypes; and/or against all pathogenia. Neisseriae. Identification of biological probes, particularly organism-specific probes. Attempts to make efficacious or medicament vaccines have also been tried but none have successfully overcome antigenic variability. The provision of further, complete sequences may provide an opportunity to identify secreted or surface exposed proteins that may be presumed targets for the immune system and which are not antigenically variable or at least more conserved than every because the conserved than antigenic variable regions.
     Scarlato V;
                                                                                                                                            Isolated nucleotide sequences of Neisseria meningitidis which can used in the diagnosis and treatment of N. meningitidis infection other Neisserial infections, for example, N.gonorrhoea - \star
  Scarselli M,
  Ratti G,
                                                                                                                                                                                                                                                        Claim 7; Page 532-547; 1760pp; English.
     Mora M,
  Galeotti C,
                             Pizza M;
                                                                                   WPI; 2000-318079/27.
Masignani V,
                             Rappuoli R,
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Sequence 52253 BP; 12877 A; 15510 C; 13103 G; 10761 T; 2 other;

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47343 TCGCCTTTGGCACTTGCCGACTTCACCATCCAAGACATCCGCGTCGAAGGCTTGCAGCGT 47402
                                                                                                                                                                                                                                                                                                                                    47556 GTTATCGAACGCCCCACCATCGGCTCGCTCAACATCACCGCGCGCAAAAATGCTGCAAAAAC 47615
                                                                                                                                                                                                                                                                                                                                                                    186
                                                                                                                                                                116 ThrProLeuSerLeuGluGluLeuPheAlaGlnGluSerThrGluMetGlyIleAsnPro 135
                                                                                                                                                                                                                                                                                                                                                                   170 AlaArgLeuPheAsnAspGlyValAsnLysValPro-----ArgLeuLysAlaLys
                                                                                                                                                                                                                                   136 AsnAsp-----TyrIleProGluTyrGlnGlyGluGlnProAsnSer
                                                                                                                                                                                                                                                                                                   GluValValValProProThrLeuGluProGluLysProGlyLeuIleLysArgLeuTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                  PheTyrGlnSerSerGlnSerGlyGluThrSerAlaIleGlySerSerHisGlnLysThr
                                                                                                                                                                                                                                                                                                                                                                                                   47496 GCCACCGGTTTCTTTGACGACGTACGCGTCGAAACTGCGGGACGGGCAGCTCCTGCTGACC
                 52253
191
121
342
278
40
                 Length:
Matches:
Conservative:
Mismatches:
                                                                                    Indels:
                                                                                                   Gaps:
                                                                                                                                 US-09-914-168-2 (1-919) x AAA81478 (1-52253)
                 1.17e-09
                             259.00
33.48%
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                                                               Best Local Similarity:
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Alignment Scores:
                                                                                    Query Match:
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47616 GACGCC-----ATTAAGAAAACCTCGAATCGTTCGGGCTGGCGAGTCGCAATAC 47666

GluProTyrAlaAsnIleLysAlaAlaLeuGluAsp-----IleThrGlnGluSerAla

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MetAsp ::: TTTAATC?	225 Metasp 236 :::             :::::               :::::
GGCAAACTCAAT	
IleAspLeuSer         ATCGACATCACG	IleaspLeuSerIleIleargasnSerIleGlyGluValaspValIleIleHisaspLeu 269 
GlyGluProVal      GCCAACCAAGTC	GlyGluProValTyrIleAspTyrArgAlaValGluValArgGlyGluGlyAlaAspAsp 289 
LysAlaPheThr	LysalaPheThrThrValalaAspGluValProLeuLeuIleGlyAspVal 306 
AsnAlaSerAl ::: GACTTCTACCA	AsnalaSeralaGluHisGlyTyrPheAspGlyArgTrpLeuAspArgSerValAspVal 340 ::: :::
IleLeuProAs AACGAAGACAA	IleLeuProAspAsnThralaAspValSerLeuIleTyrAspThrGlyThrGlnTyrArg 360
PheaspGluVal:::::::::::::::::::::::::::::::::::	PheaspGluValValPhePheThrIleaspProLysThrAsnGlnLeuThrThrAspPro 380 ::: :::    :::     :::   ::: TGGGGCAAAGTCTCCATCGAAGGCGACACCAACGAA 48131
AspLysLeuPr	AspLysLeuProValLysArgGluLeuLeuGluGlnLeuThrValAsnMetGlyGlu 400
AlaTyrAsnLe     TGGTACGAACG	AlaTyrAsnLeuGlnAlaValArgAlaLeuSerAsnAspLeuIleAlaThrArgTyrPhe 420            ::     :: TGGTACGAACGCCAGCAGATGACCGCCTTTGGGT
AsnMetValAs	AsnMetValAsnThrGluIleValPheProGluArgGluGlnIleGlnAsnAspGlnVal 440 :::         GAGATTCAGAACCGCATGGGC 48236
SerPheGluGl     TCGCCAGGCTA	SerPheGluGlnSerSerSerArgThrGluProAlaGlnValAspGluSerThrLeu 460 
GluProValII :::   :: CAGCCGCTGCC	GluProValIleGluThrValGluLeuThrAspGlyIleLeuMetAspIleSerPro 479 :::    :::
CGGAAAATCTA	480
AsnLeuValAl :::    GTCGTCCG	ASDLeuValAlaAlaLySAlaArgHisLeuTyrAspMetProAspAsp 508 
CAACGTTCCAA	
LeuGlyArgIle	LeuGlyArgileSerAspAlaValSerAlaValAlaArgAlaileLeuProAspGiuSer 543 
GluAsnGluVa]	544 GluAsnGluValIleAspLeuProGluArgThrAlaLeuAlaAsnArgLysThrProAla 563

QΩ	) 48531GTCGATTTG-	:::    AACATGAGTCTGACCGAACGTTCCACC	48566
QY	y 564 AspValTyrGlnSerLysLysV	alProLeuTyrValPheValAlaSerAspLysProArg	583
qq	b 48566		48566
QY	584 AS	pGlyGlnIleGlyLeuGlyTrpGlySerAspThrGlyThrArgLeuValThr	601
qq	48567		48617
QΥ	602 L	ysPheGluHisAsnLeuIleAsnArgAspGlyTyrGlnAlaGlyAlaGluLeuArgLeu	621
QQ	48618 T	ACCTGTTCGGTACGGCCAAGTCGGCCGCACTGCGCCCC	48677
ΟÝ	622 S	erGluAspLysLysGlyValLysLeuTyrAlaThrLysProLeuSerHisProLeuAsn	641
qq	48678 T	ACCACGCTTAACGCCTCGCTGTGTTACTGACCCGTACTTC	48731
Οy	642	AspGlnLeuArgAlaThrLeuGlyTyrGlnGlnGluValPheGlyHisSerThrAsnGly	661
qq	48732	SCTACGATGTTTACGAAAAGCCTTCGACCCG	48785
Qy	662	PheAspLeuSerThrArgThrLeuGluHisGluIleSerArgSerIleIleGlnAsnGly	681
QΩ	48786	AACAATATAAAACCACGGCAGGC	48833
Οy	682	ThrTyrSerLeuArgTyrArgLeuAspLysLeu	969
qq	48834	GCAGGCATCCGCATGAGCGTGCCTGTTACCGAATACGACCGCGTGAATTTCGGTTTGGTG	48893
Qy	697 LY	sThrGlnAlaProProGluThrTrpGlnAspLeuProValAspPheVal	713
qq	48894 GC		48953
QY	714	AsnGlyLysProSerGlnGluAlaLeuLeuAlaGlyValAlaValHisLys	730
qq	48954	SCACAGACGCCAGCTTCAAAGGCTGGCTGTACAAAGGT	49013
Qγ	731	ThrValAlaAspAsnLeuValAsnProMetArgGlyTyrArg	744
qq	49014	AAACCGACAGCGCGTTATGGCCGACGCGCGCTAC	49070
ΟŸ	745 GlnArgTyrSerLeuGluVal	GlySerSerGlyLeuValSerAspAlaAsnMetAlaIle	764
QQ	b 49071	CTGACGGCGTGAACGCCGAAATC	49094
ΟY	y 765 AlaArgAlaGlyIleSerGlyValTyrS	erP	784
QQ	49095	ATACTACTCGCC	49130
ογ	y 785 AlaHisGlnMetThrGly		790
QQ	49131	ACCCACAACCAAAACTIGGTTCTTCCCCTGAGCAAAACCTTCACGCTGATGCTTGGGCGGC	49190
δλ	y 791GlylleGlnAlaGlyTyrlleT	rIleTrpSerAspAsnPheAsnHisValProTyrArg	808
Dp	49191	GGCAGAACCAAAGAAATCCCCTT	49241
δ	808	pGlnSerIleArgGlyTyrAlaHisAspSerLeuSer	828
qq	49242	GAAAACTTCTACGGCGGCGGCCTGGGTTCGGTGCGGGATACGAAAGCGGCACGCTCGGT	49301
Qy	829 Proiles	erAspLysGlyTyrLeuThrGlyGlyGlnValLeuAlaValGly	845
qa	49302 CCG	CGAATACGGCGAAAAATCAGCTACGGCGGCAACAAA	49352
Οy	y 846 ThralaGluTyrasnTyrGluPhemet		856
QQ	49353	GCTCTTCCCGATGCCCGGCGCGAAAGACGCGCGCACC	49412
Οy	y 857 LeuArgLeuAlaValPheGlyAspIleGlyAsnAlaTyrAsp :::	pplleGlyAsnAlaTyrAsp	870

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes the full length genome of
Neisseria menigitidis B (NMB). The sequences in AAF21544 and AAF21607
Neisseria menigitidis B (NMB). The sequences in AAF21544 and AAF21607
to AAF21613 represent fragments of the NMB genomic sequence, as the
sequence was too long to go in a record on its own it was split into 8
sequences which overlap each other at the beginning and end of each
sequences which overlap each other at the beginning and end of each
sequences which overlap each other at the beginning of AAF21607, the last 49980 bp of AAF2164 is repeated at
the beginning of AAF21607, the last 49980 bp of AAF21540 are repeated at
the beginning of AAF21607, and so on). AAF21555 to AAF21589 encode the
Neisseria proteins given in AAB58550 to AAB58593, and AAF21589 to
AAF21606 represent PCR primers which are used in the exemplification of
the present invention. The NMB genome and fragments from it have
antibacterial activity, and can be used in vaccines and gene therapy.
Weisseria nucleic acids, proteins and/or antibadies which binds to the
proteins can be used in compositions for treating or preventing infection
due to Neisserial bacteria or as a diagnostic reagent for detecting the
                                                                                                                        GTCCGCCTGAGCCTGTTTGCCGACGCAGCGAGCGTGTGGGACGGCAAAACCTACGACGAC 49472
                                                                                                                                                                                                49593 CCTTTAGGCCCGATGAAATTCAGCTACGCCTACCCGCTGAAGAAAAACCGGAAGACGAA 49652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Masignani V;
Rappuoli R;
                                                                49473 AACAGCAGTICCGCGACCGGCGGCGGGTTCAAAACATTTACGGCGCCGGCAATACCCAT 49532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neisseria meningitidis; Neisseria gonorrheae; immunogenic; vaccine; diagnosis; antigen; detection; infection; gene therapy; antibacterial;
                                                                                                                                                                  ProvalGlyGlnValArgValAspValAlaThrGlyValLysGlu-----GluGlyAsn 907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neisseria meningitidis B full length genome sequence and open readi
frames are used to detect, treat and prevent Neisserial infections
                                                                                                   ---LysGlyPheThrAsnAspThrLysIleGlyAlaGlyValGlyValArgTrpAlaSer
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Scarlato V,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Neisseria meningitidis B nucleotide sequence SEQ ID NO:1.
                                                                                                                                                                                                                                                                   49653 ATCCAACGCTTCCAATTCCAACTCGGCACGACGTTC 49688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , Tettelin H,
Scarselli M,
                                                                                                                                                                                                                                     908 ProlleLysLeuHisPhePheIleGlyThrProPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 7; Appendix A; 692pp; English.
                                                                                                                                                                                                                                                                                                                                     AAF21544 standard; DNA; 349980 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hickey E, Peterson J,
C, Mora M, Ratti G, S
M, Grandi G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-APR-1999; 99US-0132068.
08-0CT-1999; 99WO-US23573.
28-FEB-2000; 2000GB-0004695.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-MAR-2000; 2000WO-US05928
                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neisseria meningitidis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200066791-A1.
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Frazer CM,
                                                                                                                                                                                                                                                                                                                                                                     AAF21544;
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49413
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presence of Neisserial bacteria or of antibodies raised to Neisserial bacteria. Computers, computer storage medium or computer databases can be used in a search to identify open reading frames (ORFs) or coding sequences within the NMB genome. The DNA sequences provide further opportunities to find antigenic or immunogenic proteins which are more effective in vaccines than the outer membrane proteins currently used.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 180761 TCGCCTTTGGCACTTGCCGACTTCACCATCCGAGACATCCGCGTCGAAGGCTTGCAGCGT 180702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GACTICIACCAAAATAACGGCTACTTCGATTTCCGTATCCTCGATACCGACAFCCAAACC 180069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 180701 ACCGAGCCGAGTACCGTATTCAACTACCTGCCCGTCAAAGTCGGCGACACCTACAAC--- 180645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db 180377 GGCAAACTCAATATCCAAATCACGCCCAAAGTAACCAAAATTGGCCGGCAACCGCGTCGAC 180318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 ThrProLeuSerLeuGluGluLeuPheAlaGlnGluSerThrGluMetGlyIleAsnPro 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               321 AsnAlaSerAlaGluHisGlyTyrPheAspGlyArgTrpLeuAspArgSerValAspVal 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              341 IleLeuProAspAsnThrAlaAspValSerLeuIleTyrAspThrGlyThrGlnTyrArg 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136 ASDASP------TyrIleProGluTyrGlnGlyGluBroAsnSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GluValValValProProThrLeuGluProGluLysProGlyLeuIleLysArgLeuTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170 AlaArgLeuPheAsnAspGlyValAsnLysValPro-----ArgLeuLysAlaLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCACCGGTTTCTTTGACGACGTACGCGTCGAAACTGCGGACGGGCAGCTCCTGCTGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LysAlaPheThrThrValAlaAspGluValProLeuLeuIleGlyAspVal-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---ThrAlaLeuValAlaAlaArgAlaValGlyTyrTyrAsp
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                                                                                                                                                                                                                                                                                                                                                                          Sequence 349980 BP; 83241 A; 85091 C; 95206 G; 86442 T; 0 other;
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179270 GCAGGCATCCGCATGAGCGTGCCTGTTACCGAATACGACCGCGTGAATTTCGGTTTGGTG 17	09/ LYSTINFOLIGATAFIOFFGOLUTHTIFPOLIGASPLEUPTOVALASPENEVAL	714 179150	Qy 731 ThrValAlaAspAsnLeuValAsnProMetArgGlyTyrArg 744	Qy 745 GinargTyrSerLeuGluValGlySerSerGlyLeuValSerAspalaAsnMetalaile 764	Qy 765 AlaArgAlaGlyIleSerGlyValTyrSerPheGlyAspAsnAlaTyrGlySerAsnArg 784	Qy 785 AlaHisGlnMetThrGly790  Db 178973 ACCCACAACCTGGTTCTTCCCCTGAGCAAAACTTCACGCTGATGCTCGGCGGC 178914	Qy 791GlyIleGlnAlaGlyTyrIleTrpSerAspAsnPheAsnHisValProTyrArg 808	Qy 809 LeuargPhePheAlaGlyGlyAspGlnSerIleargGlyTyralaHisAspSerLeuSer 828	Qy 829 ProlleSerAspLysGlyTyrLeuThrGlyGlyGlnValLeuAlaValGly 845	Oy 846 ThralaGluTyrAsnTyrGluPheMet	857 LeuargLeualaValDheGlyAspileClyAsnalaTyrAsp	QY 870 870  Db 178631 AACAGCAGTTCGCGACGGCGGGGGTTCAAAACATTTACGGCGCGGGAATACCCAT 178572	Oy 871LysGlyPheThrAsnAspThrLysIleGlyAlaGlyValGlyValArgTrpAlaSer 889  Db 178571 AAATCCACCTTACCAACGAATTGCGCTATTCCGCCGGCGGGGGGGG	Oy 890 ProvalGlyGlnValArgValAspValAlaThrGlyValLysGluGluGlyAsn 907	Qy 908 ProlleLysLeuHisPhePhelleGlyThrProPhe 919 :::      :::          Db 178451 ATCCAACGCTTCCAACTCGGCACGACGTTC 178416	SUL A15	XX XX 21-AUG-2000 (first entry)	DE DNA encoding outer membrane protein (omp) 85. XX KW Outer membrane protein; omp85; gonococcal infection; symptomatic disease;
Db 180068 AACGAAGACAAAACCAAGCAGACCATCAAAATCACCGTCCACGAAGGCGGACGTTCCGT 180009	Qy 361 PheaspGluValValPhePheThrIleAspProLysThrAsnGlnLeuThrThrAspPro 380 ::: :::    :::	Oy 381 AspLysLeuProValLysArgGluLeuGluGluGluLeuThrValAsnMetGlyGlu 400	Qy 401 AlaTyrAsnLeuGlnAlaValArgAlaLeuSerAsnAspLeuIleAlaThrArgTyrPhe 420 	Qy 421 AsnMetValAsnThrGluIleValPheProGluArgGluGInIleGlnAsnAspGlnVal 440 Db 179888GAGATTCGCGCTGGGG	Oy 441 SerpheGluGlnSerSerSerSerArgThrGluProAlaGlnValAspGluSerThrLeu 460	Qy 461 GluProValIleGluThrValGluLeuThrAspGlyIleLeuMetAspIleSerPro 479 ::::	OY 480	CTG	509ArgValLeuAlaIleAsnHisAspAspGlyValAsnArgSerIle 179660 CAACGTTCCAAAGAGGGGGGGGGGGGGGGGGGGGGGGGG	524 LeuGlyArglleSerAspAlaValSerAlaValAlaArgAlaIleLeuProAspGluSer 179609TTTGARGCTGTCCCGCTTGCCGCACGACAA	544 GluAsnGluValIleAspLeuProGluArgThrAlaLeuAlaAsnArgLysThrProAla :::	Qy 564 AspValTyrGlnSerLysLysValProLeuTyrValPheValAlaSerAspLysProArg 583 Db 179538 179538	584 AspGlyGlnIleGlyLeuGlyTrpGlySerAspThrGlyThrArgLeuValThr 119537GTTCCTGGATTGGGGTTGGGTTCAAAPACGGGTTGGTCAG	AlaGluLeuArgLeu 621 	641	Oy 642 AspGlnLeuargalaThrLeuGlyTyrGlnGlnGluValPheGlyHisSerThrasnGly 661 :::	Oy 662 PheAspLeuSerThrArgThrLeuGluHisGluIleSerArgSerIleIleGlnAsnGly 681	ArgLeuAspLysLeu

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                                                                                                                                                                                                                                                                                                                                                                     The present sequence encodes an outer membrane protein (omp) 85 of Neisseria meningitidis. The omp polypeptides and polynucleotides are useful in compositions for use in the prevention, treatment and diagnosis of non-symptomatic genococcal infection or meningococcal infection and symptomatic disease. They are also useful for the detection of hybridisation complexes, Antiqens and antibodies specific omp proteins also provide diagnostic, therapeutic and prophylactic compositions for the treatment or prevention of the infections described above. The antibodies are useful for inducing a protective immune response in humans or animals with N. gonorrhoeae, N. meningitidis, or other Neisseria species. The proteins, antibodies and polynucleotide sequences of the present invention may also be used in the screening and development of chemical compounds such as drugs or vaccines.
                                                                                                                                                                                                                                                                                             New isolated outer membrane protein 85 of Neisseria gonorrhoeae and N. meningitidis useful for vaccine, therapeutic and diagnostic compositions for gonococcal or meningococcal infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 ThrProLeuSerLeuGluGluLeuPheAlaGlnGluSerThrGluMetGlyIleAsnPro 135
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meningococcal infection; protective immune response; vaccine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----GAAATCAGGGTA
                                                                                                                                               GluProTyrAlaAsnIleLysAlaAlaLeuGluAsp-----IleThrGlnGluSerAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----ThrAlaLeuValAlaAargAlaValGlyTyrTyrAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGCAAACTCAATATCCAAATCACGCCCAAAGTAACCAAAACTCGCCCGCAACCGCGTCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGACACGAAGCAACCAATTCAACGAGCAGAAATTTGCCCAAGACATGGAAAAAGTAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               321 AsnAlaSerAlaGluHisGlyTyrPheAspGlyArgTrpLeuAspArgSerValAspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AACGAAGACAAAACCAAGCAGACCATCAAAATCACCGTCCACGAAGGCGGACGTTTCCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTTAATCAGGCGACACTCAATCAGGCAGTCGCCGGCCTGAAAGAAGAATACCTCGGGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       490 ATCGACATCACGATTGACGAGGGCAAATCCGCCAAAATCACCGACATCGAATTTGAA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LysAlaPheThrThrValAlaAspGluValProLeuLleGlyAspVal------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AsnLeuValAlaAlaLysAlaArgHisLeuTyrAspMetProAspAsp---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGGGCAAAGTC-----TCCATCGAAGGCGACACCAACGAA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          883 TGGTACGAACGCCAGCAGATGACCGCCGTTTTGGGT------
                                                                                                                                                                                                                                                                                                                                                                                                                          -----LeuAsnGlySerIleProArgLeuArgGln--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCAACCAAGTCTATTCCGACCGCAAACTGATGCGG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCGGCAGGCTACGCATACAGC
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Dp	1147	CAACGCTCCAAAGAGCGCGTCGAGCTTTTGGGCTACTTCGACAACGTACAG 1197	
0λ	524	LeuGlyArgIleSerAspAlaValSerAlaValAlaArgAlaIleLeuProAspGluSer 543	
QQ	1198	TTTGATGCCGTCCCGCTTGCCGCACACAA 1233	
οy	544	GluAsnGluValileAspLeuProGluArgThrAlaLeuAlaAsnArgLysThrProAla 563	
QQ	1234	GTCGATTTGAACATGAGCCTGACGAACGTTCCACC 1269	
ογ	564	AspValTyrGlnSerLysLysValProLeuTyrValPheValAlaSerAspLysProArg 583	
qq	1269	1269	
οy	584	AspGlyGlnIleGlyLeuGlyTrpGlySerAspThrGlyThrArgLeuValThr 601	
QQ	1270	GCTCGCTCGATTGAGCGCGGGCTACAGGATACCGGCCTGGTCATG 1320	
ογ	602	LysPheGluHisAsnLeuIleAsnArgAspGlyTyrGlnAlaGlyAlaGluLeuArgLeu 621	
QQ	1321	TCCGCAGGCGTTTCCCAAGACAACCTGTTCGGTACGGCCAAGTCGGCCGCCCTGCGCGCCC 1380	
οy	622	SerGluAspLysLysGlyValLysLeuTyrAlaThrLysProLeuSerHisProLeuAsn 641	
QQ	1381	TCACGAAGCAAAACCACGCTCAACGCCTCGTCGTTTACCGACCCCGTACTTC 1434	
οy	642	AspGlnLeuArgAlaThrLeuGlyTyrGlnGlnGluValPheGlyHisSerThrAsnGly 661	
g	1435	ACGCCAGACGGGTCAGCCTGGGCTACGATGTTTACGGAAAAGCCTTCGACCCG 1488	
οy	662	PheAspLeuSerThrArgThrLeuGluHisGluIleSerArgSerIleIleGlnAsnGly 681	
QQ	1489	CGCAAAGCATCGACCAGCATCAAACAATATAAAACCACCACGGCAGGC 1536	
δλ	682	GlyTrpAsnArgThrTyrSerLeuArgTyrArgLeuAspLysLeu 696	
QQ	1537	GCAGGCATCCGCATGAGCGTGCCTGTTACCGAATACGACCGCGTGAATTTCGGTTTGGTG 1596	
Οy	697	LysThrGlnAlaProProGluThrTrpGlnAspLeuProValAspPheVal 713	
q	1597	GCAGAACACCTGACCGTCAACAACAACAAGCGCCCAAACACTATGCCGACTTTATC 1656	
δy	714	AsnGlyLysProSerGlnGluAlaLeuLeuAlaGlyValAlaValHisLys 730	
qq	1657	AAGAAATACGGCAAGACGGCACAGGCAGCTTCAAAGGCTGGCT	
٥y	731	ThrValAlaAspAsnLeuValAsnProMetArgGlyTyrArg 744	
qq	1717	ACCGTCGGCTGGGGGCGCACAAAACCGACAGCGCGTTATGGCCGACGCGCGGCTAC 1773	
Oy	745	GlnArgTyrSerLeuGluValGlySerSerGlyLeuValSerAspAlaAsnMetAlaIle 764	
QQ	1774	GGCGTGAACGCCGAA	
٥y	765	AlaArgAlaGlyIleSerGlyValTyrSerPheGlyAspAsnAlaTyrGlySerAsnArg 784	
q	1798	GCCCTGCCCGGCAGCAAACTGCAATACTACTCCGCC 1833	
Οy	785	AlaHisGlnMetThrGly790	
QQ	1834	ACCCACAACCAAACCTGGTTCTTCCCCTTAAGCAAAACCTTCACGCTGATGCTCGGCGGC 1893	
δ	791	GlylleGlnAlaGlyTyrIleTrpSerAspAsnPheAsnHisValProTyrArg 808	
qq	1894	GAAGTCGGCATTGCGGGCGGCTACGGCAGAACCAAAGAAATCCCCTTCTT 1944	
οy	809	LeuargPhePheAlaGlyGlyAspGlnSerIleArgGlyTyrAlaHisAspSerLeuSer 828	
qq	1945	GAAAACTTCTACGGCGGCGGCTGGGTTCGGTGCGGGATACGAAAGCGGCACGCTCGGT 2004	
οy	829	ProlleSerAspLysGlyTyrLeuThrGlyGlyGlnValLeuAlaValGly 845	
QQ	2005		

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The present invention provides isolated polynucleotides encoding HtrA, PonA, HypC, LysS, YefW, ABC1 or Omp100 protein of Lawsonia intracellularis. The sequences can be used in vaccines for the prevention of Lawsonia intracellularis infection. The present sequence is a coding sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HtrA; PonA; HypC; YefW; ABC1; Omp100; Lawsonia intracellularis infection;
                       2056 AAAGCCAACGTCTCCGCGAGCTGCTTCCCGATGCCTGGCGCGAAAGACGCGCGCACC 2115
                                                                        2236 AAATCCACCTTAACCAAGGAATTGCGCCTATTCCGCGGCGCGCGGTTACCTGGCTCG 2295
                                                                                                                                                                                                                                                    2296 CCTTTAGGCCCGATGAAATTCAGGTACGCCTACCCGCTGAAGAAAAAACCGGAAGACGAA 2355
                                                                                                                                        2176 AACAGCAGTTCCGCGACCGGCGGCGGGTTCAAAACATTTACGGCGCCGGCAATACCCAT 2235
                                                                                                               870
                                                      870
--LysAsp 856
                                                                                                                                                                                                                             890 ProValGlyGlnValArgValAspValAlaThrGlyValLysGlu-----GluGlyAsn 907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lawsonia intracellularis polynucleotide and encoded protein, used to prevent Lawsonia intracellularis infection
                                                                                                                                                                      871 ---LysGlyPheThrAsnAspThrLysIleGlyAlaGlyValGlyValArgTrpAlaSer
                                                      LeuArgLeuAlaValPheGlyAspIleGlyAsnAlaTyrAsp--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6617 BP; 2216 A; 1153 C; 1142 G; 2106 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lawsonia intracellularis coding sequence SEQ ID NO: 1.
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198
137
391
239
38
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                    2356 ATCCAACGCTTCCAATTCCAACTCGGCACGACGTTC 2391
                                                                                                                                                                                                                                                                                    908 ProlleLysLeuHisPhePhelleGlyThrProPhe 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Page 37-39; 67pp; Japanese.
 846 ThrAlaGluTyrAsnTyrGluPheMet-
                                                                                                                                                                                                                                                                                                                                                                     AAI97964 standard; DNA; 6617 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.65e-09
238.50
34.72%
20.52%
5.05%
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                                                                                                                                                                                                                                                                                                                                                                                                                            20-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lawsonia intracellularis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PFIZ ) PFIZER PROD INC.
                                                                                                             870 -----
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Best Local Similarity:
Query Match:
DB:
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-----TCAGITAITAGIGAIAGACIAITGICCCAAGAIAITCAAAAAAITACCGAC 4528 3824 ICAAAIGAIGAAGAAGIIACAAACAGAACIACCAAIGCIICIIGCAACIGCAIIAAAGAAI 3883 ------AAGGGA 3889 TITCGIGICALTAAAATCIGCATTAAAICIT-----CIATATAAAAATATC 3943 3944 TCCCAACTTAATATTTCTACTGCAAAAAGGTA-------GCTCAACAACTCCAT 3991 -----TTTAGT 4042 4160 -----AATGGCCTTATAAAGAAA---AACACTATTGCTGATGTACGTATTCATGGGCTT 4210 4211 AAAGTICTIGAICCTGAIGIAAICCTIACACGACTCACTAITAAIAAGGGAGAICAIACT 4270 4376 TTTACTGTACAAGAAAGCCTAAAATTACAGATGTTGTTGTTCAAGGCTCAAAAGCTGTA 4435 1529 CTCTATAGAAAAGAAGGCTACTATCTCGCTGAA-----GTTAATTATGAAATAAAAGAG 4582 1271 GATCATGCCAAAATTAATGCAGAAATCAAAAAATATGGGAATTAGGA-----TATTTT 4324 109 MetSerVallleGluGluThrThrProLeuSerLeuGluGluLeuPheAlaGlnGluSer 128 294 ThrValAlaAspGluValProLeuLeuIleGlyAspValPheHisHisGlyLysTyrGlu 313 ThrGluMetGlyIleAsnProAsnAspTyrIleProGluTyrGlnGlyGluGlnProAsn 148 SerGluValValValProProThrLeuGluProGluLysProGlyLeuIleLysArgLeu 168 TyrAlaArgLeuPheAsnAspGlyValAsnLysValProArgLeuLysAlaLysPheTyr 188 ThrGluProTyrAlaAsnIleLysAlaAlaLeuGluAspIleThrGlnGluSerAlaMet 225 226 AspLeuAsnGlySerIleProArgLeuArgGlnThrAlaLeuValAlaAlaArgAlaVal 245 314 ThrLysLysAsnLeuIleGluAsnAlaSerAlaGluHisGlyTyrPheAspGlyArgTrp 333 89 PheAspAspGlnSerProIleSerArgIleGlyGluGlnSerProProLeuGlyLeuAsp 108 GlnSerSerGlnSerGlyGluThrSerAlaIleGlySerSer------HisGlnLys 205 334 LeuAspArgSerVal-----AspValIleLeuProAspAsnThrAlaAspValSerLeu 351 352 IleTyrAspThrGlyThrGlnTyrArgPheAspGluValValPhePheThrIleAspPro 371 LysThrAsnGlnLeuThrThrAspProAspLysLeuProValLysArgGluLeuLeuGlu 391 AsnGlnAlaLysAlaGlyAsnProProValLeuLeuThrProGluGlnIleGlnAlaArg 69 246 GlyTyrTyrAspIleAspLeuSerIleIleArgAsnSerIleGlyGluValAspValIle IleAspTyrArgAla---ValGluValArgGlyGluGlyAlaAspAspLysAlaPheThr 70 LeuAsnAlaAlaGlyLeuAsnAlaLys---ProGlnSerGlnAlaLeuAspValValAsn AAACCAAAATTTAATGAGCTAAATATTGCTGTAACAGAACTTGCTGAACGTATAAGT---4007 TACGGCAGTTTCAATCAAACAGGTGAAAAT-----3992 GCTGACTATGTAGTA-----US-09-914-168-2 (1-919) x AAI97964 (1-6617) AAAGAAAATACTTCTTGCA---206 20 3890 129 189 4103 4478 372 4583 149 169 Db qq pp qq a Op qq qq qq qq g, QQ ŏ qq δ Q ò g ð g ŏ ŏ ŏ å ò ò ò ò ò

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Qy	392	<pre>lnLeuLeuThrValAsnMetGlyGluAlaTyrAsnLeuGlnAlaValArgAlaLe</pre>	411
qq	4607	:::	4
Qy	412	AsnAspLeulleAlaThrArgTyrPheAsnMetValAsnThrGluIleValPheProGlu	4
qq	4667	:::      GAAACAATAAAAGCTAAAACTTTAAAAAAAGAGTTAGCATT	4
QY	432		437
qq	4718	TTTACTGGAACAGGTGTATTACGTGAAGAA	4
Qy	438	ValSerPheGluGlnSerSerSerArgThrGluF	4
qq	7	TCTGCCTATGCCATGAATCATGGC	4
Οy	458	val11.eG	4
QQ	4829	AACATTCAATGAAAAGGAATTGTTATTACAYTTAG	48
Qy	470	aSe	489
QQ	4889	ATTAGGAAAATAGACTTTAAAGGAGATCTTATTGA	9
Qy	490	aAlaLysAlaArgHisLeuTyrAspMet	509
QQ	4949		5008
Оу	510	pGlyValAsnArgSerIleLeuGlyArgIleS	529
qq	5009	TGTAAAAGCATTAACAGATTTTAAT	50
Οy	530	530 AlaValSerAlaValAlaArgAlaIleLeuProAspGluSerGluAsnGlu	
q	5063	AGATCTTGAAACAACCAAAAATGAAGAAC	5.1
Qy	547	eAspLeuProGluArgThrAlaLeu	
qq	5120	   TGATAAAAAAAAAGTCTTTCTTCGTAGA	51
Oy	557	oAlaAspValTyr	56
qa	5180	AGATAATGTTATCCTCCGTGAATTACGCCTTGC	
Qy	266		26
QQ	5240	TCTCCGACGCTCTAATGAATGCCTTAACCGCCT	52
Qy	267	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	57
qq	5300	TACACTGCCTACAGGGAAGGATGATGAAGTTGA	53
Qy	574	sProArgAspGlyGl	593
qa	5360	AAGTTCAAGAAGCTCGAACAGGTC	54
ΟŊ	594	lyThrArgLeuValThrLysF	6.1
qq	5414	3GTGTTTCAGGAAGTATCT	5.4
QY	611	AspGlyTyrGlnAlaGlyAlaGluLeuArgLeuSerGluAspLysLysGlyValLysLeu	63
qq	5474	  TTATATTTAAGTATTGAAGGTTTTTATTTCTA	
Οy	631	LysProLeuSerHisProLeuAsnAspC	65
qq	5531	TTTACCAATCCTCGTGTTTATGATACAGAC	55
Oy	651	GlnGluValPheGlyHisSerThrAsnGlyPheA	664
qq	5564	TITGGCTTTAGTAACATTTATACGCTACGAGATGA	561.1

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                                                                                                                                                                                                                     777
                                                                                                                                                                                                                                                                                                            817
                                                                                                                                                                                                                                                                                                                                                                                                                                            874
 ---SerThrArgThrLeuGluHisGluIleSerArgSerIle 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                       |||| ::: |||||:::||||:::
                                                                                                          5708 CTATATGATATTCCATCTACAGCACCACGCTCTTATCTTGACTAT----CAAGGGAAAAAT
                                                                                                                             SerGlnGluAlaLeuLeuAlaGlyValAlaValHisLysThrValAlaAspAsnLeuVal
                                                                                                                                                   5765 ATTICTAGIGIAGIAGIGGIGGITTIACTITIGATICIACA-----GACAGICGIGAG
                                                                                                                                                                                               5819 AGACCATCTAAAGGGCATATTGCAAAACTAATTGTTGAATATGGAGGTGGTGTTTTGGT
                                                                                                                                                                                                                     758 SerAspAlaAsnMetAlaIleAlaArgAlaGlyIleSerGlyValTyrSerPheGlyAsp
                                                                                                                                                                                                                                                                778 AsnAlaTyrGlySerAsnArgAlaHisGlnMetThrGlyGlyIleGlnAlaGlyTyrIle
                                                                                                                                                                                                                                                                                      -----TCAAGAAGTAAAAACCATATAATACATTGGCGTACACGTGCAGGTGCAGCT
                                                                                                                                                                                                                                                                                                           TrpSerAspAsnPheAsnHisValProTyrArgLeuArgPhePheAlaGlyGlyAspGln
                                                                                                                                                                                                                                                                                                                                 AsnAsp.....ThrLysIleGlyAlaGlyValGlyValArgTrpAlaSerPro
                                         678 IleGlnAsnGlyGlyTrpAsnArgThrTyrSerLeuArgTyrArgLeuAspLysLeuLys
                                                                                    698 ThrGlnAlaProProGluThrTrpGlnAspLeuProValAspPheValAsnGlyLysPro
                                                                                                                                                                          AsnProMetArgGlyTyrArgGlnArgTyrSerLeuGluValGlySerSerGlyLeuVal
                                                                                                                                                                                                                                                                                                                                                      SerIleArgGlyTyrAlaHisAspSerLeuSerProIleSerAspLys---GlyTyrLeu
                                                                                                                                                                                                                                                                                                                                                                                                 ThrGlyGlyGlnValLeuAlaValGlyThrAlaGluTyrAsnTyrGluPheMetLysAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTAGGTCTTGCATTCCATTCTATGACATAGGATTCCAAACAGATTCTGTACAAACT
                                                                                                                                                                                                                                          GGTAATGATAACTTCTTCAAGCCAATTGCTGAACTACAAGGATTTTACTCAATT---
                    5612 TTCCGTAAAAAACTTATGGAGATACCATACGTCTATTTCACCCTATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding novel human diagnostic protein #17701.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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6284 ATGGGAGATTTGCGA 6298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ValGlyGlnValArg 895
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerasae chain reaction (PGR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical magning of sites expressing (II). (I) and (II) are useful in medical activity. The polypeptide and polynucleotide sequences have applications in disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and and cond sequences. A&Sé4197-A&S4564 represent novel human caid sequences and for his patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences.
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AGCGACTTTAAAACCGGTACCGGGGTCGCCTGCGCATCGCCCGGTCGGCCAATC
                                                                                                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
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235.50
57.26%
45.16%
31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
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                                                                                                  (HYSE-) HYSEQ INC
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815 GlyAspGlnSerIleArgGlyTyrAlaHisAspSerLeuSerProIleSerAspLysGly 834
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                                                                                                                                                                                                            1014 GACCTGAAAGGGGCCTCGAAGTTGATAACCGGATCGCTGGAATACCAGTACAACGTGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Porphorymonas gingivalis protein PG45 encoding DNA.
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                  Indels:
                                                                    US-09-914-168-2 (1-919) x AAS93087 (1-1425)
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Webb EA;
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97AU-0000839.
97AU-0001182.
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98AU-0003338
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98AU-0002911
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98AU-0004917
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783 TTTTACATCGGA 772
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Ross BC, Rothel LJ,
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30-JAN-1998;
10-MAR-1998;
09-APR-1998;
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05-MAY-1998;
22-MAY-1998;
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              Query Match:
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592 AAACTCGATTTTGCCGTACCGGTCGCGGATAAAGACGAACACGGG------TTACAG 642
                                                                                                                                                                                                                                                                                                                 Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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Conservative:
Mismatches:
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                                                                                                                                                          AAS93087 standard; cDNA; 1425 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tang YT;
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23-AUG-2000; 2000US-0649167.
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235.50
57.26%
45.16%
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|643 TTTTACATCGGA 654
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Best Local Similarity:
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Patterson MA;

Score:

Antigenic Porphorymonas gingivalis peptides for preventing gingivitis Claim 12; Page 222-223; 588pp; English.	do Oy	931 CGGCAGAAA 939 509 ArgValLeuAlaIleAsnHisAspAspGlyValAsnArgSerIleLeuGlyArgIleSer 528
AAX91536 to AAX91801 encode two hundred and sixty six antigenic Porphorymonas gingivalis (PG) polypeptide sequences given in AAX34318 to AAX34583. AAX31802 to AAX91809 represent PCR primers used in the solution of the PG polypeptides. The PG polypeptides have antibacterial	Db Oy Db	940
used as vaccines especially against Porphorymonas gingivalis. Probes can be used as vaccines especially against Porphorymonas gingivalis in standard hybridisation assays. Porphorymonas gingivalis is involved in periodontal disease especially gingivitis.	QY	
Sequence 2325 BP; 575 A; 636 C; 547 G; 567 T; 0 other;	QQ O	564 AspValTyrGlnSerLysLysValProLeuTyrValPhevalala 578 ::::::
Artigument Scores: 5.53e-09 Length: 2325 Score: 229.00 Matches: 161 Percent Similarity: 32.99% Conservative: 93 Percent Food Matches: 63	Q <sub>y</sub>	579 SeraspLysProargaspGlyGlnIleGlyLeuGlyTrpGlySer 593 
4.84% Indels:	Oy Op	594AspThrGlyThrArgLeuValThrLysPheGluHisAsnLeuIleAsnArgAspGly 612 :::
US-09-914-168-2 (1-919) x AAX91724 (1-2325)  OY 300 ProLeuLeuLleGlyAspValPheHisHisGlyLysTyrGluThrLysLysAsnLeuIle 319	o d	TyrGlnAlaGlyAlaGluLeuArgLeuSerGluAspLysLysGlyValLysLeuTyrAla
CCGGTTTTCATCAGGTCAGGTCAAATCCGATAGCCGGGCTAAGGTGGCG 372 GluAsnAlaSerAlaGluHisGlyTyrPheAspGlyArgTrpLeuAspArgSerValAsp 339	oy da	ThrLysProLeuSerHisProLeuAsnAspGlnLeuArgAlaThr
	QQ Oy	647 647 1384 AGGCACACTATTAGCATGTACTCTTTCGGCTTTTCGACCACCTACGAATTTCAGCCC 1443
hrihr	QY	648
LeuGluGlnLeuLeuThrVal?	Qy	658 SerThrasnGlyPheaspLeuSerThrargThrLeuGluHisGluIleSer 674
GlnAlaValArgAlaLeuSer	Qy	675 ArgSerIleIleGlnAsnGlyGlyTrpAsnArgThrTyrSerLeuArgTyrArg 692 
	QY	693
GlnIleGlnAsnAspGlnValSerPheGluGlnSerSerSerArgThrGlu	QQ DP	708 LeuprovalAspPhevalAsnGlyLysProSerGlnGluAlaLeuLeuAlaGly 725 :::
	da	726valalavalHis-LysTh 731 ::::::
7000	Qy Db	731 rValAlaAspAsnLeuValAsnProMetArgGlyTyrArgGlnArgTyrSerLeuGluVa 751             1761 CACGGGAGAA
SCANDARAGECTCGACATCGCTCGAGGGGGGGGGGGGGGGGGGGGGG	da .	751 1GlySerSerGlyLeuValSerAspalaAsnMetAlaileAlaArgAlaGly1leSe 770
	Qy	770 rGlyValTyrSerPheGlyAspAsnAlaTyrGlySerAsnArgAlaHisGlnMetThrGl 790  :::       :::    1830 CGTGATATATAGCTATGGC

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2057
                        ------AATATGCGAGTGGCACCCTATAGCGAGCA 1877
                                                                                                          ACGGITCAAICCGGAITCCGACAAICCAGIICCIAIIIGGAICAGGIGGGCGAAITCAA 1997
                                                                                                                                                                                                             CCTCGATGCGGGCAACGTTTGGCTCTTGAGGAGGATTCTTCCCGTCCGGGCGGTGCTCT 2117
                                                                                                                                                                                                                                                            GTCCGAAGTGGGATCGGTGAGCAATTTCCTGAATAGCATCGCTCTCTCGGCACCGGTGTCGG 2177
                                                                                                                                                                                                                                                                                                                                                      2238 TCCTTACAATACGGGTAAGAAAGGTTACTACAATATCCCACGCTTTAAGGATGCCATCGG 2297
                                                                                                                                           862
                                                                                                                                                                                        869
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                                                                   ACTCGAAGCCAACGTGGAATATAGAGGCAAGCTTTTCGGGGATCTCCACGCGTTTT
yGlyIleGlnAlaGlyTyrIleTrpSerAspAsnPheAsnHisValProTyrArgLeuAr
                                              gPhePheAlaGlyGlyAspGlnSerIleArgGlyTyrAlaHisAspSerLeu-----
                                                                                            -----SerProlleSerAspLysGlyTyrLeu------ThrGlyGlyGlyGlnValLe
                                                                                                                                        uAlaValGlyThrAlaGluTyrAsnTyrGluPheMetLysAspLeuArgLeuAlaValPh
                                                                                                                                                                                                                                    ------AspLysGlyPheThrAsnAspThrLysIleGlyAlaGlyValGl
                                                                                                                                                                                                                                                                                                eGlyAspIleGlyAsnAlaTyr------
                                                                                                                                                                                                                                                                                  yValArgTrpAlaSerProValGlyGlnValArgValAspValAlaThrGlyValLys--
                                                                                                                                                                                                                                                                                                                                 ----GluGluGly-----AsnProlleLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Porphorymonas gingivalis; PG; periodontal disease; gingivitis; vaccine; antigenic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patterson MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Porphorymonas gingivalis protein PG45 ORF encoding DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Margetts MB,
                                                                                                                                                                                                                                                                                                                                                                                                      2325
                                                                                                                                                                                                                                                                                                                                                                              sLeuHisPhePheIleGlyThrProPhe 919
                                                                                                                                                                                                                                                                                                                                                                                              2298 TTTCCATTTGGCTGTCGGCTATCCCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hocking DM,
Webb EA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAX91597 standard; DNA; 2409
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98AU-0002264.
98AU-0002911.
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98AU-0003654
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Porphorymonas gingivalis
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Rothel LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CSLC-) CSL LTD.
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22-MAY-1998;
29-JUL-1998;
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31-DEC-1997;
30-JAN-1998;
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09-APR-1998;
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Ross BC,
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Porphorymonas gingivalis (PG) polypeptide sequences given in AAY34318 to AAY34893. AAX91802 to AAX91899 repersent PGR primers used in the isolation of the PG polypeptides. The PG polypeptides have antibacterial activity with a vaccine mechanism of action. The PG polypeptides can be used as vaccines sepecially against Porphorymonas gingivalis. Probes can be used to detect Porphorymonas gingivalis in standard hybridisation assays. Porphorymonas gingivalis is involved in periodontal disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProLeuLeuIleGlyAspValPheHisHisGlyLysTyrGluThrLysLysAsnLeuIle 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AspProAspLysLeuProValLysArgGluLeuLeuGluGlnLeuLeuThrValAsnMet 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           412 AsnAspLeuIleAlaThrArgTyrPheAsnMetValAsnThrGluIleValPheProGlu 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            774
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              432 ArgGluGlnIleGlnAsnAspGlnValSerPheGluGlnSerSerSerArgThrGlu 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATACCCTCCTCGTAAGAGGTGCCGTATGCCTGCGAGCCAAGCTCTCGGAAGATACTCCA 834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GluAsnAlaSerAlaGluHisGlyTyrPheAspGlyArgTrpLeuAspArgSerValAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TATCATTACGACAGCATCATTCCCTTACCGATC------AGCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGAGACCAGTTCAATTTGGCAAAGCTGCACGAAGAGCGTCAGACCATCAGTGCCCTGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        457 ACGAACATCCTCCGCGAACACGGGTACTTCGATGCTAAA....GTAAAAAGCAGTGTGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ValileLeuProAspAsn---ThrAlaAspValSerLeuIleTyrAspThrGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlyGluAlaTyrAsnLeu------GlyGluAlaValArgAlaLeuSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TyrArgPheAspGluValValPhePheThrIleAspProLysThrAsnGlnLeuThrThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    613 TTCCCCGACAGCATTCTGGCTTACAGGCAGACTCCGTCT----TTGATCAGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCCCAAGCCATGCGCCCGTGGAGGATAGGGAAACGGACAGCAGTCCTGCTCGCAATGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---GluProValIleGluThrValGluLeuThrAsp---GlyIleLeu------
                                                                                                                                                  AAX91536 to AAX91801 encode two hundred and sixty six antigenic
                                                                 Antigenic Porphorymonas gingivalis peptides for preventing
                                                                                                                                                                                                                                                                                                                           Sequence 2409 BP; 603 A; 657 C; 569 G; 580 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                  Claim 12; Page 136-137; 588pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (1-2409)
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32.99%
20.91%
4.84%
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                                                                                                                                                                                                                                                                                        especially gingivitis
            WPI; 1999-385613/32.
P-PSDB; AAY34379.
                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                   gingivitis
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                                                                                                                                                             The present sequence is a putative version of the Neisseria meningitidis strain ATCC13090 BASB040 coding sequence. The protein produced from this gene is similar to the D15 outer membrane protein of the bacterium. The gene, its protein, antibodies, antagonists and agonists can be used to diagnose and treat bacterial diseases such as those leading to upper respiratory tract infections, bacteraemia and meningitis. In addition, they can be used in vaccines for use against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          364 TATACGGTACACATCACACCGGGCCCGCGCACCAAAATCGCCAACGTCGGTGTCGCCATC 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   712 CAAATCGTCTCCGGCCTGGCGCGTTCCAACCGGGCACGCCTTACGACCTCGACTGCTG 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProValIleGluThrValGluLeuThrAspGlyIleLeuMetAspIleSerProIleGlu 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 CCCGACACCGAATCAGTTAAATTAAAATTCCCCGTCCGCATCGACACGCAGGAT 183
                                                     Novel BASB040 polypeptides of Neisseria meningitidis useful for diagnostic, prophylactic and therapeutic purposes against microbial diseases comprise a specific amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----LeuVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 PheSerAlaSerAsnLeuIleGlnAspLysLeuAsnLeuValAlaAlaLysAlaArgHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 AGTGAAATCAAAGATATGGTCGAAGAACACCTGCCGCTCATCACGCAGCAGCAGGAAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .----ValProLeuTyrValPheValAlaSerAspLysPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LeuProAspGluSerGluAsnGluValIleAspLeuProGluArgThrAlaLeuAlaAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   544 GTCCTCGGCGCGGTAACGCGAAAAGGCTACCCGCTTGCCAAGCTCGGCAACACCCCGGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   583 ArgAspGlyGlnIleGlyLeuGlyTrpGlySerAspThrGlyThrArg------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SerIle-----LeuGlyArgIleSerAspAlaValSerAla-----
                                                                                                                                                                                                                                                                                                                                       Sequence 1830 BP; 440 A; 603 C; 461 G; 326 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                            1830
135
72
218
178
19
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Conservative:
Mismatches:
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                                                                                                                               Claim 14; Page 59; 98pp; English
                                                                                                                                                                                                                                                                                                  cancer and autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                          9.4e-09
224.50
34.33%
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4.75%
2000-423426/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity:
                 P-PSDB; AAY99623
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Best Local Similari
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1177 GCCAGGCTGGGGGCAGAGTTTCTCGCAGAAGGCCGGAAAATCCCCGGC-----TCGGAT 1230
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                                                               CTCGACTTCCAACAGGCACTC - - - GAACAAAACGGGCATTATTCCGGCGCGTCCGTACAA
                                                                                                                                  -----ArgleuSerGluAspLysLysGlyValLysLeuTyrAlaThrLysPro
                                                                                                                                                                                                  829 GCCGACTTCGACCGTCTCCCAAGGCGACCGCGTCCCGTCAAAGTCAGCGTAACCGAGGTC
                                                                                                                                                                                                                                                                     LeuSerHisProLeuAsnAspGlnLeuArgAlaThrLeuGlyTyrGlnGlnGluValPhe
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601 ThrLysPheGluHisAsnLeuIleAsnArgAspGlyTyrGlnAlaGlyAlaGluLeu-
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The present sequence is a putative version of the Neisseria menighidis strain ATCL3090 BASB040 coding sequence. The protein produced from this gene is similar to the D15 outer membrane protein of the bacterium. The gene, its protein, antibodies, antagonists and agonists can be used to diagnose and treat bacterial diseases such as those leading to upper respiratory tract infections, bacteraemia and meningitis. In addition, they can be used in vaccines for use against
                  AlaThrGlyValLysGluGluGlyAsnProIleLysLeuHisPhePheIleGlyThrPro 918
                                                                                                                                                                                                                                            tract infection; bacteraemia; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnostic, prophylactic and therapeutic purposes against microbial diseases comprise a specific amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel BASB040 polypeptides of Neisseria meningitidis useful for
                                                                                                                                                                                                                     Neisseria meningitidis BASB040 putative coding sequence #2
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                               bacterial disease; respiratory is; cancer; autoimmune disease;
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                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1..1830
/*tag= a
                                                                                                                                                                                                                                                                                                                                                            /product= "BASB040"
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                                                                                                                                    AAA48508 standard; DNA; 1830 BP
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Best Local Similari
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------AAACCACGCTTGCCGCCGGCATCAGCCGCGCGCGCAACTATCGGGGC 1068
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482 PheSerAlaSerAsnLeuIleGlnAspLysLeuAsnLeuValAlaAlaLysAlaArgHis 501
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                                                                                          LeuTyrAspMetProAspAspArgValLeuAlalleAsnHisAspAspGlyValAsnArg
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LeuThrValAsnMetGlyGluAlaTyrAsnLeuGlnAlaValArgAlaLeuSerAsnAsp 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 TIGITCAAAAACAAAAGCCCCGACACACCGAATCAGTTAAATTAAAACCC---AAAATTCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 ATCACGCAGCAGCAGGAAGAAGTATTGGACAAGGAACAGACGGGCTTCCTCGCCGAAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
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                                                                                                                                                                                                                                                                                   1471 GCCCGCGACAATGCCGACGTTCCTTCAGGGCTGATGTTCCGCAGCGGCGGCGGGGTCTTCC 1530
                                                                                                                                                                                                                                                                                                                                                                                       1591 GAACGCCCCTCCTGGTGGGCAGCCTGGAATACCAACTGCCGTTTACGCGCACCCTTTCC 1650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia; antibacterial; gene therapy; ds.
740 tArgGlyTyrArgGlnArgTyrSerLeuGluValGlySerSer--GlyLeuValSerAsp 759
                                                760 AlaAsnMetAlaIleAlaArgAlaGlyIle-----SerGlyValTyrSerPheGly 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neisseria meningitidis ORF 286 partial DNA sequence SEQ ID NO:1197
                                                                                                                            1291 AACAACGTGCTGCATCCCGAAAACGGCCATTACCTCGACGGCAAAATCGGTACGACTTTG
                                                                                                                                                                                                                                                                                                             819 IleArgGlyTyrAlaHisAspSerLeuSerProIleSerAspLysGlyTyrLeuThrGly
                                                                                                                                                                                                                                                                                                                                                             839 GlyGlnValLeuAlaValGlyThrAlaGluTyrAsnTyrGluPheMetLysAspLeuArg
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                        1177 GCCAGGCTGGGGCAGAGTTTCTCGCAGAAGGCCGGAAAATCCCCGGC----TCGGAT
                                                                                                                                                                                                      -----GlnAlaGlyTyrIleTrp
                                                                                                                                                                                                                                                         799 SerAspAsnPheAsnHisValProTyrArgLeuArgPhePheAlaGlyGlyAspGlnSer
                                                                                                   AspAsnAlaTyrGlySerAsnArgAlaHisGlnMetThrGlyGlyIle-
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98US-0098994.
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31-JUL-1998;
02-SEP-1998;
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1848 146 98 232 181 29

Conservative: Mismatches:

1,39e-08 222.50 37.20% 22.26%

Indels:

Length: Matches:

445

453

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AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ55473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves may also have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
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Scarselli
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Scalato E, S
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                                                                                                                                                                                                                                                                                                      Hickey
Ratti
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                                                                                                                                                                                                                                                                                               Fraser C, Galeotti C, Grandi G, Petersen J, Pizza M, Rappuoli R, Tettelin H, Venter JC;
98US-0099062.
98US-0103749.
98US-0103794.
98US-0103796.
99US-0121528.
                                                                                                                                                                                                  (CHIR ) CHIRON CORP. (GENO-) INST GENOMIC RES.
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                                                                 09-OCT-1998;
09-OCT-1998;
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qq	454CTTTCAGACGGCAACCTCGCCGAATACTACCGCAACGCGCTGGAAAACTGG 504	(	i i	
Qy	478SerProlleGluPheSerAlaSerAsnLeuIleGlnAspLysLeuAsnLeu 494	δλ		i
QQ	::: :::      :::       :::::::           ::::::	ପ୍ର	1395 GATCCGCACCTC	Ĕ
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ò	533 AlaValAla-ArgAlaIleLeuProAspGluSerGluAsnGluValIleAspLeuProGl 552	Oy	826 rLeuSerProl	н
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à à	YTYGIDAIGGLYAIGGLULEUAFGLEUSEGLUASPLYSGI	qa	:   1810AAAATCC	Ŭ
Q C	822 GCATTATTCCGGCGCGCGTCCGTACAAGCCGACTTCGACCCCCTCCAAGGCGACCGCGTCCC 881	RES	JLT 27	
δŏ	yvalLysLeuTyrAlaThrLysProLeuSerHisProLeuAsnAspGlnLeuArgAlaTh	AAA	AAA48509 ID AAA48509 standard	ŭ
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δλ	647 rLeuGlyTyrGlnGlnGluValPheGlyHisSerThrAsnGly	XX	03-JAN-2001 (fi)	.,
qq	942 TTCGGAATAC	XX	4	i E
ΟŊ	662 -PheAspLeu-SerThrArgThrLeuGluHisGluIleSerArgSerIleIleGlnAsnG 681	XX	Netesetta menting	,
qq	981 TTACAACCTCTTCAACAAAGGCTATA		BASBU40; Dacteria meningitis; cance	ĕΰ
δλ	681 lyGlyTrpAsnArgThrTyrSerLeuArgTyrArgLeuAspLysLeuLysThrGlnAlap 701	SS \$	Neisseria mening	Ď.
QQ	1023 GGATATGGACAAATACGAAACCACGCTTGC 1052	Y E	Key	'
Qy	701 roProGluThrTrpGlnAspLeuProValAspPheValAsnGlyLysProSerGlnGluA 721	. 5. 5		
QQ	1053 CGCCGCCATCAGCCAGCCGCCCAACTATCGGGGCAACTACTGGACAAGCAA 1103	.E.		•
δλ	721 laLeuLeuAlaGlyValAlaValHisLySThrValAlaAspAsnLeuValAsnPro 739	V Z	WO200034480-A1.	
qq	1104 CGTTTCCTACAACCGTTCGACCACCCAAAACCTCGAAAAACGCGCCTTCTCCGGCGG 1160	Υ Q ?	15-JUN-2000.	
Óγ	rArgGlnArg	AA PF	02-DEC-1999;	9.
qq	1161 CATCTGGTATGTGCGCGACCGCGGGCATCGATGCCAGGCTGGGGGGCGGAGTTTCTCGC 1220	XX RA	07-DEC-1998; 9	5
Qγ	a)	AA H	(SMIK ) SMITHKLI	Ħ
qq	1221 AGAAGGCCGGAAAATCCCCGGCTCGGATATCGATTTGGGCAACAGCCCGCCAC 1274	VY Id	Ruelle J;	
QY	768 ylleSerGlyValTyrSerPheGlyAspAsnAlaTyrGlySerAsnArgAl 785		WPI; 2000-423426,	ுல்
QQ	1275 GATGCTGACCGCCTCTTGGAAACGCCAGCTGCTCAACAACGTGCTGCATCCCGAAAACGG 1334	XX	Nows page 040 20	າ 'ຄ
ογ	785 aHisGlnMetThrGlyGlyIle 792	2 2 2	NOVEL BASBU4U PO. diagnostic, propl diseases comprise	၁ဩ၈
qq	1335 CCATTACCTCGACGGCAAAATCGGTACGACTTTGGGCGCATTCCTGTCCTCCACCGCGCT 1394	××	•	

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UTGCCCGCGCAGGTTATTTCTTCACGCCCGAAAAACAAAAAACTCGGCAC 1454
                           eSerAspLysGlyTyrLeuThrGlyGlyGlnValLeuAlaValGlyTh 846
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                                                                                                                                                                                                                                                                                                                                oValGlyGlnValArgValAspValAlaThrGlyValLysGluGluGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           al disease; respiratory tract infection; bacteraemia; er; autoimmune disease; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lypeptides of Neisseria meningitidis useful for hylactic and therapeutic purposes against microbial e a specific amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             itidis BASB040 putative coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                              SCTGGCACATCAGCTTGGGACGCGCTTC 1845
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XX SQ Sequence 1764 BP; 424 A; 581 C; 451 G; 308 T; 0 other;

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Align Pred. Score Percei Best J Query	Alignment Sc Pred. No.: Score: Percent Simi Best Local & Query Match.	nment Scores: . No.: ent Similarity: Local Similarity: y Match:	4.02e-08 216.50 34.87% 22.37% 4.58%	Length: Matches: Conservative: Mismatches: Indels: Gaps:	1764 136 208 188 21	
ns.	09-914	-168-2 (1-919)	x AAA48509 (1-	1764)		
60 G	462		ProValileGluThrValGluLeuThrAspGlyIleLeuWetAspIleSerProIleGlu	uLeuThrAspGlyIleLeuMetAspIl :	1.48	
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λ a	482		aSerAsnLeutlieGlnAspLysLeuAsnLeuValAlaAlaLysAlaArgii 	/sLeuAsnLeuValA] 	PheSerAlaSerAshGeulleGlnAspLysLeuAsnLeuvalAlaAlaLysAlaArgHis 501 	
ογ	502		roAspAspArgValLe	euAlaIleAsnHisAs	pAspGlyValAsnArg 521	
q	178		  AACAGACGGGCTTCCT	  CGCCGAAGAAGCGCC	:::                     GARTHGGACAAGGACGTTAAAACG 237	
Οy	522	SerIle	-LeuGlyArgIleSerAspAlaVa	lserAla-	533	
qa	238		   AAGGCTATTTCAGCAG	 	::: ATGCTCCGCAGCAAAGGCTATTTCAGCAGCAAAGTCAGCCTGACGGAAAAAGACGGAGCT 297	
Οy	534				-ValAlaArgAlaile 538	
qa	298		TCACACCGGGCCCGCG	SCACCAAAATCGCCAA	 TATACGGTACACATCACACCGGGCCCGCGCACCAAAATCGCCAACGTCGGGGTTGGCCATC 357	
Qγ	539		erGluAsnGluValIl	eAspLeuProGluAr	uArgThrAlaLeuAlaAsn 558	
q	358		CTCGGCGACATCCTTTCAGACGCCAACCTCGCCGAAT	CGCCGAATACTACCG	ACTACCGCAACGCGCTGGAAAAC 417	
δλ	559		1a	AspValTyrGlnSerLy	nSerLysLys 570	
QQ	418		TAGGCAGCGATTTCGA	TCAGGACAGTTGGG	TGGCAGCAGCAGCAGCAGCATTCGATCAGGACAGTTGGGAAAACAGCAAAACTTCC 477	
δy	570				0.22	
qq	478		GTCCTCGGCGCGGTAACGCGCAAAGCCTACCCGCTTGCCAAGCTCGGCAATACGCAGGCG	CCCGCTTGCCAAGCT	CGGCAATACGCAGGCG 537	
Qy	571		ValPro	oLeuTyrValPheVa	alProLeuTyrValPheValAlaSerAspLysPro 582	
QQ	538		ATACCGCCACCGCCGA	TTTGAACGTCGTCGT	GCCGTCAACCCCGATACCGCCACCGCGATTGAACGTCGTCGTCGACAGCGGCCGCCCC 597	
δλ	583	ArgAspGlyGln	pGlyGlnIleGlyLeuGlyTrpGlySerAspThrGlyThrArg	ySerAspThrGlyTh	rArg 598	
qo	598		   TCGCCTTCGGCGACTT	TGAAATCACCGGCAC	   ATCGCCTTCGGCGACTTTGAAATCACCGGCACACAGCGTTACCCCGAA 645	
Qγ	599					
QΩ	646		::   Caaatcgtctccggccttgcgcgtttccagcccggtatgccgtacgacctcgacctgct	GCCCGGTATGCCGTA	CGACCTCGACCTGCTG 705	
٥y	601		11	gAspGlyTyrGlnAl	aGlyAlaGluLeu 619	
DÞ	706	CTCGACTTCCAACAGGCGCTC	;	.::::   :::: AAACGGCATTATTC	-GAACAAAACGGGCATTATTCCGGCGCGTCCGTACAA 762	
δy	620	1	D	sLysGlyValLysLe :	LeuSerGluAspLysLysGlyValLysLeuTyrAlaThrLysPro 635	

QQ	763	GCCGACTTCGACCGCCTCCAAGGCGACCGCGTCCCGTCAAAGTCAGCGTAACCGAGGTC 82
Qy	636	LeuSerHisProLeuAsnAspGlnLeuArgAlaThrLeuGlyTyrGlnGluVal
qq	823	AAACGCCACAACTCGAAACCGGCATCCGCCTCG
Qy	959	GlyHisSerThrAsnGlyPheAspLeu-SerThrA≹gThrL
qq	868	  GGTTTGGGCGGCAAAATCGCCTACGACT
Qy	699	uGluHisGluIleSerArgSerIleIleGlnAsn
QQ	922	TCGGTTCGGTC
Qy	689	lLeuAspLysLeuLys6
qq	926	
Qγ	869	ThrGlnAlaProProGluThrTrpGlnAspLeuProValAspPh 712
qa	1015	AGCAACGTTTCCTACAACGTTCGACCCAAAAACCTCGAAAAACGCGCGTTTTTCCTGCGGC 1074
Qy	712	eValAsnGlyLysProse 718
QQ	1075	GGCGTCTGGTATGTGCGCGACCGCGGGCATCGATGCCAGGCTGGGGGGGG
Qy	718	rGlnGluAlaLeuLeuAlaGlyValAlaVal
qq	1135	GCAGAAGGCCGGAAAATCCCCGGCTCGGCTGTCGATTTGGGCAACAGCCACGCCACGATG 1194
Qy	732	732
qq	1195	CTGACCGCCTCTTGGAAACGCCAGCTGCTCAACAACGTGCTGCTCCCGAAAACGGCCAT 1254
٥'n	744	ArgGlnArgTyrSerLeuGluValGLySerSerGlyLeuVal 757
qq	1255	TACCTCGACGGCAAAATCGGTACGACTTTGGGCACATTCCTGTCCTCCACCGCGCTGATC 1314
Qy	758	SerAspAlaAsnMetAlaIleAlaArgAlaGlyIleSerGlyValTyrSerPheGlyAsp 777
QQ	1315	CGCACCTCTGCCCGTGCAGGT
ОУ.		AsnAlaTyrGlySerAsnArgAlaHisGlnMetThrGlyGlyIleGln 793
Db	1336	TATTTCTTCACGCCCGAAAAAAACTCGGCACGTTCATCATACGCGGACAA 1389
δy	794	AlaGlyTyrIleTrpSerAspAsnPheAsnHisValProTyrArgLeuArgPhePheAla 813
QQ	1390	GCGGGTTACACCGTTGCCCGCGACATGCCGACGTTCCTTCAGGGCTGATGTTCCGCAGC 1449
Qy	814	GlyGlyAspGlnSerIleArgGlyTyrAlaHisAspSerLeuSerProIleSerAspLys 833
qq	1450	GGCGCGCGCTTTCCGTGCGCGGTTACGAACTCGACAGCATCGGACTTGCCGGCCCGAAC 1509
Oy	834	GlyTyrLeuThrGlyGlyGlnValLeuAlaValGlyThrAlaGluTyrAsnTyrGluPhe 853
qq	1510	GGATCGGTCCTGCCCGAACGCGCCCTCCTGGTGGGCAGCCTGGAATACCAACTGCCGTTT 1569
Οy	854	MetLysaspLeuargLeualavalPheGlyaspIleGlyasnAlaTyrAspLysGlyPhe 873
qq	1570	ACGCGCACCCTTTCCGGCGCGCGTTTCCACATATGGGCGATGCCGCCGCCAATTTCAAA 1629
Qy	874	ThrAsnAspThrLysIleGlyAlaGlyValGlyValArgTrpAlaSerProValGlyGln 893
QQ	1630	CGTATGAAGCTGAACACGGTTCGGGACTGGGCGTGGTTCTTTTTTTT
Οy	894	ValArgValAspValAlaThrGlyValLySGluGluGluGlyAsnProIleLySLeuHisPhe 913
qq	1690	TTTTCCTTCGACATGGCTACGGGCACAGCGATAAGAAAATCCGCTGGCACATC 1743
Qy	914	PhelleGlyThrProPhe 919
qa	1744	SGGAACACGCTTC 17

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462 ProvalileGluThrValGluLeuThrAspGlyIleLeuMetAspIleSerProileGlu 481
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                                                                                                                                                                                                                                            Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia; antibacterial; gene therapy; ds.
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Scarselli M;
                                                                                                                                                                                                    SEQ ID NO:1195
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Scalato E, S
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                                                                                                                                                                                                  Neisseria meningitidis ORF 286 partial DNA sequence
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Ratti
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   Pizza M, Rappuoli R,
   Venter JC;
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                                                               AA253623 standard; DNA; 1848 BP
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98US-0098869.
98US-0098994.
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(GENO-) INST GENOMIC RES.
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P-PSDB; AAY74861.
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Tettelin H,
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25-FEB-1999;
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                                                                                                          AGTGAAATCAAAGATATGGTCGAAGAACACCTGCCGCTCATCACGCAGCAGCAGGAAGAA
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                                                                                                                                                                                                                                           262 GTATTGGACAAGGAACAGACGGGCTTCCTCGCCGAAGAAGGCGCCGGACAACGTTAAAACG
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142 CCCGACACCGAATCAGTCAAATTAAAACCCAAATTCCCCGTCCTCATCGACACGCAGGAC
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                                               GCAGAAGGCCGGAAAATCCCCGGCTCGGCTGTCGATTTGGGCAACAGCCACGCCACGATG 1278
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                                                                     -----ValAlaAspAsnLeuValAsnProMetArgGlyTyr 743
                                                                                                                                                                                               778 AsnAlaTyrGlySerAsnArgAlaHisGlnMetThrGlyGlyIle------Gln 793
                          rGlnGluAla--LeuLeuAlaGlyValAlaVal-------HisLysThr--- 731
                                                                                                                                                       SerAspAlaAsnMetAlaIleAlaArgAlaGlyIleSerGlyValTyrSerPheGlyAsp 777
                                                                                                                                                                                                                                         AlaGlyTyrIleTrpSerAspAsnPheAsnHisValProTyrArgLeuArgPhePheAla 813
                                                                                                                                                                                                                                                                                   GlyGlyAspGlnSerIleArgGlyTyrAlaHisAspSerLeuSerProIleSerAspLys 833
                                                                                                                                                                                                                                                                                                                                                                                                               ThrAsnAspThrLysIleGlyAlaGlyValGlyValArgTrpAlaSerProValGlyGln 893
                                                                                                                                                                                                                                                                                                                                                 GGATCGGTCCTGCCGGAACGCGCCCTCCTGGTGGGCAGCCTGGAATACCAACTGCCGTTT
                                                                                                              GlyTyrLeuThrGlyGlyGlnValLeuAlaValGlyThrAlaGluTyrAsnTyrGluPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ValArgValAspValAlaThrGlyValLysGluGluGlyAsnProIleLysLeuHisPhe
                                                                                                                                                                                                                                                                                                                                                                      MetLysAspLeuArgLeuAlaValPheGlyAspIleGlyAsnAlaTyrAspLysGlyPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                   1714 CGTATGAAGCTGAAACACGGTTCGGGACTGGGCGTGCGTTCAGCCCGCTTGCGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N. meningitidis partial DNA sequence gnm_21 SEQ ID NO:21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA81473 standard; DNA; 92934 BP
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1828 AGCTTGGGAACGCGCTTC 1845
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-DEC-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   914 PhelleGlyThrProPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neisseria meningitidis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA81473;
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                                               1219
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The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. AAA81453 to AAA82414

Proteins from Neisseria genomic sequences. AAA81453 to AAA82414

represent specifically claimed Neisseria meningtidia genomic DNA sequences; AAA81260 to AAA8120 and AAB25620 to AAB2563 represent Neisseria DNA sequences and their corresponding proteins; AAA81254 to AAA81259 and AAA81304 to AAA81321 represent PCR primers used in the isolation of Neisseria meningtidia DNA sequences; and AAA8132 to AAA81452 represent Neisseria meningtidia DNA sequences; and AAA8132 to AAA81452 represent Neisseria meningtidia MenB polynucleotide ORF sequences, which are all used in the exemplification of the present invention. The nucleic acid sequences, protein sequences, and antibodies against them, can be used in the manufacture of a composition can be used as a medicament (or in the manufacture of a medicament) for treating, preventing or diagnosing infection due to Neisserial bacteria. For example, some of the identified proteins could be components of vaccines against Meningococcus B; against all serotypes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and/or against all pathogenic Neissaniae. Identification of sequences from the bacterium will also facilitate production of biological probes, particularly organism-specific probes. Attempts to make efficacious Meningococcus B vaccines have failed mainly due to antigen tolerance. Multivalent vaccines have also been tried but none have successfully overcome antigenic variability. The provision of further, complete sequences may provide an opportunity to identify secreted or surface exposed proteins that may be presumed targets for the immune system and which are not antigenically variable or at least more conserved than
                                                                                                                    Scarlato V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38451 AGTGAAATCAAAGATATGGTCGAAGAACACCTGCCGCTCATCACGCAGCAGCAGGAAGAA 38510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38570
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                                                                                                                                                                                                                                                                                           Isolated nucleotide sequences of Neisseria meningitidis which can be used in the diagnosis and treatment of N. meningitidis infection and other Neisserial infections, for example, N.gonorrhoea -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LeuTyrAspMetProAspAspArgValLeuAlaIleAsnHisAspAspGlyValAsnArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               482 PheSerAlaSerAsnLeuIleGlnAspLysLeuAsnLeuValAlaAlaLysAlaArgHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --ValAlaArgAlaile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 92934 BP; 24051 A; 24249 C; 21902 G; 22730 T; 2 other;
                                                                             Tettelin H, Venter JC;
Ratti G, Scarselli M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              522 SerIle-----LeuGlyArgIleSerAspAlaValSerAla-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative:
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Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 7; Page 471-498; 1760pp; English.
                                                                             Peterson J,
C, Mora M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       other more variable regions
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34.87%
22.37%
4.58%
                                                                                                                Galeotti
                                                                                                    , V, Garca
R, Pizza M;
                                                                             Hickey E,
(CHIR ) CHIRON CORP.
                                                                                                                                                                                                                         WPI; 2000-318079/27.
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Best Local Similarity:
                                                                                                                                               Rappuoli R,
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                                                                             Frazer CM,
                                                                                                                    Masignani
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Db 38631 TATACGGTACACATCACACCGGGCCCGCGCACCAAAATCGCCAACGTCGGCGTCGCCATC 38690	Ov 778 ASDAlaTyrGlySerAsDArgAlaHisGlnMetThrGlyGlyIleGln 793
Dy 539 LeuProAspGluSerGluAsnGluValIleAspLeuProGluArgThrAlaLeuAlaAsn 558	39669
559 ArgLysThrProAla	Oy 794 AlaGlyTyrIleTrpSerAspAsnPheAsnHisValProTyrArgLeuArgPhePheAla 813
56751	814 GlyGlyAspGlnSerIleArgGlyTyrAlaHisAspSerLeuSerProIleSerAspLys 833
Db 38811 GTCCTCGGCGGGTAACGCGCAAAGCCTACCCGCTTGCCAAGCTCGGCAATACGCAGGCG 38870	39783
Sy 571ValProLeuTyrValPheValAlaSerAspLysPro 582	GLYTY LEUTINGLYGLYGLYGLYGLYGLYTINGLAGGUNY ASDIY FOLUNGE
583 ArgaspGlyGlnIleGlyLeuGlyTrpGlySerAspThrGlyThrArg	Qy 854 MetLysAspLeuArgLeuAlaValPheGlyAspIleGlyAsnAlaTyrAspLysGlyPhe 873 ::
Db 38931ATCGCCTTCGGCGACTTTGAAATCACCGGCACACAGGGTTACCCCGAA 38978 Dv 599LeuVal 600	Oy 874 ThrasnaspThrLysIleGlyAlaGlyValGlyValArgTrpAlaSerProValGlyGln 893
38979 CAAATCGTCCGGCCTTGCGGCGTTTCCAGCCCGGTATGCCGTACGACCTCGACCTGCTG	39963 CGTATGAAGCTGAAACACGGTTCGGGACTGGGCGTGCGTTCAGCCCGCTTGCGCCG 40
Oy 601 ThrLysPheGluHisAsnLeuIleAsnArgAspGlyTyrGlnAlaGlyAlaGluLeu 619	Qy 894 ValArgValAspValAlaThrGlyValLysGluGluGluGlyAsnProIleLysLe@HisPhe 913
620ArgineuSerGluAspLysLysGlyValLysLeuTyrAlaThrLysPro 635	Oy 914 PheileGlyThrProPhe 919  :::
39096 GCCGACTTCGACCGCCTCCAAGGCGCGCGTCCCCGTCAAGTCAGCGTAACCGAGGTC 636 LeuSerHisProLeuAsnAspGlnLeuArgAlaThrLeuGlyTyrGlnGlnGluValPhe 111 111	RESULT 30 AAF21613 ID AAF21613 standard; DNA; 172325 BP.
DD 39196 AAACGCCACAAACTCGAAACCGGCATCCGCTTCGGATAC39200 Ov 656 GlvHisserThrAsnGlvPheaspleu-SerThrArdThrIe 669	XX AC AAF21613; XX
39201GGTTTGGGCGGCAAATCGCCTACGACTATTACAACCTCTTCAACAAGGCTAT	13-MAR-2001 (first ent
Qy     669 uGluHisGluIleSerArgSerIleIleGlnAsnGlyGlyTrpAsnArgThrTyrSerLe 689       Db     39255 A 3928	DE Nelsseria meningitidis B nucleotide sequence SEQ ID NO:114.  XX KW Neisseria meningitidis; Neisseria gonorrheae; immunogenic; vaccine; KW diagnosis: antigen: detection: infection: gene therapy: antibacterial:
689 uArgTyrArgLeuAspLysLeuLys	
Db 39289 -AAACCAGGCTTGCCGCGGCGTCAGCCAGCGGCAACTATCGGGGCAACTACTGGACA 39347	
Oy 698ThrGlnAlaProProGluThrTrpGlnAspLeuProValAspPh 712	09-NOV-2000.
712	08-MAR-2000; 30-APR-1999;
39408 GCCGTCTGGTATGTGCGCCGCCGCGCGCATCCATGCCAGGCTGGGGGCGGAATTTCTC	PR 08-OCT-1999; 99WO-US23573. PR 28-FEB-2000; 2000GB-0004695.
<pre>Qy 718 rGlnGluAlaLeuLeuAlaGlyValAlaValHisLySThr 731                                      </pre>	XX PA (CHIR ) CHIRON CORP. PA (GENO-) INST GENOMIC RES.
Oy 732	AA Pizza M, Hickey E, Peterson J, Tettelin H, Venter JC, Masignani V;   PI Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V, Rappuoli R;
CTGACCGCCTCTTGGAA	Frazer CM, Grandi G;
744ArgGlnArgTyrSerLeuGluValGlySerSerGlyLeuVal	WPI; 2000-647603/62.
39588 TACCTCGACGCCAAAATCGGTACGACTTTGGGCACATTCCTGTCCTCCACCGCGCTGATC	PT Neisseria meningitidis B full length genome sequence and open reading PT frames are used to detect, treat and prevent Neisserial infections -
Qy 758 SerAspAlaAsnMetAlaIleAlaArgAlaGlyIleSerGlyValTyrSerPheGlyAsp 777 ::::	ix A; 692pp; English.
23048 CGCACCICI	vv -

The present Arreltion describes the full femyling yellow.

Neisseria meningitidis B (NMB). The sequences in AAPZ1544 and AAFZ1607

to AAFZ1613 represent fragments of the NMB genomic sequence, as the sequence was too long to go in a record on its own it was split into 8 sequences which overlap each other at the beginning and each of each sequences which overlap each other at the beginning and each of each sequence by 49980 bp (i.e. the last 49980 bp of AAFZ1544 is repeated at the beginning of AAFZ1609, and so on). AAFZ1545 to AAFZ1588 encode the Neisseria proteins given in AABS8550 to AABS8593, and AAFZ1589 to the present invention. The NMB genome and fragments from it have attabacterial activity, and can be used in vaccines and gene therapy.

Neisseria nucleic acids, proteins and/or antibodies which binds to the proteins can be used in compositions for treating or preventing infection due to Neisserial bacteria or of antibodies raised to Neisserial activity, and as adiagnostic reagent for detecting the presence of Neisserial bacteria or of antibodies raised to Neisserial activity of a search to identify open reading frames (ORFs) or coding sequences within the NMB genome. The DNA sequences provide further opportunities to find antiganic or immunogenic proteins which are more effective in vaccines than the outer membrane proteins currently used. present invention describes the full length genome of 

Sequence 172325 BP; 43072 A; 47583 C; 41465 G; 40205 T; 0 other;

Db 142058 CCCGACACCGAATCAGTCAAATTAAAACCCAAATTCCCCGTCCTCATCGACACGCAGGAC 142117 Db 142358 CTCGGCGACATCCTTTCAGACGGCAACCTCGCCGAATACTACCGCAACGCGCTGGAAAAC 142417 Db 142538 GCCGTCAACCCCGATACCGCCACCGCCGATTTGAACGTCGTCGTGGACAGCGGCCGCCCC 142597 Db 142118 AGTGAAATCAAAGATATGGTCGAAGAACACCTGCCGCTCATCACGCAGCAGCAGGAAGAA 142177 ::: |||| | Db 142178 GTATTGGACAAGGAACAGACGGGCTTCCTCGCCGAAGAAGCGCCGGACAACGTTAAAACG 142237 Db 142418 TGGCAGCAGCCGGTAGGCAGCGATTTCGATCAGGACAGTTGGGAAAACAGCAAAACTTCC 142477 Db 142478 GTCCTCGGCGCGGGTAACGCGCAAAGCCTACCCGCTTGCCAAGCTCGGCAATACGCAGGCG 142537 Db 142238 ATGCTCCGCAGCAAAGGCTATTTCAGCAGCAAAGTCAGCCTGACGGAAAAAAGACGGAGCT 142297 Db 142298 TATACGGTACACATCACACCGGGCCCGCGCACCAAAATCGCCAACGTCGGCGTCGCCATC 142357 462 ProvalileGluThrValGluLeuThrAspGlyIleLeuMetAspIl'eSerProileGlu 481 482 PheSerAlaSerAsnLeuIleGlnAspLysLeuAsnLeuValAlaAlaLysAlaArgHis 501 539 LeuProAspGluSerGluAsnGluValIleAspLeuProGluArgThrAlaLeuAlaAsn 502 LeuTyrAspMetProAspAspArgValLeuAlaIleAsnHisAspAspGlyValAsnArg 522 SerIle-----LeuGlyArgIleSerAspAlaValSerAla-----LeuGlyArgIleSerAspAlaValSerAla-559 ArgLysThrProAla-------AspValTyrGlnSerLysLys----583 ArgaspGlyGlnIleGlyLeuGlyTrpGlySerAspThrGlyThrArg------Length:
Matches:
Conservative:
Mismatches:
Indels: US-09-914-168-2 (1-919) x AAF21613 (1-172325) 1.62e-05 216.50 34.87% 22.37% 4.58% Best Local Similarity: Query Match: Percent Similarity: Alignment Scores: 570 571 534 δ ö δ ò ò ò ő δŏ ó õ

a	14.2598	AICGCCTTCGGCGAATCACGCACACACGCGTTACCCGAAA	142045
Oy	599	Tennen	009
qq	142646 (	CAAATCGTCTCCGGCCTTGCGCGTTTCCAGCCCGGTATGCCGTACGACCTCGACCTGCTG	142705
Qy de	601	ThrLysPheGluHisAsnLeuIleAsnArgAspGlyTyrGlnAlaGlyAlaGluLeu	619
3 3	00/4	1011-000-1000-000-00-1-11-1-1000-00-00-0	
CY Db	- - m	GCCGACTTCGACCCCTCCAAGCGCACCCCGTCCAAAGTCAGCGTAACGTC GCCGACTTCGACCCCTCCAAGCGCACCCCGTCCAAAGTCAGCGTAACCGAGGTC	. <b>4</b>
ΟY	636	LeuSerHisProLeuAsnAspGlnLeuArgAlaThrLeuGlyTyrGlnGlnGluValPhe	655
qq	142823	AAACGCCACAAAACTGGCATCCGCCTCGATTCGGAATAC	142867
Qγ	959		699
Dp	142868	AACA/	1.4
Qy Ph	669 1	uGluHisGluIleSerArgSerIleIleGlnAsnGlyGlyTrpAsnArgThrTyrSerLe : :: -	689
ò	689	ArgTyrArg LeuAspLysLeuLys	, ,
qα	56	ACCACGCTTGCCGCCGGCATC	143014
ΟŊ	869	luT	712
Pρ	143015	:::       AAAACCTCGAAAAACGCGCC	143074
QY	712	Lyspros	718
QQ	143075 (	GGCGTCTGGTATGTGCGCGCGCGCGCGCGATCCATGCCAGGCTGGGGGCGGAATTTCTC	143134
QY	718	rGlnGluAlaLeubeuAlaGlyValAlaVal	731 143194
Qy	732	AspAsnLeuValA	743
ΩD	143195	TGCTCAACACGTGCTGCATCCCGAAAACGGCCA	143254
Οy	744	ArgGlnArgTyrSerLeuGluValGlySerSerGlyLeuVal	757
qq	143255	GTCCTCCAC	143314
Οy	758	SerAspAlaAsnMetAlalleAlaArgAlaGlyIleSerGlyValTyrSerPheGlyAsp	777
qq	143315 (	CGCACCTCTGCCCGTGCAGGT	143335
Οy	778	AsnAlaTyrGlySerAsnArgAlaHisGlnMetThrGlyGlyIleGln	793
qq	143336	TATTTCTTCACGCCCGAAAACAAAAACTCGGCACGTTCATACGGGGACAA	143389
ΟY	794	nHisValPro	813
qu	143390	ACCGTTGCCCGCGACAATGCC	143449
٥y	814	GlyGlyAspGlnSerIleArgGlyTyrAlaHisAspSerLeuSerProIleSerAspLys	833
Dp	143450	deddecerritedrocederracaaerredaeae	143509
ΟY	834 (	1G1yT	82
QQ	10	GCAGCCTGGAATACCAACT	4
Οy	854	MetLysAspLeuArgLeuAlaValPheGlyAspIleGlyAsnAlaTyrAspLysGlyPhe :::	m
q	143570	ACGCGCACCCTTTCCGGCGCGCTGTTCCACGATATGGGCCGATGCCGCCGCCAATTTCAAA	143629

Tue May

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producing fusion proteins carrying foreign peptide sequences that can also be useful in epitope mapping, screening of antibody libraries and as immunogens. The present sequence represents the specifically claimed Methylococcus capsulatus surface protein-antigen D15 nucleotide sequence,
                                      143630 CGTATGAAGCTGAAAACACGGTTCGGGACTGGGCGTGGCTTCAGCCCGCTTGCGCCG 143689
                                                                                                                                                                                                               Db 143690 TTTTCCTTCGACATCGCCTACGGGCACAGCGATAAG-----AAAATCCGCTGGCACATC 143743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence that codes for any of the 14 Methylococcus capsulatus nucleotide sequences given in ABQ72976 to ABQ72989. Also described is a method for producing a desired protein in a bacterial host cell, comprising: (a) transforming a bacterial host cell, which comprising a first nucleotide sequence selected from the vector comprising a first nucleotide sequence selected from the group of 14 Methylococcus capsulatus, and comprising a nucleotide encoding the desired protein linked in frame to the first nucleotide sequence; and (b) culturing the transformed host cell in a medium under conditions that allow the expression of the protein. (I) can be used in vaccine production. The nucleic acids or the proteins from the present invention can be used in manufacturing vaccines that can be administered in animals, fish or humans. The method is useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a nucleotide molecule (I) comprising a
874 ThrAsnAspThrLysIleGlyAlaGlyValGlyValArgTrpAlaSerProValGlyGln 893
                                                                                                                                                  913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Methylococcus capsulatus surface protein-antigen D15 DNA SEQ ID NO:5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleotide molecule encoding a surface exposed protein and is incorporated and expressed in Methylococcus capsulatus, useful in manufacturing vaccines that can be administered orally in animals,
                                                                                                                                              ValArgValAspValAlaThrGlyValLysGluGluGlyAsnProIleLysLeuHisPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eidhammer I, Jonassen I, Jensen HB, Lien T
Lossius I, Eisen JA, Fraser CM, Durkin AS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Methylococcus capsulatus; methanotropic bacterium; MopC; Mog
MopF; D15; surface protein antigen; helper protein; vaccine;
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qq	799	TACGTCAATTTCGAAATCGAGTCCACCCAGGTATCGATCACGCCCAAC 846		
οy	446	SerSerArgThrGluProAla	Qy	717 oSerGlnGluA
qa	847	AAGAAAGAAATATATC 864	QQ ·	
оу	466	ThrvalGluLeuThrAspGlyIleLeuMetAspIleSerProlleGluPheSerAlaSer 485	Oy B	737 lAsnProMetA             1795 TGGACCCATGA
q	865	ACCATCAACGTTA	ò	
δ d	486	AsnLeulleGinAspLysLeuAsnLeuValAlaAlaLysAlaArgHisLeuTyr 503 ::::: :::::::::::::::::::::::::::::::	7 A	
γò	504	ASPMetProAspAspArgValLeualaIleAsnHisAspAspGlyValAsnArGerIle	Oy	775
q	985	TCCAGAAACTGGCGACAGAAACCCAGAAAGGGC	qq	1878 CAGCACCCTGC
δλ	524	LeuGlyArgIleSerAspAlaValSerAlaValAlaArgAlaIleLeuProAspGluSer 543	Oy	176
qq	1018		qo :	
yo d	544	GluAsnGluVallleAspLeuProGluArgThrAlaLeuAlaAsnArgLysThrProAla 563	à d	/88 LINIGIYGIYI         1978GGCGGCT
8 8	564	AspValTvrGlnSerLvsL	Oy	808 gLeuArgPheP
7 d	1075	GACATCAATCAGGAGAAGACCGTAAACATCACCTTTTTCGTCGATCGGGCAAACAG	qa	2019 GGAACACTTTT
o y	573	LeuTyrValPheValAlaSerAspLysProArgAsp	Oy Dp	828 rProlleserA     2079 GCCCAGGGACA
2	6511	GICTACGTGAGGGGAATTTCCAGGGCAATACCAAGACGCGTGACGAAGTGCTGCGC	Qy	848 uTyrAsnTyr-
oy Dp	585 1195	GlyGhlleGlyLeuGlyTrpGlySerAspThrGlyThrArgLeuValThr 601 AGGGAAATGCGGCAGAGGGGGCGTGGGCGTCGACGGG 1236	qq	
νο 4	602	LysPheGluHisAsnLeulleAsnArgAspGlyTyrGlnAlaGlyAlaGluLeu	Qy Db	862 eGlyAspileG          2199 CGTCGACGCC
a è	1630	AMBATICAMBEGGITCCAMBACCTUCAMBCGTCTCGGCTATTTCCAMBATGTCAACGTG	QY	881 aGlyvalGlyv
g 8	1297		QQ	2259 CGGCATITCGG
δ	635	ProLeuSerHisProLeuAsnAspGlnLeuArgAlaThrLeuGlyTyr 650	δλ	901 yvalLysGluG
qq			qu	2319 GCTCAACTCCC
, oy	651		RESC ABQ9	
qq	1405	GGCATCATATTCAATGCGGCGGTCACCCAGGACAACATTTTCGGCAGCGGCAAGCGTGTC 1464	Q X X	ABO90024 standar
δy	658	829 028	XX	
QQ	1465	AGTTTCAATTTCAACAACAGCCAGATCAACACCATCTATGCCTTGGGGTATTTCAATCCT 1524	XX	01-001-2002 (11
Οy	629		X	M. capsulatus ge
qq	1525	TACGCCACCCTGGATGGCATCAGCAGTGGTTTCGACATCAGCTATCGCGACACCAACACC 1584	X X C	Micro array; gen
QY	672		8 <b>X</b> 8	Metnylococcus ca
qq	1585	GGCTATTCGAACTATGCCAACTACCATTACCAATGTGTTCCAGGTGGGCGCAACTGG 1644	x x a	18-TH -2003
o y	684	AsnArgThrTyrLysLeuLargTyrArgLeuAspLysLeuLys	X X	14-JAN-2002; 200
an i			P.K.	12-JAN-2001; 200
oy B	1705	698 -ThrGinAlaProProGluThrTrpGinAspLeuProValAspPheValAsnGlyLysPr 717   ::::::	PR XX PA	12-JAN-2001; 200 (UNIF-) UNIFOB S
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ACACCCTGAATCGGGCGATATTCG------1828
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                                                                                                                                                                                                                                                                                                                                            CTGTGGTTGAATGGCGATTTCGGTTACGGC-------1977
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                                                                                                                                                                                                                                                                       CAGTATTACAAGGCCAACGTGCGCCTGGAGCAGTATTTTCCGCTGACCCA 1937
AlaLeuLeuAlaGlyValAlaValHisLysThrValAlaAspAsnLeuVa 737
                                                                       ArgGlyTyrArgGlnArgTyrSerLeuGluValGlySerSerGlyLeuVa 757
                                                                                                                                                                                                                                                                                                          -----GlyAspAsnAlaTyrGlySerAsnArgAlaHisGlnMe 788
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CAGAGCGGGACCGAATTCAGCATTT 2355
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The invention relates to a novel DNA array giving a representation of a number of Methylococcus capsulatus genes. The method of the invention is useful for determination of the differential expression of the genes of M. capsulatus, and for studying gene expression on a genomic scale and in gene expression assays of M. capsulatus genes. The sequences shown in ABO90016-ABO91855 represent M. capsulatus genes for use in arrays of the
                                                                                                         wovel DNA array useful for determining differential expression of Methylococcus capsulatus genes, comprises polynucleotides or oligonucleotides representative for a selective number of Methylococcus capsulatus genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ValAlaAspGluValProLeu---LeuIleGlyAspValPheHisHisGlyLysTyrGlu 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AlaIleGlySerSerHisGlnLysThrGluProTyrAlaAsnIleLysAlaAlaLeuGlu
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                              HB, Lien T
Durkin AS;
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187
108
316
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43
                              I, Jensen
Fraser CM,
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Matches:
Conservative:
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                             Eidhammer I, Jonassen
Lossius I, Eisen JA,
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Query Match:
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                           Birkeland NK,
Lillehaug JR,
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(TIGR-) TIGR
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                                                          Salzberg
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                                                                                                                                                                                                                                                                                                                                                                                                                                              SerSerSerArgThrGluProAlaGlnValAspGluSerThrLeuGluProValIleGlu
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                                 LeuAspArgSerValAspValIleLeuProAspAsnThrAlaAspValSerLeuIleTyr
                                                                  -----CTGCCCCGGAACCGTGTGGCGGTGAATATCAATATC
                                                                                                AspThrGlyThrGlnTyrArgPheAspGluValValPhe--------PheThr
                                                                                                                                  GCGGAGGGGCGCGTTGCTCGCATAAAACAGATCAATATCGTCGGAAATAATGCATTTAGT
                                                                                                                                                                                                                                                                      ------GAGCTGAGTACATCTCCTGTCTTTCTATACCAAGGATGATCAGTAT
                                                                                                                                                                                                                                                                                                        406 AlaValArgAlaLeuSerAsnAspLeuIleAlaThrArgTyrPheAsnMetValAsnThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----AAAGAAATATATC
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RESU AAP2 ID XX XX AC AC AC	DE XX XX XX XX XX XX XX XX XX XX XX XX XX	XX O XX	X Q X Z	X X X X X X X X X X X X X X X X X X X	XAAX	N X I	X E E E	XX PS	<b>\$</b> 0.8			3888		UUX OS	Alig Pred Scor	Pero Best Quer DB:	US-0
651	9ThrasnGlypheaspLeuSerThrargThrLeuGluHis :::::	672 GlulleSerargrrp 683 	684 ASNArgthrTyrSerLeuargtyrargLeuaspLysLeuLys 697 	698 -ThrGlnalaProProGluThrTrpGlnaspLeuProValaspPheValasnGlyLysPr 717	717 oserGinGlualaLeuLeuAlaGlyValAlaValHisLysThrValAlaAspAsnLeuVa 737 	737 lAsnProMetargGlyTyrArgGlnArgTyrSerLeuGluValGlySerSerGlyLeuVa 757            1795 TGGACCCATGACACCCTGAATGGGGGGATATTCG	757 lSeraspalaasnMetalaIlealaargalaglyIleSerGlyValTyrSerPhe 775    :::      :: :::::	775 775	1878 CAGCACCTGCAGTATTACAAGGCCAACGTGCGCCTGGAGCAGTATTTTCCGCTGACCCA 1937	776	788 tThrGlyGlyIleGlnAlaGlyTyrIleTrpSerAspAsnPheAsnHisValProTyrar 808         :::    :::	808 gLeuargPhePhealaGlyGlyAspGlnSerIleargGlyTyralaHisAspSerLeuSe 828 	828 rProlleSerAspLysGlyTyrLeuThrGlyGlnValLeuAlaValGlyThrAlaGl 848	848 uTyrasnTyr	862 eGlyaspileGlyasnalaTyraspLysGlyPheThrasnaspThrLysIleGlyal 881	881 aGlyValGlyValArgTrpAlaSerProValGlyGlnValArgValAspValAlaThrGl 901 	901 yValLysGluGluGlyAsnProlleLysLeuHisPhe 913 ::::::::::::::::::::::::::::::::::::
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Qy Db 1	Oy Db 1	Oy Db 1	Oy Db 1	Oy Db 1	Oy 07	Oy 10	ογ	Db 1	Qy Db 1	Oy Db 1	Oy Dp	Oy Db	0y Db 2	Oy Db 2	Oy Db	Oy

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This invention describes a novel preparation of an agent (A) for detection, prevention and/or treatment of microbial infection by:

(i) identifying essential genes (I) and corresponding polypeptides

(II): (ii) identifying essential genes (I) and corresponding polypeptides

(II): (iii) identifying compounds that are directed against (II) and inactivate the microbe; (iii) testing these for sultability for use; and corresponding selected (A). Identifying essential genes (I) comprises preparation of gene-deficient microorganisms by conditional antisense inhibition of gene-deficient microorganisms by conditional antisense inhibition (AI) and/or survival of the deficient organisms. The products of the invention have antibacterial activity. (A) (which may be a nucleic acid (Ia), vector or host cell containing (Ia), derived polypeptide (IIa), or fragments. (IIa)-specific antibodies or their collypeptide (IIa) are used in DNA, subunit or live vaccines. The method infection by Halicobacter pylori: Particularly conditions are used in DNA, subunit or live vaccines. The method identifies essential genes, including those that have homologs in other species, so identified (A) should have a broad spectrum of activity. Many gene-deficient cells can be screened quickly, in an automated process, and the identified genes can be used for screening without purification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Preparing an agent for diagnosis or control of microbial infection, useful particularly against Helicobacter, based on identification of essential genes in defective mutants -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Microbial infection; antibacterial; Helicobacter pylori infection; vaccine; screening; ds.
                                                              41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Apfel H, Fuchs TM, Gibbs CP, Hueck CJ, Meyer TF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN (CREA-) CREATOGEN GMBH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 37; Page 232-236; 366pp; German.
AAF25588 standard; DNA; 2751 BP.
                                                                                                                                                                                                            H. pylori HPS120 encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99DE-1024965.
99DE-1027740.
99DE-1034029.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAY-2000; 2000WO-EP05024
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206.50
32.98%
19.31%
4.37%
                                                                                                                                      05-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                    Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-049948/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cent Similarity:
t Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAB46311.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200073502-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAY-1999;
17-JUN-1999;
21-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-DEC-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gnment Scores:
                                                                     AAF25588;
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qc	91	TTGACTTCTCCAAAAGAAGCCTCTCAAGAATCTCAAAAAAATGAAGCTCCA 141	
27	4 4	AlaHisAspThrAlaIleAsnGlnAlaLysAlaGlyAsnProProValLeuLeuThrPro 63	
qC	142	AAAAATGAAGTTCAAAGAAATGAAGCTCAAAAAGAAACCCCCCAATCCAATCAAACGCCT 201	
λχ	64	GluGlnIleGlnAlaArgLeuAsnAlaAlaGlyLeuAsnAlaLysProGlnSerGln 82	
q	202	AAAGAAATGAAAGTCAAGTTCCTTATGTCGGGCTTTCTTACATGTCTGACATGCTC 261	
λλ	83	<pre>leSerArgIleGlyGluGlnSer    :::    :::</pre>	
g Q	262	GCTAATGAAATTGTAAAGATT	
λ	103	ProProLeuGlyLeuAspMetSerVallleGluGluThrThrProLeuSerLeuGluGlu 122	
qc	301	GATICTAAAAAATAGACACCGCTGTTTTGGCT 333	
λ	123	LeuPheAlaGlnGluSerThrGluMetGlyIleAsnProAsnAspTyrIleProGluTyr 142	
qc	334	TTGTTCAATCAA 345	
27	143	GlnGlyGluGlnProAsnSerGluValValValProProThrLeuGluProGluLysPro 162	
q	345	345	
ζ	163	GlyLeuIleLysArgLeuTyrAlaArgLeuPheAsnAspGlyValAsnLysValProArg 182	
ą	346	  GGGTATTTTAAAGACGTTTATGCCACTTTTGAAGGCGGCATA 387	
λχ	183	LeuLysAlaLysPheTyrGlnSerSerGlnSerGlyGluThrSerAlalleGly 200	
ą	388	TTAGAGTTTCATTTTGATGAAAAAGCCAGGATTGCCGGGGTAGAAATCAAGGGTTATGGG 447	
λ̈	201	SerSerHisGlnLysThrGluProTyrAlaAsnIleLysAlaAlaLeuGluAspIleThr 220	
ક	448	ACTGAAAAAGGAAAAAAGGCTTAAAATCCCAAATGGGGATCAAAAAGGGCGGCGTTT 507	
χ̈́	221	GlnGluSerAlaMetAspLeuAsnGlySerIleProArgLeuArgGlnThrAlaLeu 239	
q	508	GATGAGCAAAAATTAGAGCATGCTAAAACGGCTTTAAAA 546	
λ	240	ValAlaalaargalaValGlyTyrTyrAspIleAspLeuSerIleIleArgAsnSerIle 259	
q	547		
λ	260	GlyGluValAspValIleIleHisAspLeuGlyGluProValTyrIleAspTyrArgAla 279	
q	574	GGGAGCGTG	
λ. 90	280	ValGluValargGlyGluGlyAlaAspAspLysAlaPheThrThrValAlaAsp 297 	
>	298	GluValProfention() vasnValPheHisHisGlv[vsTvrG]uThr[vs[vs 3]	
, A	643	AGGGGGATAGCATTATATCAAACAATCCATTTATGAGGGAAGCGCGAAATTAAAAACGC 70	
χ̈́	317	AsnLeuIleGluAsnAlaSerAlaGluHis	
q	703	:::      :::   CGCATGATTGAATCTTTGAGTGCGAACAAGCAACGAGATTTCATGGGCTGGATGTG	
λά	328		
q	763	TTGAATGACGGGAAATTGCGTTTAGATCAACTAGAATACGATTC	
λά	333	ValileLeuProAspArgSerValAspValileLeuProAsp 344	
qc	823	GIGIATAIGCGIAGGGGITACTIAGACGCICATAITICIICGCCITITITGAAAACGGAI 882	
λα	345	AsnThralaAspValSerLeuIleTyrAspThrGlyThrGlnTyrArgPhe 361	
QQ	883		

Qy	362	AspGluValValPhePheThrIleAspProLysThrAsnGlnLeuThrThrAspProAsp 381
QQ	943	AGAGATTG
QY	382	LysLeuProValLysArgGluLeuGluGluGlnLeuLeuThrValAsnMetGlyGluAla 401
qq	973	ACCTTAGAAAAAGCGC
δλ	402	TyrAsnLeuGlnAlaValArgAlaLeuSerAsnAspLeuIleAlaThrArg 418
qq	1027	TTTAATATTGAGCATTTAAGAGCGGATGCCCAAATTTTAAAAACCGAAATCGCCGATAAG 1086
Qγ	419	TyrPheAsnMetValAsnThrGluIleValPheProGluArgGluGInIleGlnAsnAsp 438
Op	1087	GGTTATGCGTTTGCGGTGGTGAAGCCAGACTTGGATAAA1125
οy	439	GlnValSerPheGluGlnSerSerSerArgThrGluProAlaGlnValAspGluSer 458
Op	1126	GATGAAAA 1134
Οy	459	ThrLeuGluProVallleGluThrValGluLeuThrAspGlyIleLeuMetAsp 476
QC	1135	.AACGGGCTTGTGAAAGTCATTTATCGTATTGAAGTGGGCGATATGGTGTATATCAATGAT 1194
Qy	477	1leserProlleGluPheSerAlaSerAsnLeuIle 488
q	1195	GTCATCATTACAGGGAACCACGCACGAGGGATAGGATCATTAGAAGGGAGTTATTGTTA 1254
ΟŊ	489	GlnAspLysLeuAsnLeuValAlaAlaLysAlaArgHisLeuTyrAspMetPro 506
QΩ	1255	GGGCCTAAGGATAAATACAACTTGACCAAACTGAGA
οy	507	AspAspArgValLeuAlaIleAsnHisAspAspGlyValAsnArgSerIleLeuGlyArg 526
Dp	1291	TTA
δy	527	IleSerAspAlaValSerAlaValAlaArgAlaIleLeuProAspGluSerGluAsnGlu 546
Dp	1324	TICICITAAAGTCAAAATIGAAGAAAAAGGGTTAATAGCTCA 1365
δy	547	ValileAspLeuProGluArgThrAlaLeuAlaAsnArgLysThrProAlaAspValTyr 566
QQ	1366	CTCATGGATTA1377
δy	567	GlnSerLysLysValProLeuTyrValPheValAlaSerAspLysProArgAspGlyGln 586
Ωp	1378	TTAGTGAGCGTAGAAGAGGGGCGTACTGGCGAG 1410
δy	587	IleGlyLeuGlyTrpGlySerAspThrGlyThrArgLeuValThrLySPheGlu 604
QQ	1411	TGGCTCTTATGGAGGCTTATG
οy	605	HisAsnLeulleAsnArgAspGlyTyrGlnAlaGlyAlaGluLeuArgLeuSerGluAsp 624
QQ	1459	GGGAGCGTGAGCGAAAGCATTTTTGGCACAGGCAAAGCATGAGCTTGTATGCTAAC 1518
Qy	625	LysLysGlyValLysLeuTyrAlaThrLysPro
QQ	1519	ATCGCTACAGGGGGGGGTAGATCTTATCCGGGCATGCCAAAAGGAGCGGGGGGGTATGTT 1578
Qy	636	
qq	1579	GCCGGGAATTTGAGCTTGACTAATCCA1605
Qy	651	GlnGlnGluValPheGlyHisSerThrAsnGlyPheAspLeuSerThrArgThrLeu 669
Op	1606	GACAGCTGGTATAGCTCTACGATCAACCT
ΟŊ	670	GluHisGluIleSerArgSerIleIleGlnAsnGlyGly
qq	1648	GCGGATTACAGGATAAGCTACCAATACATCCAACAAGGCGGGGGGCCTTTGGGGTGAATGTC 1707

XX KW GHPO 107; infection; therapy; diagnosis; vaccine; gastritis; ulcer; KW SS. XX OS Helicobacter pylor1.	XX FH Key Location/Qualifiers FT CDS 1422685 FT XX XX	WO9821225-A1. 22-MAY-1998.	PF 14-NOV-1997; 97WO-US21353.  XX	01-APR-1997; 01-APR-1997; 24-JUN-1997;	PA (HUMA-) HUMAN GENOME SCI INC. PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN. PA (INMR ) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS. XX		P-PSD Helic treat	CC GHPO 107 (see AAW71477). 85 Polynuclectides (see AAV52009-v52093) CC encoding claimed Helicobacter polypeptides (see AAW71474-W71558) have CC been identified in the H. pylori genome using a transposon shuttle CC mutagenesis method in which ThMax9 mini-blaw was used for			or delivered with a delivery vehicle), polypeptides or monos antibodies; methods for detecting the presence of Helicobact	CC in samples using e.g. polynuclectide molecules; and methods for CC purifying polypeptides of the invention.	SQ Sequence 3012 BP; 896 A; 555 C; 735 G; 826 T; 0 other; Alignment Scores:	Indels: Gaps:	US-09-914-168-2 (1-919) x AAV52012 (1-3012)	24 MetThrSerGlnAlaLeuAlaGlnGlnAsnAsnProAlaAsnIleIleAsnHisValPro 4 :::	Db 25 TTGACTTCTCCAAAAGAAGCTCTCAAGAATCTCAAAAAAATGAAGCTCCA 75	Qy 44 AlaHisAspThrAlaTleAsnGlnAlaLysAlaGlyAsnProProValLeuLeuThrPro 63
Oy 683TrpAsnArgThrTyrSerLeuArgTyrArgLeuAspLysLeuLys 697	Db 1768 CTCCTTGGTTTCAGCAGCCCTTTATACAACCGCTACTATTCCTCTGTTAATGAAGTGGTT 1827  Qy 716 LysProSerGlnGluAlaLeuLeuAlaGlyValAlaValHisLysThrValAla 733	1828 TCTCCAAGGCAATGTTCTACCCCCGCATCGGTGATTATCAATCGCTTATCAGGCGGTAAA 734AspAsnLeuValAsnPro	DD 1888 ACCCCTTACAACCTGAAAGCTGTTCTAGTCCTGGAGCGATCACCACTTCACCAGAAATA 1947  Qy 741 ArgGlyTyrargGlnArgTyrSerLeuGluVal 751	Qy 752 Gly	Qy 762 MetAlaIleAlaArgAlaGlyIleSerGlyValTyrSerPheGlyAsp 777 :::     :::      :::	ACCAC	Qy 792	816 AspGlnSerIleArgGlyTyrAlaHisAspSerLeuSerProlleSerAspLysGlyTyr	Qy 836 LeuThrGlyGlyGlnValLeuAlaValGlyThrAlaGluTyrAsnTyrGluPheMetLys 855	CCCCA	867ASn	Db 2473 ACTAGAGGGAGTTTTTTTTAAGGCTCCTGTTACGACAGCGAATTTTAAAGATTATGGC 2532	Oy 868 AlaTyrAspLysGlyPheThrAsnAspThrLysIleGlyAlaGlyValGlyValArg 886	RESULT 34 AAV52012	ID AAV52012 standard; DNA; 3012 BP.	AAV52012;	09-NOV-1998	DE Helicobacter polypeptide GHPO 107 DNA.

  AATCAAACGCCT 135	ProGlnSerGln 82 TCTGACATGCTC 195	rargileGlyGluGlnSer 102    :::   :: -CGTGTGGGCGATATTGTG 234	SerLeuGluGlu 122				LysValProArg 182 321	SeralaileGly 200      AAGGGTTATGG 381		44	gLeuArgGlnThrAlaLeu 239 :::	: Φ	507	Ø	516	AlaAsp 297      TTTGATGTGAAT 576	GluThrLysLys 316 :::    ::: AAATTAAAAGG 636			332	CGTATCCAAGAT 756	IleLeuProAsp 344	::: TTGAAAACGGAT 816	36	20	
	GluGlnIleGlnAlaArgLeuAsnAlaAlaGlyLeuAsnAlaLysProGlnSerGln ::::::::::::::::::::::::::::::::::::	spAspGlnSerProlleSe	ProProLeuGlyLeuAspMetSerVallleGluGluThrThrProLeuSerLeuGluGlu   :::      :::   GATTCTAAAAAAAAAACGCTGTTTTGCT	leAsnProAsnAspT	oAsnSerGluValValValProProThrLeuGlu		GlyLeuIleLysArgLeuTyrAlaArgLeuPheAsnAspGlyValAsnLysValProArg 	LeuLysAlaLysPheTyrGlnSerSerGlnSerGlyGluThrSerAlaileGly     :::	erSerHisGlnLvsThrGluProTvrAlaAsnIleLvsAlaAlaLeuGluAsDIleThr	::: :::     actgaaaaggaaaaagacggcttaaaatcccaaatggggatcaaaagggggacgttt	AsnGlySerIleProAr	TyrTyrAspileAspLe	GCAGGGCTATTAT	lileileHisAspLeuGlyGluProValTy		ValGluValargGlyGluGlyAlaAspÅspLysAlaPheThrThrValAlaAsp 	GluValProLeuLeuIleGlyAspValPheHisHisGlyLysTyrGluThrLysLys 	AsnLeuIleGluAsnAlaSerAlaGluHis			:: TTGAATGACGGGAAATTGCGTTTAGATCAACTAGAATACGATTCTATGCGTATCCAAGAT	ValleLeuProAsp	GGGTTACTTAGACGCTCATATTTCTTCGCCTTTT	AsnThrAlaAspValSerLeuIleTyrAspThrGlyThrGlnTyrArgPhe	CGCTAAGCTTCATTATAAAGTCAAAGAGGGATC	AsnGluValValValbbobbombrIleAssporoTvsmbrAssoCluIoumbrAssDroAss
AAAATGAAGTTCA	GluGlnIleGlnAlaArg	AlaLeuAspValValAsnPheA.      :::::    GCTAATGAAATTGTAAAGATT-	ProProLeuGlyLeu :: GATTCTAAAAAAT	LeuPheAlaGlnGlu	TTGTTCAATCAAGlnGlnGlnPro	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	GlyLeuIleLysArg       GGTATTTTAAAGAG	LeuLysAlaLysPho     :::  THGAGTTTCATTT	SerSerHisGlnLvs	::: ACTGAAAAGGAAAA	GlnGluSerAlaMetAspLeu      	ValAlaAlaArgAla	ACCGCTTTAGAGGGGCAGGGCTATTAT	GlyGluValAspVa.	GGGAGCGTG	ValGluValArgGl	GluValProLev :: AGGGGGGATAGCAT	AsnLeulleGluAsı	::      :: CGCATGATTGAATC	TyrPheAspGlyArg-	TTGAATGACGGGAA		GTGTATATGCGTAG	AsnThrAlaAsi	TITICIACCCATGA	AcneliuValValDha
16	136	83 196	103	123	268	279	163	183	201	382	221	. 4	481	260	208	280	298	317	637	328	697	333	757	345	91/	262
qq	Qy Db	Qy Dp	Qy Db	οχ	g ò	og o	Qy Dp	oy B	6	g	۶ و۲	δ	qq	οy	qq	Qy Db	ر م	δλ	Op	ογ	QQ	ογ	qq	δ d	2 .	ċ

qq	877	TCAGACATTTTAATAGAGATTGACAACCCG 906
οy	382	ArgGlu
qq	907	GTAGTCCCCTTAAAAAACCTTAGAAAAGCGCTTAAAGTGAAAAGGAAAGATGTC 960
δy	402	TyrAsnLeuGlnAlaValArgAlaLeuSerAsnAspLeuIleAlaThrArg 418
Dp	961	TTTAATATTGAGCATTTAAGAGGGGATGCGCAAATTTTAAAAACCGAAATCGCCGATAAG 1020
οy	419	rPheasnmetValasnThrGlulleValPheProGluargGluGlnIleGlnAsnAsp 438
ga	1021	GTTATGCGTTTGCGGTGGTGAAGCCAGACTTGGATAAA 10
οy	439	lnValSerPheGluGln
qq	1060	
οy	459	ThrLeuGluProValIleGluThrValGluLeuThrAspGlyIleLeuMetAsp 476
QQ	1069	AACGGGCTTGTGAAAGTCATTTATCGTATTGAAGTGGGGGGATATGGTGTATTCAATGAT 1128
Qγ	477	IleserProlleGluPheSerAlaSerAsnLeuIle
QQ	1129	GTCATCATTICAGGGAACCAGGCGACGGATAGGATCATTAGAAGGGAGTTATTGTTA 1188
Oy	489	GlnAspLysLeuAsnLeuValAlaAlaLysAlaArgHisLeuTyrAspMetPro 506
qq	1189	GGGCCTAAGGATAAATACAACTTGACCAAACTGAGA
ολ	507	AspaspargValLeualaIleAsnHisAspAspGlyValAsnArgSerIleLeuGlyArg 526
qq	1225	}
δλ	527	IleSerAspAlaValSerAlaValAlaArgAlaIleLeuProAspGluSerGluAsnGlu 546
Op	1258	TTCTCTAAAGTCAAAATTGAAGAAAAAAGGGTTAATAGCTCA 1299
οy	547	VallleAspLeuProGluArgThrAlaLeuAlaAsnArgLysThrProAlaAspValTyr 566
QQ	1300	CTCATGGATTA1311
Qy	292	GlnSerLysLysValProLeuTyrValPheValAlaSerAspLysProArgAspGlyGln 586
QQ	1312	TTAGTGAGGGTAGAGAGGGGGGTACTTAGTGAGAGAGAGGGGGGGTACTTGGGGGGGG
Qy	587	IleGlyLeuGlyTrpGlySerAspThrGlyThrArgLeuValThrLysPheGlu 604
qq	1345	TTGCAATTTGGGTTAGGCTCTTATGGAGGCCTTATGCTTAAT 1392
Οy	605	HisAsnLeuIleAsnArgAspGlyTyrGlnAlaGlyAlaGluLeuArgLeuSerGluAsp 624
qq	1393	GGGAGCGTGAGCGAAAGAAACCTTTTTGGCACAGGGCAAAGCATGAGCTTGTATGCTAAC 1452
Οŷ	625	LysLysGlyValLysLeuTyrAlaThrLysPro635
QQ	1453	ATCGCTACAGGGGGGGGTTTTTTCCGGGCATGCCAAAAGGAGGGGGGGG
ōλ	636	
qq	1513	GCCGGGAATTTGAGCTTGACTAATCCA1539
Οy	651	GlnGlnGluValPheGlyHisSerThrAsnGlyPheAspLeuSerThrArgThrLeu 669
qq	1540	GACAGCTGTATAGCTCTACGATCAACCT
Οy	670	GluHisGluIleSerArgSerILeIleGlnAsnGlyGly
QQ	1582	GCGGATTACAGGATAAGCTACCAATACATCCAACAAGGCGGGGGGCTTTGGGGTGAATGTC 1641
Óλ	683	TrpAsnArgThrTyrSerLeuArgTyrArgLeuAspLysLeuLys 697
qq	1642	GGGCGCATGCTGGGTAATAGAACCCATGTGAGCTTAGGGTATAACTTGAATGTTACCAAA 1701

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US-09-914-168-2 (1-919) x AAV25138 (1-2778)
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2347 GCGGCTAAAATGCGCTTAGCGTGGTTTTTTGACTTTGGTTTCTTAACCTTTAAAACCCCA 2406
                                                                   2047 AACGGGTTAGGCGGGAATGTCCGTAACACCAAAGTTTATGGTAAATTCGCCGCTTACCAC 2106
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                               1702 CTCCTTGGTTTCAGCAGCCCTTTATACAACCGCTACTATTCCTCTGTTAATGAAGTGGTT 1761
                                                                                                                     1822 ACCCCCTTACAACCTGAAAGCTGTTCTAGTCCTGGAGCGATCACCACTTCACCAGAAATA 1881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytoplasmic; vaccine; prevention; treatment; infection; envelope; identification; binding compound; bacteria; life cycle; activator;
                                                                                                                                                                                                                                                                                                                                                                               1942 AGCTATGACAACACCGATGATTATTACTTCCCTAGAAATGGGGTTATCTTTAGT-----
                                                                                                                                                                                                                                              -IleGlnAlaGlyTyr
                                                                                                                                                                                                                                                                                                                                                                                                            816 AspGlnSerIleArgGlyTyrAlaHisAspSerLeuSerProIleSerAspLysGlyTyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----AspLeuArgLeuAlaValPheGlyAspIleGly------
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                                                                                                                                                                                       ---SerSerGlyLeuValSerAspAlaAsn
                                                                                                                                                                                                                                                                                                                                                                IleTrpSerAspAsnPhe---AsnHisValProTyrArgLeuArgPhePheAlaGlyGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2287 TGGCTTGGAGGCGATGGGATTTTTACCGCTTCTACTGAATTGAGCTATGGGGTGCTAAAG
                                                                                                                                           -----TyrSerLeuGluVal
                                                                                                                                                                                                                                 762 MetalalleAlaArgAlaGlyIleSerGlyValTyrSerPheGlyAsp------
                                                                                                                                                                                                                                                                            778 AsnAlaTyrGlySerAsnArgAlaHisGlnMetThrGlyGly-------
                                                    LysProSerGlnGluAlaLeuLeuAlaGlyValAlaValHisLysThrValAla-----
          698 ThrGlnAlaProProGluThrTrpGlnAspLeuProValAspPheValAsnGly---
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                                                                                                 -----AspAsnLeuValAsnPro----
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This sequence encodes a H. pylori cell envelope outer membrane protein having a terminal Phe residue.

The protein having a terminal Phe residue.

The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, infection or to identify H. pylori life cycle activators or inhibitors. The company probes derived from it may be used for the identification of H. pylori in a sample and the diagnosis of H. pylori infection. Nucleic acid sequences complementary to the DNA act as antisense sequences and can be used to prevent the translation of H. pylori infection. Nucleic and distribution of H. pylori-specific antigens. The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for computer evaluation. To identify likely H. pylori antigens for vaccine development, the aminon acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of membrane proteins. Having identified and determined the sequences of miterest, particular regions can be isolated from H. Pylori B. P
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inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis; cell envelope outer membrane protein; OMP; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polypeptide(s) - useful in vaccines to treat or prevent H. infection and for diagnosis of H. pylori infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               681 G; 770 T; 0 other;
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1..2778
/*tag= a
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960S-0625811.
960S-0758731.
960S-0736905.
960S-0738859.
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                                                                                                                                          Helicobacter pylori.
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29-MAR-1996;
02-APR-1996;
25-OCT-1996;
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-----ATTTGGCTTCTCCAAAAGAAACCC 169

47 ThralalleAsnGlnAlaLysAlaGlyAsnProProValLeuLeuThrProGluGlnIle 66

2778 206 143 318 352 51

Matches: Conservative: Mismatches:

1.61e-06 200.00 34.32% 20.26% 4.23%

Indels:

Length:

86

67 GlnAlaArgLeuAsnAlaAlaGlyLeuAsnAlaLysProGlnSerGlnAlaLeuAspVal

ACGGCTCTAAACCAAACG--

100

QΩ	1006 CCCTTAAAAACCTTAGAAAAGCGCTTAAAGTTAAAAGGAAAGATGTCTTTAAT 1059
Qy	404 LeuGlnalaValArgAlaLeuSerAsnAspLeuIlealaThrArgTyrPhe 420
qq	1060 ATTGAGCATTTAAGAGCGGATGCGCAAATTTTAAAAACCGAAATCGCCGATAAGGGCTAT 1119
Qγ	snThrGluIleValPheProGluArgGluGlnIl
qq	9C
Qy	lnSerSerSerArgThrGluProAlaGlnV
qq	
ΟŊ	ThrValGluLeuThrAspGlyIl
qq	AAAGTCATTTATCGTATTGAAGTGGGCGAT
QY	AsnLeuVal
QQ	1222 GTCATCATTTCAGGGAACCAGCGCACGAGCGATAGGATCATTAGG 1266
Óγ	500 ArgHisLeuTyrAspMetProAspAspArgValLeuAlaIleAsnHisAsp 516
QQ	1267 AGGGAATTGTTACTAGGGCCTAAAGATAAATACAACTTGACCAAAACTGAGAAATTCCGAA 1326
Οy	517 AspGlyValAsnArgSerIleLeuGlyArgIleSerAspAlaValSerAlaValAlaArg 536
qq	1327 AATTCTTTGAGGCGTTTAGGGTTTTTCTCTAAAGTCAAGATTGAAGAAAAAAGG 1380
Qy	537 AlaileLeuProAspGluSerGluAsnGluValileAspLeuProGluArgThrAlaLeu 556
qa	1381 GTC
Οy	557 AlaAsnArgLysThrProAlaAspValTyrGlnSerLysLysValProLeuTyrValPhe 576
qa	
Óγ	577 ValalaSerAspLysProArgAspGlyGlnIleGlyLeuGlyTrpGlySerAsp 594
qq	1408 GTGAGCGTAGAAGAGGGGCGCACCGGGCAGTTGCAATTGGGCTATGGCTGTAT 1467
Qy	h
qq	AATGGGAGCGTGAGCGAAGGAATCTTT
Οy	615 AlaGlyAlaGluLeuArgLeuSerGluAspLysLysGlyValLysLeuTyrAla 632
qq	1516 ACAGGGCAAAGCATGTATGTTATGCTAACATTGCCACAGGGGGGGG
Qy	633 ThrLysPro
qa	1576 GGCATGCCAAAAGGGGGGGGGGGTATGTTGGCGGGAATTTGAGCTTGACTAATCCA 1632
Qy	641 AsnAspGlnLeuArgAlaThrLeuGlyTyrGlnGlnGluValPheGlyHisSerThrAsn 660
qa	1633GAC 1644
Οy	661 GlyPheAspLeuSerThrArgThrLeuGluHisGluIleSerArgSerIleIle 678
qq	1645 AGCTGGTATAGCTCTACGATCAATCTTTATGCGGATAACGGATAAAGCTACCAATACATC 1704
Qy	679 GlnAsnGlyGly
QQ	1705 CAACAAGGGGGGGGTTTTGGGGTGAATGTCGGGCGCATGCTGGGTAATAGAACCCATGTG 1764
Qy	688 SerLeuArgTyrArgLeuAspLysLeu-LysThrGlnAlaProProGluThrTr 705
qq	1765 AGCTTAGGGTATAACTTGAATGTTACCAAACTCCTTGGTTTCAGCAGCCCCTTATACAAC 1824
δλ	705 pGlnAspLeuProValAspPheValAsnGlyLysProSerGlnGluAlaLeuLeuAlaGl 725
qq	1825 CGCTACTATICCICTGTTAATGAAGTG-GCCTCTCCAAGGCAATGTTCCACACCCCCATC 1883

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membrane polypeptide; OMP; vaccine; H. pylori infection; humoral; lar immune response; ds.
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                       1884 GGTGATTATCAACCGCTTATCAGGCGGTAGAACTCCATTGGTTCCTGAAAGCTGTTCTAG 1943
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                                                                       1944 TCCTGGAGCGATCACCACTTCACCAGAAATAAAAGGTATTTGGGATAGGGATTACCACAC 2003
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 -ThrValAlaAspAsnLeuValAs 738
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---TCCTATGCGACAATGTCTGG
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                                                  ----MetArgGlyTyrArgGlnArg
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                                                                                                    2064 CCCTAGAAATGGGGTTATCTTTAGT---
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yValAlaValHisLys---
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The invention relates to a vaccine for preventing or treating infections by Helicobacter pylori. The vaccine contains at least one isolated the pylori polypeptide, or its fragments, in a carrier, where the carrier is a Salmonella, vibrio cholerae or Shiqella vector containing a nucleic acid encoding the H. pylori polypeptide. The vaccines induce humoral and cellular immune responses. The vaccines are used to treat or prevent infections by H. pylori. Sequences AAX75779 to AAX75837 represent nucleic acid sequences encoding H. pylori outer membrane polypeptides (OMPs) AAX17160 to AAY17218.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GATATGGTGGATTCTAAAAAATAGACACCGCTGTTTTAGCTTTGTTCAACCAAGGGTAT 378
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                                                                                                   Smith
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Mismatches:
                                                                                                                                                                                   Cellular vaccine against Helicobacter pylori
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                                                                (GENO-) GENOME THERAPEUTICS CORP
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٥y	517	AspClyValAsnArgSerIleLeuGlyArgIleSerAspAlaValSerAlaValAlaArg 536	
οp	1327		
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q <sub>Q</sub>	::: :::       1381 GTCAATAGCTCATTGATGGATTGG	404
QY	557 AlaAsnArgLysThrProAlaAspValTyrGlnSerLysLysValProLeuTyrValPhe 5	976
qq	1405TTA 1	1407
δ d	577 ValAlaSerAspLysProArgAspGlyGlnIleGlyLeuGlyTrpGlySerAsp 5	594
δλ	5 ThrGlyThrArgLeuValThrLysPheGluHisAsnLeuIleAsnArgAspGlyTyrGln	4
qa		1515
δλ	5 AlaGlyAlaGluLeuArgLeuSerGluAspLysLysGlyValLysLeuTyrAla	632
qq	16 ACAGGGCAAAGCATGAGCTTGTATGCTAACATTGCCACAGGGGGGGG	1575
oy d	633 ThrLysPro	640
ò	641 AsnAspGlnLeuArgAlaThrLeuGlyTyrGlnGlnGluValPheGlyHisSerThrAsn	09
qq	:::	1644
Qy	661 GlyPheAspLeuSerThrArgThrLeuGluHisGluIleSerArgSerIleIle (	829
qq		1704
Qy	79 GlnAsnGlyGlyTrpAsnArgThrTyr	87
<b>q</b> O	r o	1764
δλ.	8 SerLeuArgTyrArgLeuAspLysLeu-LysThrGlnAlaProProGluThrTr	10 (
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\ \do	5 yValAlaValHisLysThrValAlaAspAsnLeuValAs	738
qq		6
Qy	738 nPro	746
qq	1944 TCTIGGAGCGATCACCACTTCACCAGAATAAAAGGTATTTGGGATAGGATTACCACAC 2	2003
QY	47TyrSerLeuGluValGly	2
qq	2004 GCCTATCACCAGTTCTTTCACCCTTGATGTGAGCTATGACAACACGGATGATTATTATT ;	2063
Qγ	nMetalaIleAlaArgAlaGlyIleSerGl	771
QQ	TCCTATGCGACAATGTCTGG	2108
Qy	ValTyrSerPheGlyAspAsnAlaTyrGlySerAsnArgAlaHisGl	787
qq		2168
Qy	787 nMetThrGlyGly	791
qq	TTATGGTAAATTCGCCGCTTACCACATTTGCAAAAATATTTATT	2228
Qy	92IleGlnAlaGlyTyrIleTrpSerAspAsnPheAsnHisVa	0
qa	TTTAAAAACGCAAGGGGGCTATATCTTTAGGTATAACACCGATGATTACTT	2288
QY	805 lProTyrArgLeuArgPhePheAlaGlyGlyAspGlnSerIleArgGlyTyrAjaHisAs { ::::::      :::	825

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2289 GCCCTTAAACTCCACTTTCTACATGGGGGGCGTAACCACGGTGAGAGGCTTTAGGAACGG 2348
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                                                                                      2409 TICTACTGAATTGAGCTATGGGGTGTTAAAAGCGGCTAAAAATGCGTTTAGCGTGGTTTTT
                                       CTCAATCACCTAAAGATGAGTTTGCCTTGTGGCTTGGAGGCGATGGGATTTTTACCGC
                                                                                                                                                             --AsnAlaTyrAspLysGlyPheThrAsnAspTh
                                                                                                                                                                                 2529 CACCACGACGCGAATTTTAAAGATTATGGCGTTGTAGGGGCTGGGTTTGAAAGGGCGAC
                                                                   yThralaGluTyrAsnTyrGluPheMetLys-----AspLeuArgLeuAlaValPheGl
                                                                                                                                     pSerLeuSerProlleSerAspLysGlyTyrLeuThrGlyGlyGlnValLeuAlaValGl
                                                                                                                                                                                                                                                                                                                                                                    Vaccine; passive immunization; vector; antiserum; diagnosis; D15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid encoding D15 outer membrane protein – esp. of Haemophllus influenzae, and related proteins, vectors, antisera etc. useful in vaccines, for diagnosis and for passive
                                                                                                               yAspIleGly------
                                                                                                                                                                                                                     r---LysIleGlyAlaGlyValGlyValArgTrpAlaSerProValGly 892
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                                                                                                                                                                                                                                                                                                                                                                               OMP; outer membrane protein; NTHi; ss
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389.,2771
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P-PSDB; AAR53758.
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                                                                                                                                                                                                                                                                                                                  LeuAsnGlySerIleProArgLeuArgGlnThrAlaLeuValAlaAlaArgAlaValGly 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  771 ITAAATGAATTTGCCAAAAGTGTAAAAGAGCACTATGCAAGTGTAGGTCGCTAT---AAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       888 ATCAATGAAGATGATAAAGCAAAATTGGCATCATTAACTTTC-------AAG
                                                                                                                                                                                                                                                                                                                                                                                                                                    247 TyrTyrAspIleAspLeuSerIleIleArgAsnSerIle......GlyGluVal---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      263 AspValIleIleHisAspLeuGlyGluProValTyrIleAspTyrArgAla-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               446 SerSerSerArgThrGluProAlaGlnValAsp-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            492 LeuAsnLeuValAlaAlaLysAlaArgHisLeuTyrAspMetProAsp------
4
                                           2989
167
129
326
211
                                                                          Matches:
Conservative:
Mismatches:
                                                                                                                                                                Indels:
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                     3.26e-05
184.50
35.53%
20.05%
3.90%
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                                                                                                      Percent Similarity:
Best Local Similarity:
                  Alignment Scores:
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XX XX C. The invention relates to isolate	788 MetThrGlyGlyIleGlnAlaGlyTyrIleTrpSerAspAsnPheAsnHisValProTyr 807	ογ
	2211 CAGGGTTTCTACCCATTAGACAGAGATCACCGCTGGGTT 2249	qq
PT diagnostics, forensics, gene map PT responsible for genetic disorder PT biodiversity -		ολ
	754 SerGlyLeuValSerAspAlaAsnMetAlaIleAlaArgAlaGlyIle 769	ςς G
		- do
AA (HYSE-) HYSEQ INC.	2053 111661106	S
PR 31-MAR-2000; 2000US-0540217. PR 23-AUG-2000; 2000US-0649167.	714 AsnGlyLysProSerGlnGluAlaLeuLeuAlaGlyValAlaValHisLysThrValAla 733	δ δ
PF 30-MAR-2001; 2001WO-US08631.	2052 AATGGCATTAAAACAAAT	g
AA PA 11-OCT-2001.	694 AspLysLeuLysThrGlnAlaProProGluThrTrpGlnAspLeuProValAspPheVal 713	ò
PN WO200175067-A2.	2001 GCTCTAGAATATAACCGTAATTTATATATTCAATGAAATTTAAAGGT 2051	පු
OS Homo sapiens.	nG1	õ
KW Human; chromosome mapping; gene	atgaaataactcctattatgtaggattaggccatacctataataaaattagtagcatt	2 8
DE DNA encoding novel human diagnos		3 3
XX DT 13-FEB-2002 (first entry)	646 AlaThrLeuGlyTyrGlnGlnGluValPheGlyHisSerThrAsnGlyPheAspLeu 664 : ::	à
XX AC AAS89745;	1821 GATGGTGTAAGTCTTGGTGGAAATATTTTCTTTGAAAACTACGATAACTCTAAAAGTGAT 1880	g
RESULT 38 AAS89745 ID AAS89745 standard; cDNA; 2342 BP	626 LysGlyValLysLeuTyrAlaThrLysProLeuSerHisProLeuAsnAspGlnLeuArg 645	ŏ
Db 2730 GATGTCGAACAGTTCCAATTTAGTATT	ACGAAAAATGATTATGGTACGAGTGTCAATTTGGGTTATACCGAACCCTATTTACTAAA	김
Qy 907 AsnProlleLysLeuHisPhePheIle		ò
Db 2670 TCTCCTATTGGACCATTGGTATTTCT	:::     ::: ACAAGATAATTTCTTGGGAACAGGGGGGGGGAGTAAGTATAGCTGGT	5 B
Qy 889 SerProValGlyGlnValArgValAsp	1041 CGTAACACGGGTAGTAGTATCAACTITGGTATTGGTTACGGTACAGAGAGTGGTTATT 1/UU 600 VATThrtygPhaGluHisAsniantla	2 2
Db 2610 CCTGATTATGGCAAATCAAGCCGTATT	ProArgAspGlyGlnIleGlyLeuGlyTrpGlySerAspThrGlyThrArgLeu	ò
2550 T	:::	qq
Oy 869 Tyr		ò
2490 GTGAGGTAAAAAGCCAAAATA	554 Thr	à
Db 2430 GTGATTGGTGGTAATGCAATCACAACT	  1494 CAAGAAGGAACTTGGTATAATTCACAATTAGTTGAGTTAGGAAAAATTCGCTTAGATCGT 1553	QQ
Qy 838GlyGlyGlnValLeuAlaVal	541 AspGluSerGluAsnGluVallleAspLeuProGluArg 553	φ
Db 2370 GGGCCTAATGCAATTTATGCCGAACAT	525GIYALGILESELASPALAVALALARATGHATGHATGHATGHATGHATGHATGHATGHATGHATGH	<u> </u>
Qy 828 SerProIleSerAspLys	AATAAAACATTAGCGATAACCTTTGTTGTTGTTGGTGGACGACGTTTAACTGTTCGCCAA	g ,
2310	AspargvalLeualaIleasnHisAspaspGlyValasnargSerIleLeu	ò i
Db 2250 GTATCTGCAAAAGCATCTGCAGGATAT		qq
2250		

GlnSerIleArgGlyTyrAlaHisAspSerLeu 827 |||:::||||||::||||:: | GGTTCATTACGCGGTTTTGCTTATGGTAGTATT 2369 ArgLeuAlaValPheGlyAspIleGlyAsnAla 868 ||| ::::::||| ||| :: |CGAACCTCCCTATTGTTGATGCGGCAAGTGTT 2549 AATGGATTAGAGGCAAGGTCTTGAAAGACTTA 2609 SCAAATGGTTTTGGAAACAAGCGTTTACCGTTC 2309 GlyThrAlaGlu-----TyrAsnTyrGluPhe 853 698 -----ValAlaThrGlyValLys-----GluGluGly 906 mapping; gene therapy; forensic; ;; diagnostic; genetic disorder; ss. encoded polypeptides, useful in pping, identification of mutations s or other traits and to assess ed polynucleotide (I) and tic protein #25549. English.

polypeptide (II) sequences. (I) is useful as hybridisation probes,

C polymerase chain reaction (PCR) primers, oligomers, and for chromosome
and gene mapping, and in recombinant production of (II). The
polymucleotides are also used in diagnostics as expressed sequence tags

C to identifying expressed genes. (I) is useful in gene therapy techniques

C to restore normal activity of (II) or to treat disease states involving

C (II). (II) is useful for generating antibodies against it, detecting or

C quantitating a polypeptide in tissue, as molecular weight markers and as

C a food supplement. (II) and its binding partners are useful in medical

imaging of sites expressing (II). (I) and (II) are useful for treating

C disponders involving aberrant protein expression or biological activity.

C diagnostics, forensics, gene mapping, identification of mutations

C responsible for genetic disorders or other traits to assess biodiversity

and to produce other types of disorders or other traits to assess biodiversity

C and to produce other types of the invention.

C and to produce ada for this patent did not appear in the printed

Specification, but was obtained in electronic format directly from WIPO

C at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 2342 BP; 453 A; 738 C; 716 G; 435 T; 0 other;

Alignment Scores: 3.78e-05 Length: 2342 Perceit No.: 182.00 Matches: 139 Percent Similarity: 34.85% Conservative: 91 Best Local Similarity: 21.06% Mismatches: 243 Query Match: 23 S\$\$ Gaps: 25

US-09-914-168-2 (1-919) x AAS89745 (1-2342)

378 -----AAGTGCTGGGCATTGTCGGG 519 -----GlyLysTyrGluThrLysLysAsnLeu 361 GGGCGAGTTCTCCATCACCTACAAGCCCAGCGAGGCAAAAAACCAATGAATCAACCGTTA 319 IleGluAsnAlaSerAlaGluHisGlyTyrPheAspGlyArgTrpLeuAspArgSerVal nTyrArgPheAspGluValValPhePheThrIleAspProLysThrAsnGlnLeuThrTh 378 rAspProAspLysLeuProValLysArgGluLeuLeuGluGlnLeu-----LeuTh ----GGCTTTAGCGATGTCTCTTTTGATTTATGGCCGGGGG----304 GlyAspValPheHisHis--200 421 339 463 ò QQ ð QQ ò QQ q g õ Qγ

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779 1708 á P ò 809 CGCCAACCGGATCCACGACCTG-----ATGCAGCA 860 ACGICATTACGGCGATATTCGTGCCACGGGGGGAGAAGGGGGGAGAAGAGGTGGAGATTCC rAspGlyIleLeuMetAspIleSerProIleGluPheSerAlaSerAsnLeuIleGlnAs

1589 1086 ACTCGTCCCGGAGCCGCCGCAACCGCGGCGCGCCATCCCCGGGCCCCGGAGCCTGCCCA 1145 CACCCAGGGCACCCCACAGTCGGGGGCGCCCGGAGATGGCGTCAAGCTCGTCCGCCCCCGG 1205 206 CGCGCGTGACCCGAAATGAGCCCGCACCTTCCGACTCAGTAACTTTGGGGGGTTCCACACG 1265 1266 AGCCCGG-------GCCGTGTATTGG-----GACCCCAATTCTGACCTTTGTCC 1307 1323 -----TATAAATGCCGCTGCTGAAGATCCACTGGA 1355 -GACC/FGAACGA 1403 1497 1649 1748 1404 TACCGAATCTGACTCCACTACGCTG-----GTGGCTTCTCGCTACTGGGATCTCTCCAG 1457 TGTCGATTTCTCCGTTTTCCAGGCGCAGAACGTCTGGATCCGCACACTGTACGATCGC-- 1707 581 537 601 661 681 490 pLysLeuAsnLeuValAlaAlaLysAlaArgHisLeuTyrAspMetProAspAspArgVa 510 601 rLysPheGluHisAsnLeuIleAsnArgAspGlyTyrGlnAlaGlyAlaGluLeuArgLe 621 681 yGlyTrpAsnArgThrTyrSerLeuArgTyrArgLeuAspLysLeuLysThrGlnAlaPr 701 799 rAspAsnPheAsnHisValProTyrArgLeuArgPhePheAlaGlyGlyAspGlnSerIl 819 510 lLeuAlaIleAsnHisAspAspGlyValAsnArgSerIleLeuGlyArgIleSerAspAl 966 GCTGCGCGCCTGGTGGTGGTGGAACTCGCCGGGTGTGATTGTAACCTCTTCCCCAG sProArgAspGlyGlnIleGlyLeuGlyTrpGlySerAspThrGlyThrArgLeuValTh --------CACTTTACTCAGGTGAAATTACCAC ----GCCCGCAACCTGGTGACGCATCCG---AAGCTGGT ----ValTyrGlnSerLysLysValPro--........LeuTyrValPheValAlaSerAspLy uSerGluAspLysLysGlyValLysLeuTyrAlaThrLysProLeuSerHisProLeuAs 701 oProGluThrTrpGlnAspLeuProValAspPheValAsnGlyLysProSerGlnGLuAl 721 aLeuLeu-----AlaGlyValAlaValHisLySThrValAlaAspAsnLeuValAsnPr 1530 GATGCTGTTTTATCCTGGGGTGATGATTAGCCGCACGCGTTCTCGTGGTGGCCTGATGCC oMetArgGlyTyrArgGlnArgTyrSerLeuGluValGlySerSerGlyLeuValSerAs AACCTGGGGCGACTCGCAACGCTACTCTATCGACTACTCCAACACGGCCTGGGGTTCAGA ----CATCGTTTTGTTACACGCGCCACGCTGGCTTGGATTCAAAC nAspGlnLeuArgAlaThrLeuGlyTyrGlnGlnGluValPheGlyHisSerThrAsnGl 661 yPheAspLeuSerThrArgThrLeuGluHisGluIleSerArgSerIleIleGlnAsnGl pAlaAsnMetAlaIleAlaArgAlaGlyIleSerGlyValTyrSerPheGlyAspAsnAl aTyrGlySerAsnArgAlaHisGlnMetThrGlyGlyIleGlnAlaGlyTyrIleTrpSe alleLeuProAspGluSerGluAsnGluValIleAspLeuProGluArgThrAlaLeuAl 1356 ACAATATTATTTGGTGCAGGGGGGTTTTTAAGCGCACT----aAsnArgLysThrProAlaAsp-----530 avalSerAlavalAla-GACCCTCGACTTCAGC-861 GCGTTTGCAGATT --581 536 537 557 1146 573 1308 621 1324 641 906 1498 1590 739 1650 759 q g δ qq Q g qq qq ò qq qq QQ qq ò ò ò ò ò δ δ ò οy qq ò Q Ω Q δy qq ò qq ŏ Db

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and
GCCTCGAAGTTGATAACCGGATCGCTGGAATACCAGTACAACGTGACGGGAAAATGTACC 1928
                                                                                             1809 TCGTGGCTACCAATACCAAATCTATCGGTCCGAAATTACCCAACGGTGACACTGAAAGGG 1868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                    GlyGlnValLeuAlaValGlyThrAlaGluTyrAsnTyrGluPheMetLysAspLeuArg
                                                                                                                                                                                                               LeuAlaValPheGlyAspIleGlyAsnAlaTyrAspLysGlyPheThrAsnAspThrLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                         eArgGlyTyrAlaHisAsp-SerLeuSerProlleSerAspLysGly-TyrLeuThrGly
                                                                                                                                                                                                                                                                                                                                ---recerecece---eeceAegrececere 1973
                                                                                                                                                                                                                                                                                           879 IleGlyAlaGlyValGlyValArgTrpAlaSerProValGlyGlnValArgVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding novel human diagnostic protein #28892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID No 28892; 103pp; English.
                                                                                                                                                                                                                                                    AAGTGGCAGTTCGGCGAA-----
                                                                                                                                                                                                                                                                                                                                                                                                               BP
                                                                                                                                                                                                                                                                                                                                                                                                             AAS93088 standard; cDNA; 1916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAR-2001; 2001WO-US08631
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2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                           458 SerThrLeuGluProValIleGluThrValGluLeuThrAspGlyIleLeuMetAspIle 477
                                                                                                                                                                                                                                                                                                                                                                            497
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                                                                                                                                                                                                                                                                                                                              349 GCCACCGCGCAGAAGTGGCTGGAAAGAGGTGGAGATTCCCGCCAACCGGATCGAČGACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               578 AlaSerAspLysProArgAspGlyGlnIleGlyLeuGlyTrpGlySerAspThrGlyThr
                                                                                                                                                                                                                                                                                                                                                                            478 SerProlleGluPheSerAlaSerAsnLeuIleGlnAspLysLeuAsnLeuValAlaAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---GCCCGCAACCTGGTGACGCATCCG---AAGCTGGTGTTTATGGATGAACCGACCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               518 GlyvalAsnArgSerIleLeuGlyArgIleSerAspAlaValSerAlaValAlaArgAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   538 IleLeuProAspGluSerGluAsnGluValIleAspLeuProGluArgThrAlaLeuAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  558 AsnArgLysThrProAlaAspValTyrGlnSerLysLysValProLeuTyrValPheVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      598 ArgLeuValThrLysPheGluHisAsnLeuIleAsnArgAspGlyTyrGlnAlaGlyAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            638 HisProLeuAsnAspGlnLeu-----ArgAlaThrLeuGlyTyrGlnGlnGlu---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTGACCCGAAATGAGCCCGCACCTTCCGACTCAGTAACTTTGGGGGTTCCACACGAGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             847 GGGGCGTGTATTGGGACCCCAATTCTGACCTTTGTCCGACCCTCGACTTCAGCTATAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------ThrAsnGlyPhe---
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                                                                                                                                                                                                                                                                                                                                                                                                            ---CCGACCACCTTTTCCGGCGGT-----ATGCAGCAGCGTTTGCAGATT-----
amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the specification, but was obtained in electronic format directly at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                      other;
                                                                                                                                                      1916
110
61
166
166
20
                                                                                                                                                                                      Conservative:
Mismatches:
Indels:
                                                                                                      0
                                                                                                      :;
                                                                                                      582 G; 366
                                                                                                                                                        Length:
Matches:
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                                                                                                      349 A; 619 C;
                                                                                                                                                    3.51e-05
181.00
34.00%
21.87%
3.83%
                                                                                                      Sequence 1916 BP;
                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
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                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                           Query Match:
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                                         ThrGlnAlaProProGluThrTrpGlnAspLeuProValAspPheValAsnGlyLysPro
                                                                                           776 GlyAspAsnAlaTyrGlySerAsnArgAlaHisGlnMetThrGlyGlyIleGlnAlaGly
                                                                                                                                                                                                                             TyrIleTrpSerAspAsnPheAsnHisValProTyrArgLeuArgPhePheAlaGlyGly
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                                                                                                                                                                                                                                                                                                                                                                              snAspThrLysIleGlyAlaGlyValGlyValArgTrpAlaSerProValGlyGlnValA
                                                                              718 SerGlnGluAlaLeuLeu-----AlaGlyValAlaValHisLysThrValAlaAspAsn
                                                                                                                   LeuValAsnProMetArgGlyTyrArgGlnArgTyrSerLeuGluValGlySerSerGly
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                                                                                                                                                                                                            1273 TACGATCGC------CATCGTTTTGTTACACGCGGCACGCTGGGC
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                       1021 GATCTCTCCAGCGGCGTGCCATTAACCTGCGCTGGAGTCTCGAC-----
                                                                                                                                                                                                                                                                                                                                           855 ysAspLeuArgLeuAlaValPheGlyAspIleGlyAsnAlaTyrAspLysGlyPheThrA
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Outer membrane protein (OMP) D15 genes were isolated by screening chromosomal libraries of H. influenzae type b (Hib) strains Ca. Eagan and Minn A, and the non-typeable (NTHI) strains SB13 and PAK 12085. Nucleotide sequences were determined for the D15 genes (AAQ66198-202) and the corresponding as sequences were derived (ARRS1784-89). D15 OMP can be produced easily and on a large scale, free of other antigens and lipooligosaccharides, by recombinant DNA methods using the isolated genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179 LysValProArgLeuLysAlaLysPheTyrGlnSerSerGlnSerGlyGluThrSerAla 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          219 IleThrGlnGluSerAlaMetAspLeuAsnGlySerIleProArgLeuArgGlnThrAla 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        259 Ile-----GlyGluVal---AspValIleIleHisAspLeuGlyGluProValTyrIle 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         239 LeuValAlaAlaArgAlaValGlyTyrTyrAspIleAspLeuSerlleIleArgAsnSer
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Best Local Similarity:
Query Match:
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Search completed: May 6, 2003, 01:20:46 Job time : 949 secs

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Perfect score: Scoring table:

Sequence:

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Run on:

Total number Minimum DB & Maximum DB &

Searched:

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Sequence 126, Appl
Sequence 2, Appli
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Sequence 1, Appli
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Sequence 243, Appli
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Sequence 102, Appli
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APPLICANT: CHONG, Pele
APPLICANT: THOMS, Wayne
APPLICANT: THOMS, Wayne
APPLICANT: LOOSMORE, Sheena
APPLICANT: LOOSMORE, Sheena
APPLICANT: SIA, Dwo Yuan Charles
APPLICANT: KLEIN, Michel
TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 55
CORRESPONDENCES: 51m & MCBURNESS:
ADDRESSEE: Sim & MCBURNES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,522A
FILING DATE: 12-SEP-1995
CLASSIFICATION: 435
US-08-433-522A-3

US-08-135-166-3

US-08-433-522A-55

US-08-135-166-55

US-09-135-166-55

US-09-135-166-55

US-07-689-008-1

US-07-689-008-1

US-08-61-527-126

US-08-61-527-126

US-08-621-944A-2

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STREET: 6TH Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
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ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-434 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
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     RESULT 1
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-MODEL-framet-p2n.model -DEV-x1h
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-MODEL-framet-p2n.model -DEV-x1h
-MODEL-framet-p2n.model -DEV-x1h
-DE-ISSUG_PAPPO_SPOOL/US09914168/runat_28042003_151615_6807/app_query.fasta_1.1095
-DB-ISSUG_PATENTS_NA -QENT"-fastap -SUFFIX=n1 -MINNATCH=0.1 -LOOPCU=0
-LOOPEXT=0 -UNITS=blts -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cd1
-LIST=45 -DOCALIGN-200 -THR_SCORE=pct -THR_MAX=100 -THR_NIN-0 -ALIGNS=40
-USRE-US09914168_@CGN_1_1.32_@runat_28042003_151615_6807 -NCPU=6 -ICPU=3
-NO_ALDXY -NO_MANP -LARGEDGRRY -NGS_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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1 MSKPVLFANRSFMPVALAAY ......TGVKEEGNPIKLHFFIGTPF 919
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                             GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                               nucleic search, using frame_plus_p2n model
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US-09-135-166-1
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0 , Xgapext 0
Ygapop 10.0 , Ygapext 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -------AsnLeuGlnAlaValArgAlaLeuSerAsnAspLeuIleAlaThrArg
                                                                                                                                                                                                                                                                                                                                                        LysValProArgLeuLysAlaLysPheTyrGlnSerSerGlnSerGlyGluThrSerAla
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                           Gaps:
           SEQUENCE CHARACTERISTICS:
LENGTH: 2989 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOCY: linear
MOLECULE TYPE: DNA (genomic)
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INFORMATION FOR SEQ ID NO:
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Best Local Similarity:
Query Match:
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US-08-433-522A-9
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1592 2069 1412 GTTACTTTAGGTTTCCCTGTAAATGAAATAACTCCTATTATGTAGGATTAGGCCATACC 1979 1184 ------GAACGTAACACGGGTAGTATCAACTTTGGTATTGGTTACGGT 1679 ACAGAGAGTGGTATCAGTTATCAAACAAGTATTAAACAAGATAATTTCTTGGGAACAGGG 1739 1740 GCGGCAGTAAGTATAGCTGGTACGAAAATGATTATGGTACGAGTGTCAATTTGGGTTAT 1799 1860 TACGATAACTCTAAAAGTGATACATCCTCTAACTATAAGCGTACGACTTATGGAAGTAAT 1919 TATAATAAAATTAGTAACTTTGCTCTAGAA------TATAACCGTAATTTATATT 2030 1413 CGACGTTTAACTGTTCGCCAACTTCGCTTTGAAGGAAATACCGTTTCTGCTGATAGTACT 1472 1593 ATCAATGGTAGCAATGATGAAGTGGATGTCGTATATAAAGTCAAA-------1637 1065 TATTTAAATAATGGCTATGCCAAAGCACAAATCACTAAAACGGATGTTCAGCTAAATGAT 1124 1185 AGTGCACGCATTATAGGTAATCTGGGAGGTATGTCTGCCGGGCTTGAACCTTTACTTTCA 1244 484 550 608 SerGlu------AspLysClyValLysLeuTyrAlaThrLysProLeuSerHis 638 ---ThrasnGlyPheaspLeuSerThrargThr-------LeuGluHis--- 671 456 551 Pro------GluArgThr-----AlaLeuAlaAsnArgLysThrPro 562 TyrSerLeuArgTyrArgLeuAspLysLeuLysThrGlnAlaProProGluThrTrpGln 706 1533 GGAAAAATTCGCTTAGATCGTACAGGTTTCTTCGAAACAGTTGAAACCGAATTGATCCT SerAspThrGlyThrArgLeuValThrLysPhe---GluHisAsnLeuIle-----TyrPheAsnMetValAsnThrGluIleValPheProGluArgGluGlnIleGlnAsnAsp 466 ThrvalGluLeuThrAspGlyIle---LeuMetAspIleSerProIleGluPheSerAla 1353 GTACCTGATTTTGACGATGCAAATAAAACATTAGCGATAACCTTTGTTGATGCTGGA ArgSerIleLeu--------GlyArgIleSerAspAlaValSerAla ProLeuAsnAspGlnLeuArgAlaThrLeuGlyTyrGlnGlnGluValPheGlyHisSer GlnValSerPheGluGlnSerSerSerArgThrGluProAlaGlnValAsp-----1125 GAAAAAACAAAAGTTAATGTAACCATTGATGTAAATGAAGGTTTACAGTATGACCTTCGT ------GluSerThrLeuGluProValIleGlu SerAsnLeulleGlnAspLysLeuAsnLeuValAlaAlaLysAlaArgHisLeuTyrAsp 505 MetProAsp-----AspArgValLeuAlaIleAsnHisAspAspGlyValAsn 534 ValAlaArgAlaIleLeuProAspGluSer-----GluAsnGluValIleAspLeu 575 ValPheValAlaSerAspLysProArgAspGlyGlnIle-----GlyLeuGlyTrpGly -----AsnArgAspGlyTyrGlnAlaGlyAlaGluLeuArgLeu -----GluileSerArgSerIleIleGlnAsnGlyGlyTrpAsnArgThr-----1245 GCATTACATTAAATGATACTTTCCGCCGTAGTGATATTGCAGATGTAGAA-----2031 CAATCAATGAAATTTAAAGGTAATGGCATTAAAACAAAT-----1920 419 485 521 1680 439 1638 593 609 622 639 629 672 687 457 Db a ò q δy QQ δ g Db δy g OD δ q δ g g QQ Ωp Op δ g ŏ ŏ ò δ ò g ò q ò à δ οχ ò

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2130 AAAGGGGTTAAAAGCAAGTCTTGGTGGACGAGTTACTATTCCAGGTTCTGATAACAAATAC 2189
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2229 GACAGAGATCACCGCTGGGTTGTATCTGCAAAAGCATCTGCAGGATATGCAAATGGTTTT 2288
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AspLeuProValAspPheValAsnGlyLysProSerGlnGluAlaLeuLeuAlaGlyVal 726
                                                                                                                                                                                                                                                                                                                                                                                            GlyTyrAlaHisAspSerLeuSerPro-----IleSerAspLysGlyTyrLeuThr 837
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                                                             727 AlaValHisLysThrValAlaAspAsnLeuValAsnProMetArgGlyTyrArgGlnArg
                                                                                                                                                                                                                                                            AsnArgAlaHisGln-----MetThrGlyGlyIleGlnAlaGlyTyrIleTrpSerAsp
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                                                                                                                                -SerAspAlaAsnMet
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APPLICANT: CHONG, Pele
APPLICANT: THOMAS, Wayne
APPLICANT: YANG, Yan Ping
APPLICANT: YANG, Yan Ping
APPLICANT: SIA, Dwo Yuan Charles
APPLICANT: KLEIN, Michel
TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
NUMBER OF SQUENCES: 55
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Sim & McBurney
STREET: 6TH Floor, 330 University Avenue
                                                                                                                             747 TyrSerLeuGluValGlySerSerGlyLeuVal
                                --GACTTTGATTTTCTTTTGGTTGG-
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Patent No. 6083743
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COMPUTER READABLE FORM:
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179 LysValProArgLeuLysAlaLysPheTyrGlnSerSerGlnSerGlyGluThrSerAla 198
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172
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                                                                       Version #1.25
                                                                                                                                       FILING DATE:
CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/433,522
FILING DATE: 12-SEP-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/OCKET NUMBER: 1038-829 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPRAX: (416) 595-1155
TELEFAX: (416) 595-1153
TELEFAX: (416) 595-1153
TELEFAX: (416) 595-1153
TELEFAX: (416) 595-1163
SEQUENCE CHARACTERISTICS:
LENGTH: 299-base pairs
TYPE: nucleic acid
TYPE: nucleic acid
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Mismatches:
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Matches:
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MEDIUM TYPE: Floppy disk Computer: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                US/09/135,166
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181.00
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APPLICATION NUMBER: US
FILING DATE:
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION:
US-09-135-166-9
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2709 ATTABABABATGAABATGATGATGAACAGTTCCAATTTAGTATTGGGGGCTCTTTC 2768 2408 2468 CITATIGIACCAACTCCATITIGIGAGIGATAAAAGCCAAAATACAGICCGAACCTCCCTA 2528 2529 TITGTIGATGCGGCAAGTGTITGGAATACTAAATGGAAATCAGATAAAAATGGATTAGAG 2588 2289 GGAAACAAGCGTTTACCGTTCTATCAAACTTATACAGCGGGGGGTGGCATTGGTTCATTACGC 2348 ------AACTATAACAGCCTTAATAGAGGCTATTCCCAACT 2129 2130 AAAGGGGTTAAAGCAAGTCTTGGTGGACGAGTTACTATTCCAGGTTCTGATAACAAATAC 2189 :::||||||| 1980 TATAATAAATTAGTAACTTTGCTCTAGAA------TATAACCGTAATTATATATT 2030 GlyValGlyValArgTrpAlaSerProValGlyGlnValArgValAspVaLAlaThrGly 901 1860 TACGATAACTCTAAAAGTGATACATCCTCTAACTATAAGCGTACGACTTATGGAAGTAAT 1919 1920 GTTACTTTAGGTTTCCCTGTAAATGAAAATAACTCCTATTATGTAGGATTAGGCCATACC 1979 727 AlaValHisLysThrValAlaAspAsnLeuValAsnProMetArgGlyTyrArgGlnArg 746 763 AlaileAlaArgAlaGlyIleSerGlyValTyrSerPheGlyAspAsnAlaTyrGlySer 782 AsnargalaHisGln-----MetThrGlyGlyIleGlnAlaGlyTyrIleTrpSerAsp 800 837 :::||| 1800 ACCGAACCCTATTTTACTAAAGATGGTGTAAGTCTTGGTGGAAATATTTTCTTTGAAAAC 1859 TyrserLeuArgTyrArgLeuAspLysLeuLysThrGlnAlaProProGluThrTrpGln 706 AspLeuProValAspPheValAsnGlyLysProSerGlnGluAlaLeuLeuAlaGlyVal 726 PheGlyAspIleGlyAsnAlaTyr----------AspLysGlyPheThrAsnAspThrLys1leGlyAla 2589 AGCAAGGICITGAAAGACITACCIGATTATGGCAAATCAAGCCGTATTCGCGCCTCTACA 2649 GGTGTCGGATTCCAATGCCAATCTCCTATTGGACCATTGGTATTTTCTTATGCTAAACCA ValLys-----GluGluGlyAsnProlleLysLeuHisPhePheIleGlyThrProPhe -------GlyGlyGlnValLeuAlaValGlyThrAlaGlu -----TyrAsnTyrGluPheMetLysAsp------LeuArgLeuAlaVal --SerAspAlaAsnMet AsnPheAsnHisValProTyrArgLeuArgPhePheAlaGlyGlyAspClnSerlLeArg GlyTyrAlaHisAspSerLeuSerPro-----IleSerAspLysGlyTyrLeuThr ProLeuAsnAspGlnLeuArgAlaThrLeuGlyTyrGlnGlnGluValPheGlyHisSer -----GluileSerArgSerIlelleGlnAsnGlyGlyTrpAsnArgThr -----LeuGluHis---2190 TACAAACTAAGTGCAGATGTACAGGGTTTCTACCATTA----------GACTTTGATTTTTCTTTTGGTTGG--------ThrAsnGlyPheAspLeuSerThrArgThr---747 TyrSerLeuGluValGlySerSerGlyLeuVal--902 801 2349 2469 862 2070 2094 639 672 687 qq a ò QQ QQ qq ŏ g QΩ οy qq Qγ ò ŏ δλ q q ŏ q οy ò QQ g οy q ò Dp δ Ω QQ δ ò ò

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US-08-942-046-9

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969 CAAATGGAATTACAACCTGATTCTTGGTGGAAATTATGGGGAAATAAAATTTGAAGGTGCG 1028
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  582 TICGTAAGTGGTCGATTCGATGATGTGAAAGCGCATCAAGAAGGCGATGTGGTTGTTGTT 641
                                                                                                                                  276 AspTyrArgAla-----Asp 288
                                                                                                                                                             289 AspLysAlaPheThrThrValAlaAspGluValProLeuLeuIleGlyAspValPheHis 308
                                                                                                                                                                                                                                      :::||||||||||||| actgaagcataaacttagatgctaacggtttaaagttggcgatgttta--- 758
                                                                                                                                                                                                                                                                                         309 HisGlyLysTyrGluThrLysLysAsnLeuIleGluAsnAlaSerAlaGluHisGlyTyr 328
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                                                                                                                                                                                                                                                                                                                                  -----ATTCGAGAAAATTAAATGGATTTGCCAAAAGTGTAAAAGGGCACTATGCA
                                                         Ile-----GlyGluVal---AspValIleIleHisAspLeuGlyGluProValTyrIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           386 LysArgGluLeuLeuGluGlnLeuLeuThrValAsnMetGlyGluAlaTyr----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IleThrGlnGluSerAlaMetAspLeuAsnGlySerIleProArgLeuArgGlnThrAla 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  239 LeuValAlaAlaArgAlaValGlyTyrTyrAspIleAspLeuSerIleIleArgAsnSer 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            179 LysValProArgLeuLysAlaLysPheTyrGlnSerSlnSerGlyGluThrSerAla 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  378 AGGATACAATCGATGAAAAACTTCTAATCGCAAGTTTATTATTCGGTGCGACAACGACT 437
                                                                       APPLICANT: THOMAS, Wayne
APPLICANT: YANG, Yan Ping
APPLICANT: YANG, Yan Ping
APPLICANT: LOOSNORE, Sheena
APPLICANT: LAD DWO Yuan Charles
APPLICANT: KLEIN, Michel
TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2989
172
141
345
222
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                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/942,046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALIONALIZATION INFORMATION:
NAME: STEWART, Michael I.
REGISTRATION NUMBER: 24,973
REFERNEC/COCKET NUMBER: 1038-732 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1163
TELEPHONE: (416) 595-1163
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2999 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-914-168-2 (1-919) x US-08-942-046-9 (1-2989)
                                                                                                                                                                                                 STATE: Onterio
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                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/433,522
APPLICATION NUMBER: 12-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
Sequence 9, Application US/08942046
                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.11e-09
181.00
35.57%
19.55%
3.83%
                                                       CHONG, Pele
THOMAS, Wayne
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390..2768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                           Ontario
: Canada
                  atent No. 6264954
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                              M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-942-046-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              483
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qq	1533 GGAAAAATTCGCTTAGATCGTACAGGTTTCTTCGAAACAGTTGAAAACCGAATTGATCCT 1592	
Qy	563 AlaAsp	Qy 862 PheGlyAspIleGlyAsnAlaTyr
qq	::: 1593 ATCAATGGTAGCAATGATGAAGTGGATGTCGTATATAAAGTCAAA	Db 2529 TTTGTTGATGCGGCAAGTGTTTGGAATACTAA
Οy	575 ValPheValAlaSerAspLysProArgAspGlyGlnIleGlyLeuGlyTrpGly 592	870
q	1638GAACGTAACACGGTAGTATACAACTTTGGTATTGGTTACGT 1679	
δ	593 SerAspThrGlyThrArgLeuValThrLysPheGluHisAsnLeulle 608	Oy 882 GlyValGlyValArgTrpAlaSerProValGly
QQ	1680 ACAGAGAGTGGTATCAGTTATCAAAGTATTAAACAAGATATTTCTTGGGAACAGG 1739	40 0
Οy	609	CY 902 VAILYSGIUGIUGIYASHYIOITELY 
q	1740 GCGGCAGTAAGTAGCTGGTACGAAAATGATTATGGTACGAGTGTCAATTTGGGTTAT 1799	10000000000000000000000000000000000000
οy	622 SerGluAspLysLysGlyValLysLeuTyrAlaThrLysProLeuSerHis 638	US-08-13- US-08-33-522A-7
qq	1800 ACCGAACCCTATTTACTAAAGATGGTGTAAGTCTTGGTGGAAATATTTTCTTTGAAAAC 1859	; Patent No. 6013514
Οŷ	639 ProLeuAsnAspGlnLeuArgAlaThrLeuGlyTyrGlnGlnGluValPheGlyHisSer 658	APPLICANT CHONG
qq	1860 TACGATAACTCTAAAAGTGATACATCCTCTAACTATAAGCGTACGACTTATGGAAGTAAT 1919	APPLICANI: INONAS, WAYINE  APPLICANI: YANG, Yan Ping
Qy	659ThrAsnGlyPheAspLeuSerThrArgThr	APPLICANT: DOCSMORE, SHeens
qa	1920 GTTACTTTAGGTTTCCCTGTAAATGAAATAACTCCTATTATGTAGGATTAGGCCATACC 1979	; TITLE OF INVENTION: HAEMOPHILUS OUTE
Qy	snGlyGlyTr	CORRESPONDENCE ADDRESS:
q	1980 TATAATAAATTAGTAACTITGCTCTAGAATATAACGTAATTATATATT 2030	; ADDRESSEE: Sim & McBurney ; STREET: 6TH Floor, 330 University A
Qy	687 TyrSerLeuArgTyrArgLeuAspLysLeuLysThrGlnAlaProProGluThrTrpGln 706	; CITY: Toronto ; STATE: Ontario
q	2031 CAATCAATGAAATTTAAAGGTAATGGCATTAAAACAAAT	; COUNTRY: Canada ; ZIP: M5G 1R7
Qy	707 AspLeuProValAspPheValAsnGlyLySProSerGlnGluAlaLeuLeuAlaGlyVal 726	PE 9
qq	2070GACTTTGATTTTTTTTGGTTGG	IBM PC compatible SYSTEM: PC-DOS/MS-DOS
Qy	727 AlaValHisLysThrValAlaAspAsnLeuValAsnProMetArgGlyTyrArgGlnArg 746	; SOFTWARE: Patentin Release #1.0, Vortice #
QQ	2094AACTATAACAGCCTTAATAGAGGCTATTCCCAACT 2129	E 0
Qy	747 TyrSerLeuGluValGlySerSerGlyLeuValSerAspAlaAsnMet 762	CLASSIFICATION: 435 ATTORNEY AGENT INFORMATION:
qq	2130 AAAGGGGTTAAAGCAAGTCTTGGTGGACGAGTTACTATTCCAGGTTCTGATAACAAATAC 2189	
٥y	763 AlaileAlaArgAlaGlyileSerGlyValTyrSerPheGlyAspAsnAlaTyrGlySer 782	TELECOMMULCATION INFORMATION:
qa	2190 TACAAACTAAGTGCAGATGTACAGGGTTTCTACCCATTA	; TELEPHONE: (416) 595-1155 ; TELEFAX: (416) 595-1163
Qy	783 AsnArgAlaHisGlnMetThrGlyGlyIleGlnAlaGlyTyrIleTrpSerAsp 800	SEQUENCE CHARACTERS 17:
qa	2229 GACAGAGATCACCGCTGGGTTGTATCTGCAAAAGCATCTGCAGGATATGCAAATGGTTTT 2288	ucleic
Qy	801 AsnPheAsnHisValProTyrArgLeuArgPhePheAlaGlyGlyAspGlnSerIleArg 820	=
QQ	2289 GGAAACAAGCGTTTACCGTTCTATCAAACTTATACAGCGGGGGGGG	<del>γ</del>
οy	821 GLyTyrAlaHisAspSerLeuSerProIleSerAspLysGlyTyrLeuThr 837	; NAME/KEY: CDS ; LOCATION: 3862761
qq	2349 GGTTTTGCTTATGGTAGTATTGGCCCTAATGCAATTTATGCCGAACATGGTAATGGTACT 2408	US-US-433-522A-1
Οy	838	ent scores: No.:
<b>Q</b> -	2409 TTTAATAAGATAAGTTCTGATGTGATTGGTGTAATGCAATCACAACTGCGAGTGCGAGA 2468	
δ	849TyrasnTyrGluDheMetLysAspLeuArgLeuAlaVal 861	3.788 3.788
a ,	2469 CTTATTGTACCAACTCCATTTGTGAGTGATAAAGCCAAAATACAGTCCGAACCTCCCTA 2528	

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SLYPheThrAsnAspThrLyslleGlyAla 881
||| ::::::
|GCAAATCAAGCCGTATTCGCGCCTCTACA 2648
                                                                                  SLYGLOVALAEGVALASPVALALATHEGLY 901
||| ::: || || || SGACCATEGETTTECTTATGCTAAACCA 2708
AAATGGAAATCAGATAAAAATGGATTAGAG 2588
                                                                                                                                         ER MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length: 2974
Matches: 173
Conservative: 138
Mismatches: 345
Indels: 225
Gaps: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                       Avenue
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50-SD	9-914-	-168-2 (1-919) x US-08-433-522A-7 (1-2974)	
ογ	179	LysValProArgLeuLysAlaLysPheTyrGlnSerGlnSerGlyGluThrSerAla 198	
QQ	374	AGGATACAATCGAAGAAAACTTCTAATCGCAAGTTTATTATTCGGTACGACAACGACT 433	
λοί	199	LysThrGluProTyrAlaAsnileLysAlaAlaLeuGluAsp 21	
Q C	4 34	GTGTTTGCCGCA	
, da	219	IleThrGlnGluSerAlaMetAspLeuAsnGlySerIleProArgLeuArgGlnThrAla 238 :::	
> 0	239		
; 셤	521	ı ıc	
δy	259	IleGlyGluValAspValIleIleHisAspLeuGlyGluProValTyrIle 275	
g G	578	TICGIAAGIGGICGAITCGAIGAIGIGAAGCGCATCAAGAGGCGAIGIGCII ::: ::: ::: ::: ::: ::: ::: ::: :::	
οy	276	AspTyrargAlaAlaasp 288	
QQ	638	AGCGTTGTGGCTAAATCGATCATTCAGATGTTAAAATCAAAGGTAACTCTATTATTCCA 697	
οy	289	AspLysAlaPheThrThrValAlaAspGluValProLeuLeuIleGlyAspValPheHis 3 :::      :::	
a	869		
οy	309	HisGlyLysTyrGluThrLysLysAsnLeuIleGluAsnAlaSerAlaGluHisGlyTyr 328	
q	755	ATTCGAGAAAATTAAATTTGCCCAAAGTGTAAAAGAGCACTATGCA 805	
λa	329	PheAspGlyArgTrpLeuAspArgSerValAspVallleLeuProAspAsn 345	
а	908	AGTGTAGGTCGCTATAACGCAACCGTTGAACCTATTGTCAATACGCTACCAAATAAT 862	
ρλ	346	ThrAlaAspValSerLeuIleTyrAspThrGlyThrGlnTyrArgPheAspGluValVal 365	
qq	863	CGCGCTGAAATTTTAATTCAAATCAATGAAGATGATAAAGCCAAATTGGCATCATTAACT 922	
δλ	366	PhePheThrIleAspProLysThrAsnGlnLeuThrThrAspProAspLysLeuProVal 385	
qq	923	TICAAGGGGAACGAATCTGTTAGTAGCAGTACATACAAGAA 964	
οy	386	LysArgGluLeuLeuGluGlnLeuLeuThrValAsnMetGlyGluAlaTyr 402	
qq	965	::: CAAATGGAATTACAACCTGATTCTTGGTGGAAATTATGGGGAAATAAAT	
δλ	403		
qq	1025		
οy	419	TyrPheAsnMetValAsnThrGluIleValPheProGluArgGluGlnIleGlnAsnAsp 438	
qq	1061	TATTTAAATAGGCTATGCCAAAGCACAAATCACTAAAGCGGATGTTCAGCTAAATGAT 1120	
οy	439	GlnValSerPheGluGlnSerSerSerSrgThrGluProAlaGlnValAsp 456	
g	1121	GAAAAAACAAAAGITAATGIAACCATTGATGIAAATGAAGGTTTACAGTATGACCTTCGT 1180	
οy	457	GluSerThrLeuGluProValIleGlu 465	
qq	1181	AGTGCACGCATTATAGGTAATCTGGGAGGTATGTCTGCCGAGCTTGAACCTTTACTTTCA 1240	
٥y	466	ThrvalGluLeuThrAspGlyIleLeuMetAspIleSerProIleGluPheSerAla 484	•
q	1241		
٥y	485	SerAsnLeuIleGlnAspLysLeuAsnLeuValAlaAlaLysAlaArgHisLeuTyrAsp 504	
QQ	1292	AATGCAATTAAAGCAAAAGTTGGGGAACGAGGTTACGGTAACACAACAGTAAATTCT 1348	

505	MetProAspAspArgValLeuAlaIleAsnHisAspAspGlyVal :::       GTACCTGATTTTGACGATGCAAATAAAACATTAGCGATAACCTTTGTTGTTGATGCT	520 1408
	ArgSerIleLeu	533 1468
	ValalaargalaileLeuProAspGluSerGluAsnGluValIleAspLeu ::: :::::::::::::::::::::::::::::::::	550 1528
	ProGluargThrAlaLeuAlaAsnArgLySThrPro	562 1588
	ValTyrGinSerLysLysValPr         : 	574
ın •	ValPheValAlaSerAspLysProArgAspGlyGlnIleGlyLeuGly	92
<del>ه</del> ۳	GAACGIAACACGGGTAGIAICAACTITGGTATTGGTTATCGG SerAspThrClyThrArgLeuValThrLyspheGluHisAsnLeuIle	608
9	::::     ::: ACAGAGAGTGGTATTAGTTATCAAGCAAGTGTCAAACAAGATAATTTCTTGGGAA	1735
ത ശ	GCGGCAGTAAGTATGCAAAAAGGATATAGGTACAAAATGGTAATAAGGTATTAGGTAATAAAAAGGATAAAAAA	621
OI V	SerGluAspLysLySGlyValLysLeuTyrAlaThrLysPr  :::     ACCGGCCTAATTTTAACTAAAGATGGGGGAAAGTTTTTTTT	638
6	ProLeuAsnAspGlnLeuArgAlaThrLeuGlyTyrGlnGlnGluValPheGlyHisSe	ထ
LO.	:::   TACGATAACTCTAAAACTGATACATCCTCTAACT	1915
6	ThrAsnGlyPheAspLeuSerThrArgThrLeuGluHis	71
9 0	GTTACTTTAGGTTTCCCCTGTAAATGAAAATAACTCCTATTATGTAGGATTAGGCCA	Ġ G
9 9	GLULLESGEARGSGETIGLIGGIASNGLYGIPYEPSGEAGTOF :::	2026
<b>~</b> 1	TyrSerLeuargTyrArgLeuaspLysLeuLysThrGlnAlaProProGluThrTrpGli	10
- (	CANTCAATGAAATTTAAAGGTAATGGCATTAAAACAAAT	Ō
- 9	AspLeuProValAspPheValAsn61yLysProSerGinGluAlaLeuLeuAlaG1yVal 	726 2089
_	AlaValHisLysThrValAlaAspAsnLeuValAsnProMetArgGlyT	746
0	 	2125
7	TyrSerLeuGluValGlySerSerGlyLeuValS	762
S	AAAGGGGTTAAAAGCAAGTCTTGGTGGACGAGTTACAATTCCAGGTTCTG	2185
c	AlaIleAlaArgA	782
SO.	TACAAACTAAGTGCAGATGTACAGGGTTTCTA	2224
	AsnArgAlaHisGlnMetThrGlyGlyIleGlnAlaGlyTyrIleTrpSerAsp	800
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                                                                                                                                                                                                                                                                          2459 GAGTTAATTGTGCCAACTCCATTTGTGAGTGATAAGAGTCAAAATACAGTCCGAACCTCC 2518
                                                                                                                                                                                                                                                                                                                                           2699 CCAATTAAAAAATATGAAAATGATGATGATGAGAACAGTTCCAATTTAGTATTGGGGGTTCT 2758
                                                                                                                                                         847
801 AsnPheAsnHisValProTyrArgLeuArgPhePheAlaGlyGlyAspGlnSerIleArg
                                                                                                  |||:::|||:::|||2345 GGTTTGGTAGCATTGGGGCCTAACGCAATTTATCAAGGTCAAAATAATAATTT
                                                                                                                                                                                                2405 AATAAGATAAGTTCTGAT-----GTGATTGGTGGTAATGCAATCGCTACAGCTAGCGCA
                                                                                                                                                                                                                                     Glu-----TyrAsnTyrGluPheMetLysAsp------LeuArgLeuAla
                                                                                                                                                                                                                                                                                                                                                                                              .------AspLysGlyPheThrAsnAspThrLysIleGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    881 AlaGlyValGlyValArgTrpAlaSerProValGlyGlnValArgValAspValAlaThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  901 GlyValLys-----GluGluGlyAsnProIleLysLeuHisPhePheIleGlyThrPro
                                    2285 GGAAACAAGCGTTTACCGTTCTATCAAACTTATACAGCGGGTGGCATTGGTTCATTACGC
                                                                                                                                                         830 -----IleSerAspLysGlyTyrLeuThrGlyGlyGlnValLeuAlaValGlyThrAla
                                                                                                                                                                                                                                                                                                                                                                                                                                 2579 GAGAGCAATGTCTTGAAAGACTTACCCGATTATGGCAAATCAAGCCGTACTCGCGCCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/09135166
Patent No. 6083743
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CHOMAS, Wayne
APPLICANT: THOMAS, Wayne
APPLICANT: LOCSMORE, Sheena
APPLICANT: LOCSMORE, Sheena
APPLICANT: KLEIN, Michel
TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                 861 ValPheGlyAspIleGlyAsnAlaTyr-------
                                                                           GlyTyrAlaHisAspSerLeuSerPro---------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CALLCATION NUMBER: US/09/135,166
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Sim & McBurney
STREET: 6TH Floor, 330 University Avenue
STATE: Toronto
STATE: Ontario
COUNTRY: Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: STEWARY, Michael 1
REGISTRATION NUMBER: 24,913
REFERENCE/DOCKET NUMBER: 1038-829 MIS:jb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/4
FILING DATE: 12-SEP-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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M5G 1R7
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                                                                                                                                                                                                                                                                                                                                                                                            870 -----
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2759 TTC 2761
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US-09-135-166-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  259 Ile-----GlyGluVal---AspValIleIleHisAspLeuGlyGluProValTyrIle 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 276 AspTyrArgAla------AlaAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     309 HisGlyLysTyrGluThrLysLysAsnLeuIleGluAsnAlaSerAlaGluHisGlyTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PhePheThrIleAspProLysThrAsnGlnLeuThrThrAspProAspLysLeuProVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 374 AGGATACAATCGATGAAAAACTTCTAATCGCAAGTTTATTATTCGGTACGACAACGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IleThrGlnGluSerAlaMetAspLeuAsnGlySerIleProArgLeuArgGlnThrAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                239 LeuValAlaAlaArgAlaValGlyTyrTyrAspIleAspLeuSerIleIleArgAsnSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 521 GTTCGTGCCGGTCAGCGTGTGACTGACAATGATGTG----GCTAATATTGTCCGCTCTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         578 TTCGTAAGTGGTCGATTCGATGATGTGAAAGCGCATCAAGAAGCCGATGTGCTTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             638 AGCGTTGTGGCTAAATCGATCATTTCAGATGTTAAAATCAAAGGTAACTCTATTATTCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----ATTCGAGAAAATTAAATGAATTTGCCCAAAGTGTAAAAGAGCACTATGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             329 PheAspGlyArgTrpLeuAspArgSerValAspValIle------LeuProAspAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              806 AGTGTAGGTCGCTAT---AACGCAACCGTTGAACCTATTGTCAATACGCTACCAAATAAT
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GTTCAAGGTGACTTAGAACAACAATCCGAGCAAGTTTACCT---------
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173
138
345
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-914-168-2 (1-919) x US-09-135-166-7 (1-2974)
                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
TELECOMMUNICATION INFORMATION:
                  TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2974 base pairs
                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                               178.50
35.30%
19.64%
3.78%
                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                         CDS
386..2761
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                    ; NAME/KEY:
; LOCATION:
US-09-135-166-7
                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                               FEATURE
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CAATTCGA		
TyrPheAs      ATTTAA	TyrPheAsnMetValAsnThrGluIleValPheProGluArgGluGlnIleGlnAsnAsp 438 	
GlnvalSe ::: GAAAAAAC	GInValSerPheGluGlnSerSerSerArgThrGluProAlaGlnValAsp 456 :::	
AGTGCAC	GluserThrLeuGluProVallleGlu 465 ::	
ThrvalG ::: GCATTAC	ThrValGluLeuThraspGlyIleLeuMetaspIleSerProIleGluPheSerala 484 :::              GCATTACATTTCCGCCGTAGTGTATTTCCAGATGTAGAA 1291	
SerAsnI     AATC	SerAsnLeulleGlnAspLysLeuAsnLeuValAlaAlaLysAlaArgHisLeuTyrAsp 504                    - AATGCAATTAAAGCAAAACTTGGGGAACGAGGTTACGGTAACACAACAGTAAATTCT 1348	<del>-</del>
MetPro :::    GTACCT	MetProAsp      AspArgValLeuAlaIleAsnHisAspAspGlyValAsn       520         :::             ::::::                           GTACCTGATTTTGACGATGCAATAACATTAGCGATAACCTTTGTTGTTGTTGTTGTTGTGTGA       1408	
ArgSer      CGACGT	ArgSerIleLeu	
valAla ::: TTACGT	ValalaargalaileLeuproaspGluSerGluasnGluValileaspLeu 550 ::: :::::::::    TTACGTCAGGAAATGCGCCAACAAGGAACTTGGTATAATTCACAATTAGTTGATTA 1528	
Pro	ProGluArgThrAlaLeuAlaAsnArgLysThrPro 562	
AlaAsp ::: ATCAATGG	AlaaspValTyrGlnSerLysLysValProLeuTyr 574 :::	
valPhe	ValPheValAlaSerAspLysProArgAspGlyGlnIleGlyLeuGlyTrpGly 592 :::	
SerAsp :::::: ACAGAG	SerAspThrGlyThrArgLeuValThrLysPheGluHisAsnLeuIle 608 :::::    ::: ACAGAGAGTGGTATTAGTTATCAAGCAAGTGTCAAACAAGATAATTCTTGGGAACAGG 1735	
20000		
SerGl:::!!	SerGluAspLysGlyValLysLeuTyrAlaThrLysProLeuSerHis 638 :::	
ProLeu TACGAT	ProLeuAsnAspGlnLeuArgAlaThrLeuGlyTyrGlnGlnValPheGlyHisSer 658     ::: :::   ::: TACGATAACTCTAAAAGTGATACTCTCTAAAACGTATAAGCGTACGACTTATGGAAGTAAT 1915	
Thr       STTACT	ThrasnGlyPheaspLeuSerThrargThrLeuGluHis 671	
TATAAT	GlulleSerArgSerIlelleGlnasnGlyGlyTrpAsnArgThr 686 	
TyrSerI	TyrSerLeuArgTyrArgLeuAspLysLeuLysThrGlnAlaProProGluThrTrpGln 706	

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2699 CCAATTAAAAAATGATGATGATGATGATGAAGATTCCAATTTAGTATTGGGGGTTCT 2758
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2126 AAAGGGGTTAAAGCAAGTCTTGGTGGACGAGTTACAATTCCAGGTTCTGATAACAAATAC 2185
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                                                                                                                                                                            727 AlaValHisLysThrValAlaAspAsnLeuValAsnProMetArgGlyTyrArgGlnArg 746
                                                                                                                                                                                                                                                                                  747 TyrSerLeuGluValGlySerSerGlyLeuVal------SerAspAlaAsnMet 762
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                                                                       707 AspLeuProValAspPheValAsnGlyLysProSerGlnGluAlaLeuLeuAlaGlyVal 726
                                                                                                                                                                                                                                                                                                                                                                                          763 AlaileAlaArgAlaGlyIleSerGlyValTyrSerPheGlyAspAsnAlaTyrGlySer 782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AsnArgAlaHis-----GlnMetThrGlyGlyIleGlnAlaGlyTyrIleTrpSerAsp 800
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APPLICANT: CHONG, Pele
APPLICANT: THOWAS, Wayne
APPLICANT: TANG, Yan Ping
APPLICANT: YANG, Yan Ping
APPLICANT: SIA, Dwo Yuan Charles
APPLICANT: KLEIN, Michel
TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
NUMBER OF SUGUENCES: 55
CORRESPONDENCE ADDRESS:
2027 CAATCAATGAAATTTAAAGGTAATGGCATTAAAAACAAAT
                                                                                                                           -----GACTTTGATTTTCTTTTGGTTGG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          374 AGGATACAATCGATGAAAAACTTCTAATCGCAAGTTTATTATTCGGTACGACAACGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                219 IleThrGlnGluSerAlaMetAspLeuAsnGlySerIleProArgLeuArgGlnThrAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGCGTTGTGGCTAAATCGATCATTTCAGATGTTAAAATCAAAGGTAACTCTATTATTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTTCAAGGTGACTTAGAACAAATCCGAGCAAGTTTACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2974
173
138
345
225
                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/942,046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-914-168-2 (1-919) x US-08-942-046-7 (1-2974)
ADDRESSEE: Sim & McBurney
STREET: 6TH Floor, 330 University Avenue
                                                                                                                                                                                                                                                                           1038-732 MIS: jb
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps:
                                                                                                                                                           FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/433,522
FILING DATE: 12-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                          ATJURENT NOUNT TO THE STEWART, MICHAEL I REGISTRATION NUMBER: 24,973
REPRENCE/DOCKER NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1163
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2974 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
                                                                                      Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178.50
35.30%
19.64%
3.78%
                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: CDS
; LOCATION: 386..2761
US-08-942-046-7
                                    E: Ontario
IRY: Canada
M5G 1R7
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           STREET: 6TH Flc
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
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Best Local Similarit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match:
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1061 TATTTAAATAATGGCTATGCCAAAGCACAAATCACTAAAGCGGATGTTCAGCTAAATGAT 1120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1409 CGACGTTTAACTGTTCACCAACTTCGCTTTGAAGGAAATACCGTTTCTGCTGATAGTACT 1468
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------ATTCGAGAAAATTAAATGAATTTGCCCAAAGTGTAAAAGAGCACTATGCA
                                                                                                                                                                                                                              TACGTCAGGAAATGCGCCAACAAGAAGGAACTTGGTATAATTCACAATTAGTTGAGTTA
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                                                                                                                                                                                              PheAspGlyArgTrpLeuAspArgSerValAspVal11e-----LeuProAspAsn
                                                                                                                                                                                                                                                                                                            346 ThralaaspvalSerLeuIleTyraspThrGlyThrGlnTyrargPheAspGluValVal
                                                                                                                                                                                                                                                                                                                                                           CGCGCTGAAATTTTAATTCAAATCAATGAAGATGATAAAGCCAAAATTGGCATCATTAACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1349 GTACCTGATTTTGACGATGCAAATAAAACATTAGCGATAACCTTTGTTGATGCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                534 ValAlaArgAlaIleLeuProAspGluSer-----GluAsnGluValIleAspLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pro-----GluArgThr-----AlaLeuAlaAsnArgLysThrPro
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g q	GCGGCAGTAAAGTAAGGTACGAAAAAATGATTATGGTACGAGTGTAATTTGGGTTAT	2699
Oy Db	622 SerGluAspLysGlyvalLysLeuTyrAlaThrLysProLeuSerHis 638 :::	OY 519 PNB 919 DD 2759 TTC 2761
Oy Db	639 ProLeuAsnAspGlnLeuArgAlaThrLeuGlyTyrGlnGlnGluValPheGlyHisSer 658     :: ::       :::   FacgataActcTaAaAgGGATACATCTCTATAAGGCGTACGACTTATGGAAGTAAT 1915	RESULT 7 US-08-433-522A-1 Sequence 1, Application US/08 Patent No. 6013514
QY Db	659ThrasnGlyPheaspLeuSerThrargThr	; CENERAL INFORMATION: ; APPLICANT: CHONG, Pele ; APPLICANT: THOMAS, Wayne ; APPLICANT: YANG, Yan Ping
Qy	672GluileSerargSerileIleGlnAsnGlyGlyTrpAsnArgThr 686 :::        1976 TATAATAAAATTAGTAACTTTGCTCTAGAATATAACCGTAATTTATATAT 2026	; APPLICANT: LOOSMORE, Sheei ; APPLICANT: SIA, Dwo Yuan ( ; APPLICANT: KLEIN, Michel ; TITLE OF INVENTION: HAEMOI
Oy . Db	687 TyrSerLeuhrgTyrArgLeuAspLysLeuLysThrGlnAlaProProGluThrTrpGln 706    ::::::::::::::::::::::::::::::::::	CORRESPONDENCES: 55 CORRESPONDENCE ADDRESS: ADDRESSEE: Sim & McBurn STREET: 6TH Floor, 330
Qy Dp	707 AspLeuProValAspPheValAsnGlyLysProSerGlnGluAlaLeuLeuAlaGlyVal 726         2066GACTTTGATTTTTCTTTTGGTTGG	; CITY: Toronto ; STATE: Ontario ; COUNTRY: Canada ; ZIP: MSG 1R7
Qy Db	ValasnProMetargGlyTyrargGlnArg                     AACAGCCTTAATAGAGGCTATTTCCCAACT	ER REAL JM TYPE JTER:
oy og	747 TyrSerLeuGluValGlySerSerGlyLeuValSerAspAlaAsnMet 762 	SOFTWARE: PatentIr CURRENT APPLICATION I APPLICATION NUMBER: FILING DATE: 12-SI
Qy Db	763 AlaileAlaArgAlaGlyIleSerGlyValTyrSerPheGlyAspAsnAlaTyrGlySer 782 	CLASSIFICATION ATTORNEY/AGENT I NAME: STEWART REGISTRATION N
Qy	783 ASNAYGAlaHisGINMEtThrGlyGlyIleGlnalaGlyTyrIleTrpSerAsp 800 	REFERENCE/DOCKET NUMBER: FELECOMMUNICATION INFORMAT FELEPHONE: (416) 595-1163 FELEFAX: (416) 595-1163
Qy Db	801 AsnPheAsnHisValProTyrArgLeuArgPhePheAlaGlyGlyAspGlnSerIleArg 820 :::	
Oy Db	821 GlytyralahisaspSerLeuSerPro	STRANDEDNES TOPOLOGY: MOLECULE TYPE FEATURE:
Qy Db	830IleSerAspLysGlyTyrLeuThrGlyGlyGlyGlnValLeuAlaValGlyThrAla 847 :::	; NAME/KEY: CDS ; LOCATION: 752465 US-08-433-522A-1
Qy Db	848 GluTyrAsnTyrGluPheMetLysAsp	Alignment Scores: 2.03e-00 Pred. No.: 2.03e-00 Score: 172.00 Percent Similarity: 35.21%
Oy Db	861 ValPheGlyAspIleGlyAsnalaTyr	larıty:
Oy Dp	870	US-09-914-168-2 (1-919) x US-08 QY 179 LysvalProArgLeuLysAla ::::: Db 63 AGGATACAATGGATGAAAAA
3 A	ntacijyaitajyaitatyiphiasetriovaidijainiaihigvaitainiii 	Qy 199 IleGlySerSerHisGlnLys

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/sThrGluProTyrAlaAsnIleLysAlaAlaLeuGluAsp 218
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GCACCTTTTGTGGCAAAGATATTCGTGGATGGT 167 GluSerAlaMetAspLeuAsnGlySerIleProArgLeuArgGlnThrAla 238	ACAACAAATCGGAGCAAGTTTACCT20	LeuValAlaAlaArgAlaValGlyTyrTyrAspIleAspLeuSerIleIleArgAsnSer 258 :::     :::	IleGlyGluValAspValIleIleHiSAspLeuGlyGluProValTyrIle 275 	38 88	3 30	r 32 A 49.	PheAspGlyArgTrpLeuAspArgSerValAspValIleLeuProAspAsn 345         ::: ::: :::   ::	ThralaaspvalserLeulleTyraspThrGlyThrGlnTyrargPheaspGluvalval 365     :::::::::::::::::::::::::::::::::	PhePheThrIleAspFroLysThrAsnGlnLeuThrThrAspProAspLysLeuProVal 385 	71		eGlnAsnAsp 43         GCTAAATGAT 80	GlnValSerPheGluGlnSerSerSerArgThrGluProAlaGlnValAsp 456  ::		48	P 50	MetProAsp      AspargValLeualaIleasnHisAspAspClyValAsn       520         ::: I                               GTACCTGATTTTGATGATGCAATAAAACATTAGCGATAACCCTTGTTGTTGTTGATGCTGGA       1097		•
				ASpTyrArgAla     AGCGTTGTGGCTAAAT	AspLysalaPheThrT :::    ACTGAAGCACTTAAAC	HisGlyLysTyrGluT	PheaspGlyargTrpL       ::: AGTGTAGGTCGCTAT-	ThralaaspvalserL    ::::::    CGCGCTGAAATTTTAA	PhePheThrIleAspP      TTC	LysArgGluLeuLeuG :::           CAAATGGAATTACAAC	AsnL   :::    CAATTCGAGAAGATT	TyrPheAsnMetValAs       TATTTAATAATGGCT2	GlnValSerPheGluG] ::: GAAAAACAAAGTTAA	AGTGCACGCATTATAGC	ThrValGluLeuThrAs :::         GCATTACATTTAAATGA	SerAsnLeuIleGlnAs       AATGCAATTAAAGC	MetProAsp :::         STACCTGATTTTGATGA	ArgSerIleLeu     ::  CGACGTTTAACTGTTCG	
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1158   TraceCroadcaArtococcoccoccoccoccoccoccoccoccoccoccocco	2093	GGTTTTGCTTATGGTAGTATTGGACCTAACGCAATTTATGCCGAATATGGTAATGGTAGT 2	2034	qq
1158 TIAGGCGGCAAAAGCGCGCAAAAAACTCCGAAAACCGAATTACTTCGAATTACTTCGATTACTTCACAACA	Ň		2	λά
1158   TIANGCAGGGAACTAGGAACTTGGTAAATTGGAACTTGGTAATTGGAACTTGGTTA   121   1259   PTO	03		1974	qq
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1158   TINCGTCAGGAANTGCCCAACAGAGGAACTTGCTTATATTGCAATTATGCAATTATGCAATTATGCATTAT   1218   TINCGTCAGGAAATGCCTAACAGAAGCGAACTTGCATAATTCACAATTATGCAATTATTATATTATGCAATTATTATATTATGCAATTATTATATTATTATGCAATTATTATATTATTATGCAATTATTATATATTATTATGCAATTATTATATATTATTATTATTATTATTATTATTATTA	97	CTCTGGGTTGTATCTGCAAAAGCATCTGCAGGATATGGTTTT		Ωp
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1158 Tracgroscandraccocandadacancrocorandracularasularasularaspea 350 Tracgroscandraccocandadacancrocorandraco		CCATTA	7	QQ
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1158 TPACCTCAGGAAAGCCCAACAAGAGAATTCGTAAATTAATTGTACATTTATTCGTTTATTCGTATTATTCGTTTATTCGTTTTCGAACTTCGTATTATTCGTTTATTCGTTTTCGAACTTCGAATTGTTCGTTTATTCGTTTTCGTTTTCGAATTGTTCGTTTTCGTTTTCGAATTGTTCGTTTTCGAATTGTTCGTTTTCGTTTTCGTTTTCGTTTTCGTTTTCGTTTTCGTTTTCGTTTTCGTTTTCGTTTTTT	87	ATTCCAGGTTCTGATAACAAATAC		QQ
1158 TPGGTCAGGAAATGGCCAACAAAAGGAACTTGGTATAATTGACAATTTGATTATTATTATATTATTATTATTATAAAACTTGATTATATTATAAAATTTGACAATTTGACATTTATATATA	9	SerAspAlaAsnMet	4	Οy
1158 TPACGTCAGGAAATGGCCAACAAAAAGCAACTTGGTATAATTCACAATTTAGTTGAGTTA 121 1158 TPACGTCAGGAAATGCGCCAACAAAAAGCAACTTGGTATAATTCACAATTTAGTTGAGTTA 121 1218 GGAAAAATTCGCTAGATCGTACAGTTTTTTCTCGAAAACCGAATTGATCTT 127 1218 GGAAAAATTCGCTTAGATCGTACAGTTTTTTCTCGAAAACCGAATTAGTTGATTAT 121 1218 GGAAAAATTCGCTTAGATCGTACAGGTTTCTTCGAAACAGAAACCGAATTGATCTT 127 1219 ATCAATGATGATGATGATGATGATGATGGTTTCTTCGAAACCGAATTAGTTAG	8.1	::: AACTATAACAGCCTTAATAGCAGCTATTTCCCAACT	77	qq
1158 TAGGTCAGGAAATGCCCAACAAGGAACTTGGTATAATTCACAATTAGTTGGTTA 121     1158 TAGGTCAGGAAATGCCCAACAAGGAACTTGGTATAATTCACAATTAGTTGGTTA 121     1218 GGAAAAATTCGCTAGATCGTACAGGTTTCTTCGAAACGCCAAATTAGTTGTTT 127     1218 GGAAAAATTCGCTTAGATCGTTTCTTCGAAACGCCAAAATTCATTAGTTTCTT 127     1218 GGAAAAATTCGCTTAGATCGTTTCTTCGAAACGCCAAAATTCATTAGTTTCTTTC	4	laValHisLysThrValAlaAspAsnLeuValAsnProMetArgGlyTyrArgGlnArg	CI	οy
1158 TTACGTCAGGAAATGGCCCAACAACGAACTTGGTATAATTCACAATTAGTTGAGTTA 121 1218 GGAAAAATTGCCTTAGATCGTACAACTTGGTATAATTCACAATTAGTTGAGTTA 121 1218 GGAAAAATTAGTTGAGTCAGCTTTCTTCGAACTCGAAACCCAATTAGTTGAGTTA 121 1218 GGAAAAATTTGCTTAGAGTCGTTTCTTCGAACTCCAAAACCCAATTAGTTGAGTTA 121 1218 GGAAAAATTTGCTTAGAGTCGGTTTCTTCGAACTCCAAAACCCAATTAGTTGAGTTA 121 1218 ATCAATGGTAATGATGAACGGTTTCTTCGAACTCCAAAACCCAATTAGTTGAGTTA 121 1228 ATCAATGGTAATGATGAACGGTTTCTTCGAAACTCCAAAACCCAAAACCGTTAGGTTA 126 123	77	GACTTTGATTTTTCTTTTGGTTGG	L)	qq
1158   TACGGCAGAATGCCCAACAAGAACTTGCTATAATTCACAATTACTTGAGTTA   121   1218   TTACGTCAGGAATGCCCAACAAGAACGAACTTGCTATAATTCACAATTACTTGAGTTA   121   1218   GGAAAATTCGCTAACAGAACGCAACTTGTTCATAATTCACAATTACTTGAGTTA   1218   GGAAAATTCGCTAACTCGTACACTTCTTCGAACTCCAAAACGCAATTCATCACTTACTT	C	spLeuProValAspPheValAsnGlyLysProSerGlnGluAlaLeuLeuAlaGlyVa	0	δy
1158   TACGGCAGAATGCGCAACAGAAGGAACTTGGTATAATTCACAATTAGTTGAGTTA   121   1218   GGAAAATTGCGCAACAGAAGGAACTTGGTATAATTCACAATTAGTTGAGTTA   121   1218   GGAAAATTGCGCAACAGGAACGGAACTTGGTATAATTCACAATTAGTTGAGTTA   1218   GGAAAATTGCGTAGGTTTCTTCGAAACGCAATTGATTGAT	ń	:::::::::::::::::::::::::::::::::::	7.1	Dp
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1158 TTACGTCAGGAATGCGCCAACAAGAAGGAACTTGGTATAATTCACAATTAGTTCAGGTTA 12  551 Pro	6	ValPheValAlaSerAsp	575	δy
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1158 TTACGTCAGGAATGCGCCAACAAGAGGAACTTCGTATAATTCACAATTAGTTCAGTTA 12 551 Pro		AlaAsp	9	οy
1158 TTACGTCAGGAATGCGCCAACAAGAAGGAACTTGGTATAATTCACAATTAGTTGAGTTA 12 551 ProGluArgThr	2	:::          GGAAAATTCGCTTAGATCGTACAGGTT	-	qq
1158 TTACGTCAGGAAATGCCCAAAAAAAAAAAAAAAAAAAAA	٧ ,	Pro	55	ò
	S	va.thiadatgdaliiledeukroAspGluSerGluAspGluVallleAspLe TTACGTCACGAAATGCGCCAACAAGAACTTGGTATAATTCACAATTAGTAAATTAACTAAATTAA	15	B 2

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|GCTACAGCTAGCGCAGAGTTAATTGTGCCAACTCCATTTGTGAGGCGATAAGAGCCAAAAT 2207
 ----IleSerAspLysGlyTyrLeuThrGlyGlyGlnValLeu
                                                                                                                                                                           -----AsplysGlyPheThrAsn
                                                                                                                                                                                                                                                                                             ValAspValAlaThrGlyValLys-----GluGluGlyAsnProIleLysLeuHisPhe
                                                                                                                                  :::|{| :::::||| ||| ||| ||| ||| ACGGTCCGAAACTGTATTGTTGATGCGAAGTCTTTGGAAATCA
                                                          AlaValGlyThrAlaGlu-----TyrAsnTyrGluPheMetLysAsp------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: THOMAS, Wayne
APPLICANT: THOMAS, Wayne
APPLICANT: TAOMAS, Wayne
APPLICANT: TOSSWORE, Sheena
APPLICANT: SIA, DWO Yuan Charles
APPLICANT: KLEIN, Michel
TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN,
NUMBER OF SEQUENCES: 55
CORRESPONDENES: 55
ADDRESSEE: SIM & MBURINEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                    ---LeuArgLeuAlaValPheGlyAspIleGlyAsnAlaTyr--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3: Sim & McBurney
6TH Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MIS: jb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1038-829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/135,166
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09135166; Patent No. 6083743; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2949 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                 2448 AGTATTGGAGGTTCTTTC 2465
                                                                                                                                                                                                                                                                                                                                                    PhelleGlyThrProPhe 919
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FILING DATE: 12-SEP-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: Canada
2IP: M5G 1R7
COMPUTER READABLE FORM:
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CITY: Toronto
STATE: Ontario
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STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      219 IleThrGlnGluSerAlaMetAspLeuAsnGlySerIleProArgLeuArgGlnThrAla 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuValAlaAlaArgAlaValGlyTyrTyrAspIleAspLeuSerIleIleArgAsnSer 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  210 GTTCGTGCCGGTCAGCGTGTGACTGACAATGATGTG---GCTAATATTGTCCGCTCTTTA 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              309 HisGlyLysTyrGluThrLysLysAsnLeuIleGluAsnAlaSerAlaGluHisGlyTyr 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           346 ThrAlaAspValSerLeuIleTyrAspThrGlyThrGlnTyrArgPheAspGluValVal 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           386 LysArgGluLeuLeuGluGlnLeuLeuThrValAsnMetGlyGluAlaTyr------ 402
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                                                                                                                                                                                                                                                                                                                                                                                                   179 LysvalProArgLeuLysAlaLysPheTyrGlnSerSerGlnSerGlyGluThrSerAla 198
                                                                                                                                                                                                                                                                                                                                                                                                                                             63 AGGATACAATCGATGAAAAACTTCTAATCGCAAGTTTATTATTCGGTACGACAACGACT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       387 ACTGAAGCACTTAAACAAACTTAGATGCTAACGGGTTTAAAGTTGGCGATGTTTA---
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171
141
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230
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Mismatches:
Indels:
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                                                                                                                                                                                       Length:
Matches:
                          DNA (genomic)
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172.00
35.21%
19.30%
3.64%
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TOPOLOGY: linear
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Best Local Similarity:
                      MOLECULE TYPE:
FEATURE:
                                                                    NAME/KEY:
LOCATION:
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                                                                                                                us-09-135-166-1
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439 GlnValserPheGluGlnSerSerSerArgThrGluproAlaGlnValAsp 		ThrValGluLeuThrAspGlylleLeuMetAspIleSerProlleGluPheSerAla	GCATTACATTTAAATGATACTTTCCGCCGTAGTGATATTGCAGATGTAGAA	445 SerAsnLeulleGlnAspLysLeuAsnLeuValAlaAlaLysAlaArgHisLeuTyrAsp            ::         981AATGCAATTAAAGCAAAACTTGGAGAACGCGGTTACGGTAGCGCAACGGTAAATTCA				534 ValalaargalaileLeuProAspGluSerGluAsnGluValileAspLeu : ::::::::::::::::    1158 TTACGTCAGGAATGCGCCAACAAGAAAGGAACTTGGTATAATTCACAATTAGTTGAGTTA	ProGluargThrAlaLeuAlaAsnArgLysThrPro	GGAAAAATTCGCTTAGATCGTACAGGTTTCTTCGAAACAGTCGAAAACGGGAAATTGATCGT	AlaAspAlandingeringeringeringeringeringeringeringer	ValPheValAlaSerAspLysProArgAspGlyGlnIleGlyLeuGlyTrpGly	Sorasondra	SELASPITICALYTHARGLEUVALTHILLYSPHeGLUHISASNLEHILE		GCGGCAGTAAGTAAGCTGGTACGAAAAATGATTATGGTACGAGTGTCAATTTGGGTTAT	SerGluAspLysLysGlyValLysLeuTyrAlaThrLysProLeuSerHis :::	ProLeuAsnAspGlnLeuArgAlaThrLeuGlyTyrGlnGluValPheGlvHisSer	::: ::    :::       :::        :::	ThrAsnGlyPheAspLeuSerThrArgThrLeuGluHis	GTTACTTTAGGTTTCCCTGTAAATGAAATAACTCCTATTATGTAGGATTAGGTCATACC	GluIleSerArgSerIleIleGlnAsnGlyGl		TyrSerLeuArgTyrArgLeuAspLysLeuLysThrGlnAlaProProGluThrTrpGln	ASDLeuproval Asnahaval asnolytivebasessessessessessessessessessessessesses	5GACTTTGATTTTCTTTTGGTTGG	${\tt AlaValHisLysThrValAlaAspAsnLeuValAsnProMetArgGlyTyrArgGlnArg}$
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|---AACTATAACAGCCTTAATAGAGGCTATTTCCCAACT 1814
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                                                                                                          763 AlailealaargalaGlyIleSerGlyValTyrSerPheGlyAspAsnAlaTyrGlySer 782
                                                                                                                                                                           783 AsnArgAlaHis...-GlnMetThrGlyGlyIleGlnAlaGlyTyrIleTrpSerAsp 800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Sim & McBurney
STREET: 6TH Floor, 330 University Avenue
CITY: Toronto
                                                                                                                                                                                                                                                                                                              821 GlyTyrAlaHisAspSerLeuSerPro-----
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Patent No. 6584954
GENERAL INFORMATION:
APPLICANT: CHONG, Pele
APPLICANT: THOMAS, Wayne
APPLICANT: YANG, Yan Ping
APPLICANT: LOOSMORE, Sheena
APPLICANT: SIA, Dwo Yuan Charles
APPLICANT: SIA, Dwo Yuan Charles
APPLICANT: SIA, Dwo Yuan Charles
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COWNRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
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171
141
344
230
44
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/942,046
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/433,522
PRIOR APPLICATION NUMBER: 08/433,522
FILING DATE: 12-SEP-1995
CLASSIFICATION: 435
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Conservative:
Mismatches:
Indels:
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REGISTATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-732 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEFAX: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2949 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-914-168-2 (1-919) x US-08-942-046-1 (1-2949)
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35.21%
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Best Local Similarity:
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                                                                                                                      366 PhePheThrIleAspProLysThrAsnGlnLeuThrThrAspProAspLysLeuProVal 385
                                                                                                                                                                                                                         TyrPheAsnMetValAsnThrGluIleValPheProGluArgGluGlnIleGlnAsnAsp 438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----GluSerThrLeuGluProValIleGlu 465
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552 CGCGCTGAAATTTTAATTCAAATCAATGAAGATGATAAAGCAAAATTGGCATCATTAACT 611
                                                                                                                                                                                                                                                                                                                                                         870 AGTGCACGCATTATAGGTAATCTGGGAGGTATGTCTGCCGAGCTTGAACCTTTACTTTCA
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                                                 346 ThralaaspValSerLeuIleTyraspThrGlyThrGlnTyrargPheAspGluValVal
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1485 ACCGAGCCCTATTTACTAAAGATGGTGTAAGTCTTGGTGGAAATGTTTTCTTTGAAAAC 1544
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                                                                                                                                                                                                                                             1665 TATAATAAAATTAGTAACTTTGCTCTAGAA-----TATAACCGTAATTTATATATT 1715
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                                      639 ProLeuAsnAspGlnLeuArgAlaThrLeuGlyTyrGlnGlnGluValPheGlyHisSer
                                                                             1545 TACGATAACTCTAAAAGTGATACATCCTCTAACTATAAGCGTACGACTTACGGAAGTAAT
                                                                                                                                       727 AlaValHisLysThrValAlaAspAsnLeuValAsnProMetArgGlyTyrArgGlnArg
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179 LysValProArgLeuLysAlaLysPheTyrGlnSerSerGlnSerGlyGluThrSerAla 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            382 GTGTTTGCCGCA-------CTTTTGTGGCAAAAGATATTCGTGTGGATGGT 426
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                                                   APPLICANT: CHONG, Wayne
APPLICANT: THOMAS, Wayne
APPLICANT: YANG, Yan Ping
APPLICANT: SIA, Dwo Yuan Charles
APPLICANT: KLEIN, Michal
TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
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171
141
344
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,522A
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Mismatches:
Indels:
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                                                                                                                                                                                                                       ADDRESSEE: Sim & McBurney
STREET: 6TH Floor, 330 University Avenue
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1038-434 MIS: jb
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Matches:
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12-SEP-1995
Sequence 5, Application US/08433522A
Patent No. 6013514
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 12-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEO ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.03e - 08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2950 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    172.00
35.21%
19.30%
3.64%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 2950 base pai
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
334..2724
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'RY: Canada
MSG 1R7 .
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                 STATE: O
COUNTRY:
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QQ	469	GTTCGTGCCGGTCAGCGTGTGACTGACAATGATGTGGCTAATATTGTCCGCTCTTTA	525
ò	259	IleGlyGluValAspValIleIleHisAspLeuGlyGluProValTyrIle	275
qq	526	TTCGTAAGTGGATTCGATGATGATGAAAGCGCATCAAGAGGCGGATGTGTTGTT TTCGTAAGTGGCGATGTGTGAAAGCGCGATCAAGAGGCGATGTTGTT	585
οy	276	AspTyrArgAlaAspTyrArgGlyGluGlyAlaAsp	288
qq	586	AGCGTTGTGGCTAAATCGATCATTTCAGATGTTAAAATCAAAGGTAACTCTGTTATTCCC	645
οy	289	AspLysAlaPheThrThrValAlaAspGluValProLeuLeuIleGlyAspValPheHis :::	308
Ор	646	ACTGAAGCACTTAAACAAAACTTAGATGCTAACGGGTTTAAAGTTGGCGATGTTTAA	702
ò	309	HisGlyLysTyrGluThrLysLysAsnLeuIleGluAsnAlaSerAlaGluHisGlyTyr	328
QQ	703	ATTCGAGAAAATTAAATGAATTTGCCAAAAGTGTAAAAGGGCACTATGCA	753
ΟŊ	329	PheaspGlyargTrpLeuaspargSerValaspVallleLeuproaspasn	345
q	754	AGTGTAGGTCGCTATAACGCAACAGTTGAACCTATTGTCAATACGCTACCAAATAAT	810
Οy	346	ThrAlaAspValSerLeuIleTyrAspThrGlyThrGlnTyrArgPheAspGluValVal	365
qa	811	CGCGCTGAAATTTTAATTCAAATCAATGAAGATGATAAAGCAAAATTGGCATCATTAACT	870
Qγ	366	PhePheThrIleAspProLysThrAsnGlnLeuThrThrAspProAspLysLeuProVal	385
qq	871	TTCAAGGGGAACGAATCTGTTAGTAGCAGTACATAACAAGAA	912
Qy	386	LysargGluLeuLeuGluGlnLeuLeuThrValAsnMetGlyGluAlaTyr	402
qq	913	CAAATGGAATTACAACCTGATTCTTGGTGGAAATTATGGGGAAATAAAT	972
οy	403	AsnLeuGlnAlaValArgAlaLeuSerAsnAspLeuIleAlaThrArg	418
QQ	973	CAATTCGAGAAAGATTTGCAGTCAATTCGTGATTAT	1008
οy	419	TyrPheAsnMetValAsnThrGluIleValPheProGluArgGluGlnIleGlnAsnAsp	438
QQ	1009	TATTTAAATAATGCCTATGCCAAAGCACAAATTACTAAAACGGATGTTCAGCTAAATGAT	1068
ογ	439	GlnValSerPheGluGlnSerSerSerArgThrGluProAlaGlnValAsp	456
Op	1069	GAAAAAACAAAAGTTAATGTAACCATTGATGTAAATGAAGGTTTACAGTATGACGTTCGT	1128
δy	457	GluSerThrLeuGluProValIleGlu	465
οp	1129	AGTGCACGCATTATAGGTAATCTGGGAGGTATGTCTGCCGAGCTTGAACCTTTACTTCA	1188
δ	466	ThrValGluLeuThrAspGlyIleLeuMetAspIleSerProIleGluPheSerAla	484
qq	1189	GCATTACATTTAAATGATACTTTCCGCCGTAGTGATATTGCAGATGTAGAA	1239
οy	485	SerAsnLeuIleGlnAspLysLeuAsnLeuValAlaAlaLysAlaArgHisLeuTyrAsp	504
QQ	1240	AATGCAATTAAAGCAAAACTTGGAGAACGCGGTTACGGTAGCGCAACGGTAAATTCA	1296
οy	505	MetProAspAspArgValLeuAlaIleAsnHisAspAspGlyValAsn	520
QQ	1297	GTACCTGATTTTGATGATGAAAAAAAAACATTAGCGATAACCCTTGTTGTTGATGCTGGA	1356
δy	521	ArgSerIleLeuGlyArgIleSerAspAlaValSerAla	533
qq	1357	GAA	1416
οy	534	ValAlaArgAlaIleLeuProAspGluSerGluAsnGluValIleAspLeu	550
QQ	1417	TTACGTCAGGAAATGGGCCAACAAGAAGGAACTTGGTATAATTCACAATTAGTTGAGTTA	1476
٥y	551	ProGluargThrAlaLeuAlaAsnArgLysThrPro	562
g	1477	GGAAAAATTCGCTTAGATCGTACAGGTTTCTTCGAAACAGTCGAAAACCGAATTGATCCT	1536

Oy H	563	AlaAspValTyrGlnSerLysLysValProLeuTyr 574
ò	7	SerAspLysProArqAspGlyGln11eGlyLeuGlyTrpGly 592
QQ	1582	:
δō.	59	erAspThrGlyThrArgLeuValThrLysPheGluHisAsnLeulle 608
aa	1624	CAGAGAGTGGTATTAGTTATCAAGCAAGTGTTAAACAAGATAATTTCTTGGGAACAGGG 15
QV Dp	609	
Qy	622	erGluAspLysLysGlyValLysLeuTyrAlaThrLysProLeuSerHis 638
Dp	1744	:::    ACCGAGCCCTATTTACTAAAGATGTGTAAGTCTTGGTGGAAATGTTTTCTTTGAAAAC 1803
ΟŊ	639	ProLeuAsnAspGlnLeuArgAlaThrLeuGlyTyrGlnGlnGluValPheGlyHisSer 658
Q	1804	TACGATAACTCTAAAAGTGATACATCCTCTAACTATAAGCGTACGACTTACGGAAGTAAT 1863
Qy	629	ThrAsnGlyPheAspLeuSerThrArgThr
QC	1864	GTTACTTTAGGTTTCCCTGTAAATGAAATAACTCCTATTATGTAGGATTAGGTCATACC 1923
οy	672	GlulleSerArgSerIleIleGlnAsnGlyGlyTrpAsnArgThr 686
Op	1924	TATAATAAATTAGTAACTTTGCTCTAGAATATAACCGTAATTTATATATT 1974
Οy	687	TyrSerLeuArgTyrArgLeuAspLysLeuLysThrGlnAlaProProGluThrTrpGln 706
g	1975	CAATCAATGAAATTTAAAGGTAATGGCATTAAAACAAAT 2013
δy	707	AspLeuProValAspPheValAsnGlyLysProSerGlnGluAlaLeuLeuAlaGlyVal 726
qq	2014	GACTTTGATTTTCTTTTGGTTGG
Qy	727	AlaValHisLysThrValAlaAspAsnLeuValAsnProMetArgGlyTyrArgGlnArg 746
QQ	2038	AACTATAACAGCCTTAATAGGGCTATTTCCCAACT 2073
δy	747	TyrSerLeuGluValGlySerSerGlyLeuValSerAspAlaAsnMet 762
Op	2074	AAAGGGGTTAAAGCAAGTCTTGGTGGACGACGATTACTATTCCAGGTTCTGATAACAAATAC 2133
δy	763	AlaIleAlaArgAlaGlyIleSerGlyValTyrSerPheGlyAspAsnAlaTyrGlySer 782
qq	2134	TACAAACTAAGTGCAGATGTACAGGGTTTCTACCCATTA
Qy	783	AsnargalaHisGlnMetThrGlyGlyIleGlnAlaGlyTyrIleTrpSerAsp 800
Dp	2173	GACAGAGATCACCTCTGGGTTGTATCTGCAAAAGCATCTGCAGGATATGCAAATGGTTTT 2232
δy	801	PheAlaGlyGlyAspGlnSerIl
Dp	2233	GGAAACAAGCGTTTACCGTTCTATCAAACTTATACAGCGGGTGGCATCGGTTCATTACGT 2292
δλ	821	Ser
OD	2293	GTTTTGCTTATGGTA
Qy	83	
Dp	2353	Ð
οy	843	AlaValClyThrAlaGluTyrAsnTyrGluPheMetLysAsp
pp	2407	GCTACAGCTAGGGGAGAGTTAATTGTGCCAACTCCATTTGTGAGGGATAAGAGĒCAAAAT 2466

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2467 ACGGTCCGAACCTCCTTATTTGTTGATGCGGCAAGTGTTTGGAATACTAAATGGAAATCA 2526
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                                                                                                                                                                                                                                                                                                                               895
                                                                                                                                                                                                                     2527 GATAAAAATGGATTAAGAGGGGATGTATTAAAAAGATTGCCTGATTATGGCAAATCAAGC
                                                                                                                                                                     ------AspLysGlyPheThrAsn
                                                                                                                                                                                                                                                                                                876 AspThrLyslleGlyAlaGlyValGlyValArgTrpAlaSerProValGlyGlnValArg
                                                                                                                                                                                                                                                                                                                                           ValAspValAlaThrGlyValLys-----GluGluGlyAsnProlleLysLeuHisPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: CHONG, Pele
APPLICANT: THOMAS, Wayne
APPLICANT: YANG, Yan Ping
APPLICANT: LOSMORE, Sheen
APPLICANT: LOSMORE, Sheen
APPLICANT: KIEIN, Michel
TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
STRDEN: SIM & MADDRESSEE: SI
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/09/135,166
FILING DATE:
---LeuArgLeuAlaValPheGlyAspIleGlyAsnAlaTyr--
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6TH Floor, 330 University Avenue
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NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-829 MIS:jb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/433,522
FILING DATE: 12-SEP-1995
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US-09-135-166-5
; Sequence 5, Application US/09135166
; Patent No. 6083743
; GENERAL INFORMATION:
APPLICANT: CHONG, Pele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (416) 595-1155
TELERAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2950 base pairs
TYPE: nucletc acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2707 AGTATTGGAGGTTCTTTC 2724
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; LOCATION: 334..2724
US-09-135-166-5
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Alignment Scores:

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179 LysValProArgLeuLysAlaLysPheTyrGlnSerSerGlnSerGlyGluThrSerAla 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                          259 Ile-----GlyGluVal---AspValIleIleHisAspLeuGlyGluProValTyrIle 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           973 CAATICGAGAAAGATITGCAGTCAATICGT-------GATTAT 1008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -------ValGluValArgGlyGluGlyAla---Asp 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     646 ACTGAAGCACTTAAACAAAACTTAGATGCTAACGGGTTTAAAGTTGGCGATGTTTTA--- 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       309 HisGlyLysTyrGluThrLysLysAsnLeuIleGluAsnAlaSerAlaGluHisGlyTyr 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1069 GAAAAAACAAAAGTTAATGTAACCATTGATGTAAATGAAGGTTTACAGTATGACCTTCGT 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1129 AGTGCACGCATTATAGGTAATCTGGGAGGTATGTCTGCCGAGCTTGAACCTTTACTTTCA 1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       366 PhePheThrIleAspProLysThrAsnGlnLeuThrThrAspProAspLysLeuProVal 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              403 ------AsnLeuGlnAlaValArgAlaLeuSerAsnAspLeuIleAlaThrArg 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --- GluSerThrLeuGluProValIleGlu 465
                                                                                                                                                                                          322 AGGATACAATCGATGAAAAACTTCTAATCGCAAGTTTATTATTCGGTACGACAACGACT
                                                                                                                                                                                                                              199 IleGlySerSerHisGlnLysThrGluProTyrAlaAsnIleLysAlaAlaLeuGluAsp
                                                                                                                                                                                                                                                                GTGTTTGCCGCA-------CTTTTGTGCCAAAAGATATTCGTGGATGGT
                                                                                                                                                                                                                                                                                                                                                                                                      GTTCGTGCCGGTCAGCGTGACTGACAATGATGTG---GCTAATATTGTCGCGTCTTTA
                                                                                                                                                                                                                                                                                                                                                                        LeuValAlaAlaArgAlaValGlyTyrTyrAspIleAspLeuSerIleIleArgAsnSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    586 AGCGTTGTGGCTAAATCGATCATTTCAGATGTTAAAATCAAAGGTAACTCTGTTATTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AspLysAlaPheThrThrValAlaAspGluValProLeuLeuIleGlyAspValPheHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             329 PheaspGlyargTrpLeuAspArgSerValAspValIle------LeuProAspAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           754 AGTGTAGGTCGCTAT---AACGCAACAGTTGAACCTATTGTCAATACGCTACCAAATAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     811 CGCGCTGAAATTTTAATTCAAATCAATGAAGATGATAAAGCAAAATTGGCATCATTAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----ATTCGAGAAAATTAAATGAATTTGCCAAAAGTGTAAAAGAGCACTATGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            386 LysargGluLeuLeuGluGlnLeuLeuThrValAsnMetGlyGluAlaTyr-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        419 TyrPheAsnMetValAsnThrGluIleValPheProGluArgGluGlnIleGlnAsnAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlnValSerPheGluGlnSerSerSerSerArgThrGluProAlaGlnValAsp-----
                                                                                                                                                                                                                                                                                                                                    GTTCAAGGTGACTTAGAACAACAAATCCGAGCAAGTTTACCT------
     2950
171
141
344
230
44
                                     Conservative:
Mismatches:
Indels:
                                                                                                                      US-09-914-168-2 (1-919) x US-09-135-166-5 (1-2950)
   Length:
Matches:
 .03e-08
                172.00
35.21%
19.30%
3.64%
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                              Percent Similarity:
Best Local Similarity:
Query Match:
Pred. No.:
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ò	466 ThrValGluLeuThrAspGlyIleLeuMetAspIleSerProIleGluPheSerAla 484	:::
e ò	LeuTyrAsp	Qy 783 AsnargalaHisGlnMetThrGlyGl :::::: Db 2173 GACAGAGATCACCTGGGTTGTATCTGCAAA
8 8	1240AATGCAATTAAAGCAAAACTTGGAGAACGCGGTTACGGTAGCGCAACGGTAAATTCA 1296 505 MetproaspAspargValleualaileasnHisaspaspGlyValasn 520 ::::	Qy 801 AsnPheAsnHisValProTyrArgLeuArgPh :: ::         ::
G & G	521 ArgSerIleLeu	Qy 821 GlyTyrAlaHisAspSerLeuSerPro      :::   :::   SerTrTGCTTATGGTAGTATTGGACCTAAGGC
3 6 A		Oy 830
S S	ProGluargThrAlaLeualaAsnargLysThrPro :::	Oy 843 AlaValGlyThrAlaGluTyrAsnTy           :::         Db 2407 GCTACAGCTAGCGCAGAGTTAATTGTGCCAAC
oy da	AlaAspValTyrGlnSerLysLysValProLeuTyr 	Qy 857LeuargLeualaValPheGlyAspIleGl :::    ::::
Oy Bb	575 ValPheValAlaSerAspLysProArgAspGlyGlnIleGlyLeuGlyTrpGly 592 1::	QY 870DD 2527 GATAAAAATGGATTAGAGGGGATGTATAAA
oy Op	SeraspThrGlyThrArgLeuValThrLysPheGluHisAsnLeulle 608 :::::::     ACAGAGAGTGGTATTATGTTATGAGCAAGTGTTAAACAAGAATATTTCTTGGGAACAGGG 168	Qy 876 AspthrLysileGlyAlaGlyValGlyValAr::          ::
QY		Qy 896 valaspvalalarhrGlyValLysGl 
Qy	638	Qy 914 PheileGlyThrProPhe 919         Db 2707 AGTATTGGAGGTTCTTTC 2724
Oy Dp		RESULT 12 US-08-942-046-5 ; Sequence 5, Application US/08942046 ; Patent No. 6264954
oy G	659ThrasnGlyPheaspLeuSerThrargThrLeuGluHis 671	; GENERAL INFORMATION: ; APPLICANT: CHONG, Pele ; APPLICANT: THOMAS, Wayne ; APPLICANT: YANG, Yan Pinq
Oy Db		; APPLICANT: LOOSMORE, Sheena ; APPLICANT: SIA, DWO Yuan Charles ; APPLICANT: KLEIN, Michel ; TITLE OF INVENTION: HAEMOPHILUS OUTE
Oy Db	687 TyrSerLeuArgTyrArgLeuAspLysLeuLysThrGlnAlaProProGluThrTrpGln 706	; NUMBER OF SEQUENCES: 55 ; CORRESPONDENCE ADDRESS: ; ADDRESSEE: Sim & MCBurney ; STREET: 6TH Floor, 330 University
Qy Db	707 AspLeuProValAspPheValAsnGlyLysProSerGlnGluAlaLeuLeuAlaGlyVal 726	; CTTY: Toronto ; STATE: Ontario ; COUNTRY: Canada ; ZIP: MSG 1R7
, dg	727 AlaValHisLysThrValAlaAspAsnLeuValAsnProMetArgGlyTyrArgGlnArg 746 1::	
oy oy	rSerGlyLeuValSerAspAlaAsnMet	CURPWAKE: Parentin Kelease #1.0, V CURENT APPLICATION DATA:  PILING DATE: CLASSIFICATION: 435
ζŏ	763 AlaileAlaArgAlaGlyIleSerGlyValTyrSerPheGlyAspAsnAlaTyrGlySer 782	; PRIOR APPLICATION DATA:

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LysGlyTyrLeuThrGlyGlyGlyGlnValLeu 842
::: |||||||
sar----GTGATTGGTGGTAATGCAATC 2406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ArgrrpalaSerProValGlyGlnValArg 895
:::||| ||||||::||| :::
CAATGGCAATCTCCTATTGGGGCATTGGTA 2646
                                                                                                         PhePheAlaGlyGlyAspGlnSerIleArg 820
::: ||||||||||||
RATACAGCGGGTGGCATCGTTCATTACGT 2292
                                                                                                                                                                                                                                                                                                                              ||||::: ||||
| ACTCCATTTGTGAGCGATAAGAGCCAAAAT 2466
                                                                                                                                                                                                                                                                                                                                                                                                     SCAAGTGTTTGGAATACTAAATGGAAATCA 2526
                                                                                                                                                                                                                                                                                                                                                                                                                                       GluGluGlyAsnProlleLysLeuHisPhe 913
||| :: || || :: 3AAAATGATGATGAGAATTT 2706
                                                              SCAATTTATGCCGAATATGGTAATGGTAGT 2352
                                          31ylleGlnAlaGlyTyrlleTrpSerAsp 800
                                                                                                                                                                                                                                                                                                       PyrGluPheMetLysAsp------ 856
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179 LysvalproArgLeuLysAlaLysPheTyrGlnSerSerGlnSerGlyGluThrSerAla 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        219 IleThrGlnGluSerAlaMetAspLeuAsnGlySerIleProArgLeuArgGlnThrAla 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        239 LeuValalaalaargalaValGlyTyrTyrAspIleAspLeuSerIleIleArgAsnSer 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 259 Ile-----GlyGluVal---AspValIleIleHisAspLeuGlyGluProValTyrIle 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              526 Trograagiggicgaticgatgaigigaaagcgcaicaagaagcgaigigtigtigti 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         276 AspTyrArgAla----Asp 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      586 AGCGTTGTGGCTAAATCGATCATTTCAGATGTTAAAATCAAAAGGTAACTCTGTTATTCCC 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    289 AspLysAlaPheThrThrValAlaAspGluValProLeuLeuIleGlyAspValPheH1s 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                309 HisGlyLysTyrGluThrLysLysAsnLeuIleGluAsnAlaSerAlaGluHisGlyTyr 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------ATTCGAGAAAATTAAATGAATTTGCCAAAAGTGTAAAAGKGCACTATGCA 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        329 PheaspGlyArgTrpLeuAspArgSerValAspValIle------LeuProAspAsn 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              754 AGTGTAGGTCGCTAT---AACGCAACAGTTGAACCTATTGTCAATACGCTACCAAATAAT 810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 346 ThralaAspValSerLeuIleTyrAspThrGlyThrGlnTyrArgPheAspGluValVal 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            811 CGCGCTGAAATTTTAATTCAATCAATGAAGATGATAAAGCAAAATTGGCATCATTAACT 870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PhePheThrIleAspProLysThrAsnGlnLeuThrThrAspProAspLysLeuProVal 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              469 GTTCGTGCCGGTCAGCGTGTGACTGACAATGATGTG---GCTAATATTGTCCGCTCTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           427 GITCAAGGTGACITAGAACAACAAATCCGAGCAAGTITACCT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              646 ACTGAAGCACTTAAACAAAACTTAGATGCTAACGGGTTTAAAGTTGGGGATGTTTTA---
                                                                                                                                                                                                                                                                                                                                                      2950
171
141
344
230
44
                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                        ATTORNEY FACENTION: 435
ATTORNEY FACENTION: 405
NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-732 MIS:jb
TELEPHONE: (416) 595-1155
TELEPAX: (416) 595-1163
INFORMATION FOR SED ID NO: 5: SEQUENCE CHARACTERISTICS:
LENGTH: 2950 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: stranbeness: single
                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-914-168-2 (1-919) x US-08-942-046-5 (1-2950)
APPLICATION NUMBER: 08/433,522
FILING DATE: 12-SEP-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                 2.03e-08
172.00
35.218
19.308
3.648
                                                                                                                                                                                                                                                                    ; NAME/KEY: CDS
; LOCATION: 334..2724
US-08-942-046-5
                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                           Alignment Scores:
Pred. No.:
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<u> </u>	78 da	1 TTCAAGGGGAACGAATCTGTTAGTAGCAGTACATTAAAAAA 017
о —	Qy 38	GluLeuLeuGluGlnLeuLeuThrValAsnMetGlvGluAlarvr
<u> </u>	16 qa	.::            :::
οy	у 40:	3AsnLeuGlnAlaValArgAlaLeuSerAsnAspLeuI]eAlamhrara 411
q <sub>Q</sub>	97	OL JALLES GALLAL TO THE TOTAL
ογ	41	TyrPheAsnMetValAsnThrGluIleValPheProGluArgGluGlnIleGlnAsnAsp 4
q <sub>0</sub>	100	TATTTAAATAACCTATGCCAAAGCACAAATTACTAAAACGGATGTTCAGCTAAATGAT 10
å i	4.	GlnValS
ago d	106	
r a	457	
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3 dd	118	INTO THE CONTROL OF T
Qy	485	12
qa	1240	040
οy	505	٠,
qq	1297	ATGAT
QY	521	100
qq	1357	3 5
QY	534	
QQ	1417	, -
Qγ	551	562
qa	1477	, ,
Qy	563	
qq	7	ATCAATGGTAGTAATGATGAAGTGGATGTCGTATATAAAGTCAAA1583
Qy	575	502
qq	1582	ACGGGTAGTATCAACTTTGGTATTGGTTACGGT 16:
οy	m	- 608
QQ	1624 /	TTAGTTATCAAGCAAGTGTTAAACAGG
Qy	609	AsnArgAspGlyTyrGlnAlaGlyAlaGluLeuArgieu 621
QΩ	4	,
Οy	622 8	AspLysLysClyValLysLeuTyrAlaThrLysProLeuSerHis 638
QQ	44	
ΟŻ	639 P	658
qq	04	GATAACTCTAAAAGTGATACATCCTCTAACTATAAGCGTACGACTTACGGAAGTAAT 18
δy	659 -	671

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179 LysValProArgLeuLysAlaLysPheTyrGlnSerSerGlnSerGlyGluThrSerAla 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuValAlaAlaArgAlaValGlyTyrTyrAspIleAspLeuSerIleIleArgAsnSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        362 AGGATACAATCGATGAAAAAACTTCTAATCGCAAGTTTATTATTCGGTACGACAACGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      199 IleGlySerSerHisGlnLysThrGluProTyrAlaAsnIleLysAlaAlaLeuGluAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      566 TTCGTAAGTGGTCGATTCGATGTGAAAGCGCATCAAGAAGGCGATGTGCTTGTTGTT
APPLICANT: LOOSMORE, Sheena
APPLICANT: SIA, Dwo Yuan Charles
APPLICANT: KLEIN, Michel
TITLE OF INVENTION: HEMOPHILUS OUTER MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2984
171
141
344
230
44
                                                                                                                                                                                                                                                                                                                                                O'PERATING SYSTEM: PC_DOS/MS-LOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,522A
FILING DATE: 12-SEP-1995
CLASSITCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: STEARAT, Michael I
REGISTRATION NUMBER: 24,93
REFERENCE/DOCKET NUMBER: 1038-434 MIS:jb
TELEPHONE: (416) 595-1163
TELEPHONE: (416) 595-1163
INFORMATION FOR SED ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2084 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-914-168-2 (1-919) x US-08-433-522A-3 (1-2984)
                                                                                                                                  3: Sim & McBurney
6TH Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
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                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
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19.30%
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                                                                                                                                                                                                                           COUNTRY: Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity:
                                                                                                                                  ADDRESSEE: Sim
STREET: 6TH Flo
CITY: Toronto
                                                                                                                                                                                                      STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
                                                                                                                                                                                                                                                  M5G 1R7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION:
US-08-433-522A-3
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QQ		AGCGTTGTGGCTAAATCGATCATTTCAGATGTTAAAATCAAAGGTAACTCTGTTATTCCC 685
Qy	289	AspLysAlaPheThrThrValAlaAspGluValProLeuLeuIleGlyAspValPheHis 308
QQ	989	ACTGAAGCACTTAAAACAAAACTTAGATGCTAACGGGTTTAAAAGTTGGCGGTGTTTAA 742
οy	309	HisGlyLysTyrGluThrLysLysAsnLeuIleGluAsnAlaSerAlaGluHisGlyTyr 328
qa	743	::: ATTCGAGAAAATTAAATGAATTTGCCAAAAGTGTAAAAGAGGACTATGCA 793
yo q	329	PheAspGlyArgTrpLeuAspArgSerValAspVallleLeuProAspAsn 345
a è	346	82
g q	851	CGCGCTGAAATTTAATTCAAATCAAAGAAGATGAAAATTGGCATCATTAACT 910
οy	366	
qq	911	TTCAAGGGAACGAATCTGTTAGTAGCAGTACATTACAAGAA 952
οy	æ	LysArgGluLeuLeuGluGlnLeuLeuThrValAsnMetGlyGluAlaTyr 402
g	953	CAAATGGAATTACAACCTGATTCTTGGTGGAAATTATGGGGAAATAAAT
٥٨	40	
QQ	1013	CAATICGAGAAAGAITIGCAGTCAAITCGI
لام اد	419	TyrPheAsnMetValAsnThrGluIleValPheProGluArgGluGlnIleGlnAsnAsp 438
3 8		TAAATGAT 11
දු අ	439	GINVAISErPheGluGInSerSerSerSerSerArgThrGluProAlaGInValAsp 456 
Qy	457	1 7
qq	1169	0 0
οy	466	ThrValGluLeuThrAspGlyIleLeuMetAspIleSerProlleGluPheSerAla 484
qq	1229	Ö
οy	485	
q	1280	
		MetProAspAspargValLeuAlalleAsnHisAspAspGlyValAsn 520
		GTACCTGATTTTGATGATGCAAATAAAACATTAGCGATAACCCTTGTTGTTGATGCTGGA 1396
		ArgSerIleLeu
		CGACGTTTAACTGTTCGCCAACTTCGCTTTGAAGGAAATACCGTTTCTGCTGATAGCACT 1456
Οy	534	ValAlaArgAlaIleLeuProAspGluSerGluAsnGluValIleAspLeu 550
Dp 1	1457	TTACGTCAGGAAATGCGCCAACAAGAAGGAACTTGGTATAATTCACAATTAGTTGAGTTA 1516
δy	551	ProGluArgThrAlaLeuAlaAsnArgLysThrPro 562
<u>е</u>	1517 (	GITICITCGAA
δλ	263	AlaAsp
Dp 1	1577	ATCAATGGTAGTAATGATGAAGTGGATGTCGTATATAAAGTCAAA
οy	575	ValPheValAlaSerAspLysProArgAspGlyGlnIleGlyLeuGlyTrpGly 592
qo,,	. 622	GAACGTAACACGGGTAGTATCAACTTTGGTATTGGTTACGGT 1663

QY	593	SerAspThrGlyThrArgLeuValThrLysPheGluHisAsnLeuIle6 :::::::!   ::::   ACAGAGAGGGTARTPAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	0.8
ò	9		<b>\</b>
6	ં લ	GCGGCAGTAAGTATAGCTGGTACGAAAAATGATATGGTACGAGTGTCAATTTGGGTTAT	621 1783
QY	62	SerGluAspLysClyvalLysLeuTyrAlaThrLysProLeuSerH1s 6	38
an .	χ ,	ACCGAGCCCTATTTACTAAAGATGGTGTAAGTCTTGGTGGAAATGTTTTCTTTGAAAAC 1	1843
δ δ	63	ProLeuAsnAspGlnLeuArgAlaThrLeuGlyTyrGlnGlnGluValPheGlyHisSer 6	58
g à	1844 676	-	1903
S S	n o	TITASHOLYFHEASDLEUDGFIDFARGTDF	57.1 1963
δy	672	YTrpAsnArgThr6	86
qq	1964	:::        TATAATAAATTAGTAACTTTGCTCTAGAATATAACGTAATTTATATATT 20	1014
Qy	687	AlaProProGluThrTrpGln 70	90,
QQ	2015	CAATCAATGAAATTTAAAGGTAATGGCATTAAAACAAAT20	053
Qy	707	AspLeuProvalAspPheValAsnGlyLysProSerGlnGluAlaLeuLeuAlaGlyVal 72	56
qq	2054	STTTTGGTTGG2	110
ΟŊ	727	g 74	
Οp	2078	AACTATAACAGCCTTAATAGGGCTATTTCCCAACT 21	113
Qy	747	SerAspAlaAsnMet 76	62
qq	2114	CTATTCCAGGTTCTGATAACAAATAC 21	173
οy	763	GlyAspAsnAlaTyrGlySer 78	82
QQ	2174	CAGATGTACAGGGTTTCTACCCATTA	212
QY	783	AsnArgAlaHisGlnMetThrGlyGlyIleGlnAlaGlyTyrIleTrpSerAsp 800	00
Оb	2213	TCTGGGTTGTATCTGCAAAAGCATCTGCAGGATATGCAAATGGTTTT 2	272
Qy	801	AsnPheAsnHisValProTyrArgLeuArgPhePheAlaGlyGlyAspGlnSerileArg 820	20
qq	2273	GGAAACAAGCGTTTACCGTTCTATCAAACTTATACAGCGGGTGGCATCGGTTCATTACGT 233	332
Οy	821	GlyTyralaHisaspSerLeuSerPro	29
QQ	2333	23	392
ολ	830	GlyTyrLeuThrGlyGlyGlnValLeu 84	4.2
qq	2393	TGCAATC 24	446
Οy	843	laValGlyThrAlaGluTyrAsnTyrGluPheMetLysAsp 85	26
QQ	2447	GCTACAGCTAGCGCAGAGTTAATTGTGCCAACTCCATTTGTGAGCGATAAGAGCCAAAAT 250	506
δλ	857	98	99
qq	2507	TTGGAATACTAAATGGAAATCA 25	999
Οy	870	87	75
qq	2567	26	526

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TICTCTTATGCCAAACCAATTAAAAATATGAAAATGATGATGATGTCGAACAGTTCCAATTT 2746
876 AspThrLysIleGlyAlaGlyValGlyValArgTrpAlaSerProValGlyGlnValArg 895
                                                                       ValAspValAlaThrGlyValLys-----GluGluGlyAsnProlleLysLeuHisPhe 913
                                    CGTATTCGCCCCTCTACAGGTGTCGGATTCCAATGGCAATCTCCTATTGGGCCATTGGTA
                                                                                                                                                                                                                                                  Sequence 3, Application US/09135166
Patent No. 6083743
GENERAL INFORMATION:
APPLICANT: CHOMAS, Wayne
APPLICANT: THOMAS, Wayne
APPLICANT: LOOSMORE, Sheena
APPLICANT: LOOSMORE, Sheena
APPLICANT: LOOSMORE, Sheena
APPLICANT: SIA, DWO YUAN CHARL
TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2984
171
141
344
230
44
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Sim & McBurney
STREET: 6TH Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1038-829 MIS:jb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/135,166 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08/433,522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEPAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA (genomic)
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172.00
35.21%
19.30%
3.64%
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                                                                                                                                                PhelleGlyThrProPhe 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/4:
FILING DATE: 12-SEP-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 2984 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY:
; LOCATION:
US-09-135-166-3
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US-09-914-168-2 (1-919) x US-09-135-166-3 (1-2984)

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953 CAAATGGAATTACAACCTGATTCTTGGTGGAAATTATGGGGAAATAAAATTTGAAGGTGCG 1012
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1169 AGTGCACGCATTATAGGTAATCTGGGAGGTATGTCTGCCGAGCTTGAACCTTTACTTTCA 1228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1049 TATTTAAATAATGGCTATGCCAAAGCACAAATTACTAAAACGGATGTTCAGCTAAATGAT 1108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1109 GAAAAAACAAAAGTTAATGTAACCATTGATGTAAATGAAGGTTTACAGTATGACCTTCGT 1168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     911 TTC------AAGGGGAACGAA---TCTGTTAGTAGCAGTACATTACAAGAA 952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------AsnLeuGlnAlaValArgAlaLeuSerAsnAspLeuIleAlaThrArg 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          419 TyrPheAsnMetValAsnThrGluIleValPheProGluArgGluGlnIleGlnAsnAsp 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----GluSerThrLeuGluProValIleGlu 465
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                                                                                                                                                                                                                                                                                                                ::: ||| ::: ||| :509 GTTCGTGCGGTCACCGTCTTTA 565
                                                                                                                                                                                                                                                                                                                                                                                                                794 AGTGTAGGTCGCTAT---AACGCAACAGTTGAACCTATTGTCAATACGCTACCAAATAAT 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   366 PhePheThrIleAspProLysThrAsnGlnLeuThrThrAspProAspLysLeuProVal 385
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                                                                                           199 IleGlySerSerHisGlnLysThrGluProTyrAlaAsnIleLysAlaAlaLeuGluAsp 218
                                                                                                                                        422 GTGTTTGCCGCA-------CCTTTTGTGCCAAAAGATATTCGTGGATGT 466
                                                                                                                                                                                    219 IleThrGlnGluSerAlaMetAspLeuAsnGlySerIleProArgLeuArgGlnThrAla 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         276 AspTyrArgAla-----Asp 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       289 AspLysAlaPheThrThrValAlaAspGluValProLeuLeuIleGlyAspValPheHis 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                309 HisGlyLysTyrGluThrLysLysasnLeuIleGluAsnAlaSerAlaGluHisGlyTyr 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         329 PheaspGlyArgTrpLeuAspArgSerValAspValIle------LeuProAspAsn 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       346 ThrAlaAspValSerLeuIleTyrAspThrGlyThrGlnTyrArgPheAspGluValVal 365
179 LysValProArgLeuLysAlaLysPheTyrGlnSerSerGlnSerGlyGluThrSerAla 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               743 ------ATTCGAGAAAATTAAATGAATTTGCCAAAAGTGTAAAAGAGCACTATGCA 793
                                                                                                                                                                                                                                                                                  239 LeuvalAlaAlaArgAlaValGlyTyrTyrAspIleAspLeuSerIleIleArgAsnSer
                                                                                                                                                                                                                                                                                                                                                                                259 Ile-----GlyGluVal---AspValIleIleHisAspLeuGlyGluProValTyrIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         362 AGGATACAATCGATGAAAAACTTCTAATCGCAAGTTTATTATTCGGTACGACAACGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            386 LysArgGluLeuLeuGluGlnLeuLeuThrValAsnMetGlyGluAlaTyr-----
                                                                                                                                                                                                                                      467 GTTCAAGGTGACTTAGAACAACAAATCCGAGCAAGTTTACCT--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      439 GlnValSerPheGluGlnSerSerSerArgThrGluProAlaGlnValAsp-
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505 MetProAsp	334 VALALANGALAILELEUPROASPGIUSErGluAsnGluValileAspleu 550  11457 TTACGTCAGGAAATGCGCCAACAAGAAGGAACTTGGTATAATTCACAATTAGTTGAGTTA 1516  551 ProGluArghrAlaLeuAlaAsnArgLySThrPro 562  1517 GGAAAAATTCGCTTAGATCGTACAGGTTTCTCGAAACAGTCGAAATTGATTG	574 162 592 166	608 172 621 178	638 184 658	TACGATAACTCTAAAAGTGATACATCCTCTAACTAAAGCGTACGGAAGTAATThrasnGlyPheaspLeuSerThrargThr		707 AspLeuProValAspPheValAsnGlyLysProSerGlnGluAlaLeuLeuAlaGlyVal 726  [	
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	os os os	0y 0y 0b	0	Oy Oy			9y 9b 9	

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2273 GGAAACAAGGGTTTACGTTCTATCAAACTTATACAGGGGGTGGCATGGGTTCATTAGGT 2332
                                                                                111:::111:::
2333 GGTTTTGCTTATGGTAGTATTGGAGCAATTTATGCCGAATATGGTAATGGTAGT 2392
                                                                                                                                                     2393 GGTACTGGTACTTTTAAGAAGATAAGTTCTGAT-----GTGATTGGTGGTAATGCAATC 2446
                                                                                                                                                                                                                          111 ::: 111 2447 GCTACAGCTAGCGAGAGTTAATTGTGCCAACTCCATTTGTGAGCGATAAGGGCCAAAAT 2506
                                                                                                                                                                                                                                                                                                 2507 ACGGTCCGAACCTCCTTATTTGTTGATGCGGCAGTGTTTGGAATACTAAATGGAAATCA 2566
                                                                                                                                                                                                                                                                                                                                                                                    2567 GATAAAAATGGATTAGAGAGGGATGTATTAAAAAGATTGCCTGATTATGGCAAATCAAGC 2626
                                                                                                                                                                                                                                                                                                                                                                                                                                                 2687 TTCTCTTATGCCAAACCAATTAAAAATATGAAATGATGATGTCGAAGTTCCAATTT 2746
                                                   843 AlaValGlyThrAlaGlu-----TyrAsnTyrGluPheMetLysAsp------ 856
                                                                                                                                                                                                                                                                                                                                                 870 ------AspLysGlypheThrAsn 875
                                                                                                                                                                                                                                                                                                                                                                                                                        876 AspThrLysIleGlyAlaGlyValGlyValArgTrpAlaSerProValGlyGlnValArg 895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               913
                                                                                                                              896 ValAspValAlaThrGlyValLys-----GluGluGlyAsnProlleLysLenHisPhe
                                                                                                                                                                                                                                                                        857 ---LeuArgLeuAlaValPheGlyAspIleGlyAsnAlaTyr----------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/08942046
Patent No. 6564954
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: THOMAS, Wayne
APPLICANT: YANG, Yan Ping
APPLICANT: SIA, Dwo Yuan Charles
APPLICANT: KLEIN, Michel
TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPOTER: IDM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/942,046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6TH Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 12-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-732 MIS:jb
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLASSIFICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/433,522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2747 AGTATTGGAGGTTCTTTC 2764
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ZIP: MSG 1R7: COMPUTER REDABLE FORM:
MEDIUM TYPE: Flore:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Toronto
STATE: Ontario
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US-08-942-046-3
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LysValProArgLeuLysAlaLysPheTyrGlnSerSerGlnSerGlyGluThrSerAla 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                             IleThrGlnGluSerAlaMetAspLeuAsnGlySerIleProArgLeuArgGlnThrAla 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTCGTAAGTGGTCGATTCGATGATGTGAAAGCGCATCAAGAAGGCGATGTGCTTGTT 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AspLysAlaPheThrThrValAlaAspGluValProLeuLeuIleGlyAspValPheHis 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PheAspGlyArgTrpLeuAspArgSerValAspValIle-----LeuProAspAsn 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ThrAlaAspValSerLeuIleTyrAspThrGlyThrGlnTyrArgPheAspGluValVal 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||||
|TTC------AGGGGAACGAA---TCTGTTAGTAGCAGTACATTACAAGAA 952
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HisGlyLysTyrGluThrLysLysAsnLeuIleGluAsnAlaSerAlaGluHisGlyTyr 328
                                                                                                                                                                                                                                                                                                                                                        AGGATACAATCGAAGAAAAACTTCTAATCGCAAGTTTATTATTCGGTACGACAACGACT
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171
141
344
230
                                                                                                                                                                                                                                     Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                      US-09-914-168-2 (1-919) x US-08-942-046-3 (1-2984)
                                                                                                                                                                                                            Length:
Matches:
                                                                                                                                                                                                                                                                             Gaps:
                                                                  TYPE: nucleic acid
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                              2.07e-08
172.00
35.21%
19.30%
3.64%
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2984 base pairs
                                                                                                                                        CDS
374..2764
                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                      ; NAME/KEY;
; LOCATION:
US-08-942-046-3
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1456 1576 1663 GATTAT 1048 .049 TATTTAAATAATGGCTATGCCAAAGCACAAATTACTAAAACGGATGTTCAGCTAAATGAT 1108 ---AATGCAATTAAAGCAAAACTTGGAGAACGCGGTTACGGTAGCGCAACGGTAAATTCA 1336 TTACGTCAGGAAATGCGCCAACAAGAAGGAACTTGGTATAATTCACAATTAGTTGAGTTA 1516 1621 724 GCGGCAGTAAGTATAGCTGGTACGAAAATGATTATGGTACGAGTGTCAATTTGGGTTAT 1783 784 ACCGAGCCCTATTTTACTAAAGATGGTGTAAGTCTTGGTGGAAATGTTTTCTTTGAAAAC 1843 ||| ::: :: ::: ::: TACGATAACTCTAACTATAAGCGTACGACTTACGGAAGTAAT 1903 GTTACTTTAGGTTTCCCTGTAAATGAAATAACTCCTATTATGTAGGATTAGGTCATACC 1963 .964 TATAATAAAATTAGTAACTTTGCTCTAGAA------TATAACCGTAATTTATATATT 2014 592 608 TyrSerLeuArgTyrArgLeuAspLysLeuLysThrGlnAlaProProGluThrTrpGln 706 ThrValGluLeuThrAspGlyIle---LeuMetAspIleSerProIleGluPheSerAla TyrPheAsnMetValAsnThrGluIleValPheProGluArgGluGlnIleGlnAsnAsp GlnValSerPheGluGlnSerSerSerArgThrGluProAlaGlnValAsp-----GAAAAAAACAAAAGTTAATGTAACCATTGATGTAAATGAAGGTTTACAGTATGACCTTCGT -----GluSerThrLeuGluProValIleGlu SerAsnLeulleGlnAspLysLeuAsnLeuValAlaAlaLysAlaArgHisLeuTyrAsp MetProAsp.....AspArgValLeuAlaIleAsnHisAspAspGlyValAsn ArgSerIleLeu---------GlyArgIleSerAspAlaValSerAla CGACGTTTAACTGTTCGCCAACTTCGCTTTGAAGGAAATACCGTTTCTGCTGATAGCACT Pro------GluArgThr------AlaLeuAlaAsnArgLysThrPro 563 AlaAsp--------ValTyrGlnSerLysLysValProLeuTyr 575 ValPheValAlaSerAspLysProArgAspGlyGlnIle-----GlyLeuGlyTrpGly SerAspThrGlyThrArgLeuValThrLysPhe---GluHisAsnLeuIle-----622 SerGlu-----AspLysLysGlyValLysLeuTyrAlaThrLysProLeuSerHis ProLeuAsnAspGlnLeuArgAlaThrLeuGlyTyrGlnGlnGluValPhedlyHisSer ---ThrAsnGlyPheAspLeuSerThrArgThr------LeuGluHis--------GluIleSerArgSerIleIleGlnAsnGlyGlyTrpAsnArgThr-----ValAlaArgAlaIleLeuProAspGluSer-----GluAsnGluValIleAspLeu 1013 CAATTCGAGAAAGATTTGCAGTCAATTCGT :::::::= 1280 1109 1229 1397 1457 466 505 534 551 639 629 1904 419 439 457 485 521 593 609 672 687 δ g ò g δ Db δý g Qγ οg óγ q ò QΩ à g Qγ qq ò pp δy qq ò qq οy g ò qq οž q ò P ŏ QQ δ

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329 PheAspGlyArgTrpLeuAspArgSerValAspValI1e------LeuProAspAsn 345
 6TH Floor, 330 University Avenue
                                                                                                                                                                               омнек: US/08/433,522A
12-SEP-1995
                                                                                                                                                                                                                                                         ATTOKNETA MELLIA THE CHARLES

NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPAN: (416) 595-1155
TELEPAN: (416) 595-1163
INPORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 2987 base pairs
TYRE: NUCLEIC acid
STRANDENESS: SINGLE
                                                                                                       : Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 172.00
35.21%
19.30%
3.64%
                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                    : Ontario
RY: Canada
M5G 1R7
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                              FILING DATE: 1: CLASSIFICATION:
                    Toronto
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                                 STATE: OF COUNTRY:
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                                   707 AspLeuProValAspPheValAsnGlyLysProSerGlnGluAlaLeuLeuAlaGlyVal 726
                                                                                                                                                                                                                                               763 AlalleAlaArgAlaGlyIleSerGlyValTyrSerPheGlyAspAsnAlaTyrGlySer 782
                                                                                                                                                                                                                                                                                                                    783 AsnArgAlaHis-----GlnMetThrGlyGlyIleGlnAlaGlyTyrIleTrpSerAsp 800
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                                                                                                                                          -----AACTATAACAGCCTTAATAGAGGCTATTTCCCAACT
                                                                                                                                                                           747 TyrSerLeuGluValGlySerSerGlyLeuVal-----SerAspAlaAsnMet
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                                                                                                                                                                                                                                                                                 2174 TACAAACTAAGTGCAGATGTACAGGGTTTCTACCCATTA------
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2015 CAATCAATGAAATTTAAAGGTAATGGCATTAAAACAAAT-
                                                                    -----GACTTTGATTTTTCTTTTGGTTGG-----
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; Sequence 55, Application US/08433522A
; Patent No. 6013514
; GENERAL INFORMATION:
APPLICANT: CHONG, Pele
APPLICANT: THOMAS, Wayne
APPLICANT: YANO, Yan Ping
APPLICANT: LOOSMORE, Sheena
APPLICANT: SIA, DWO Yuan Charles
APPLICANT: KLEIN, Michel
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LysValProArgLeuLysAlaLysPheTyrGlnSerSerGlnSerGlyGluThrSerAla 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTGTTTGCCGCA------CCTTTTTGTGGCAAAAGATATTCGTGTGGATGGT 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239 LeuValAlaAlaArgAlaValGlyTyrTyrAspIleAspLeuSerIlelleArgAsnSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTTCGTGCCGGTCAGCGTGACAATGATGTG---GCTAATATTGTCCGCTCTTTA
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171
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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Matches:
Conservative:
Mismatches:
Indels:
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QQ	809	AGTGTAGGTCGCTAT AACGCAACAGTTGAACCTATTGTCAATACGCTACCAAATAAT	865
ογ	346	ThrAlaAspValSerLeuIleTyrAspThrGlyThrGlnTyrArgPheAspGluValVal	365
qq	998	CGCGCTGAAATTTTAATTCAAATCAATGAAGATGATAAAGCAAAATTGGCATCATTAACT	925
٥y	366	heThrIleAspPr	385
Dp	926	TTCAAGGGGAACGAATCTGTTAGTAGCAGTACATTACAAGAA	296
ò i		LysArgGluLeuLeuGluGlnLeuLeuThrValAsnMetGlyGluAlaTyr	402
a		CAAATGGAATTACAACCTGATTCTTGGTGGAAATTATGGGGAAATAAAT	1027
yo 4			418
3 8	1070	### CANTICUAGAAAGATITGCAGICAATITGTGATTAT #################################	1063
6 G		TATTTAAATAATGCCTATGCCAAAGCACAAATTACTAAAAAGGGATGTTCAGCTAAATGAT TATTTAAATAATGGCTATGCCAAAGCACAAATTACTAAAAAGGGATGTTCAGCTAAATGAT	1123
οy	439 (	GlnValSerPheGluGlnSerSerSerArgThrGluProAlaGlnValAsp	456
QQ	1124 (		1183
οy	457	GluSerThrLeuGluProValIleGlu	465
Dp	1184	AGTGCACGCATTATAGGTAATCTGGGAGGTATGTCTGCCGAGGTTGAACCTTTACTTCA	1243
ογ	466	ThrValGluLeuThrAspGlyIleLeuMetAspIleSerProIleGluPheSerAla	484
QQ	1244 (	GCATTACATTTAAATGATACTTTCCGCCGTAGTGATATTGCAGATGTAGAA	1294
δy	485	SerAsnLeuIleGlnAspLysLeuAsnLeuValAlaAlaLysAlaArgHisLeuTyrAsp	504
qq	1295	AATGCAATTAAAGCAAAACTTGGAGAACGCGGTTACGGTAGCGCAACGGTAAATTCA	1351
ογ	202	MetProAspAspArgValLeuAlaIleAsnHisAspAspGlyValAsn	520
qq	1352 (	GTACCTGATTTTGATGATGCAAATAAAACATTAGCGATAACCCTTGTTGTTGATGCTGGA	1411
Οÿ	521	ArgSerIleLeu	533
ДQ	1412 (	CGACGTTTAACTGTTCGCCAACTTCGCTTTGAAGGAAATACCGTTTCTGCTGATAGCACT	1471
Οy	534	ValAlaArgAlaIleLeuProAspGluSerGluAsnGluValIleAspLeu	550
Dp	1472	TTACGTCAGGAAATGCGCCAACAAGAAGGAACTTGGTATAATTCACAATTAGTTGAGTTA	1531
ολ	551	ProGluargThrAlaLeuAlaAsnArgLysThrPro	562
qq	1532	GGAAAAATTCGCTTAGATCGTACAGGTTTCTTCGAAACAGTCGAAAACCGAATTGATCCT	1591
Οy	563	AlaAspyalTyrGlnSerLysLysValProLeuTyr	574
Dp	1592	ATCAATGGTAGTAGTGATGATGTCGTATATAAAGTCAAA	1636
οy	575	ValPheValAlaSerAspLysProArgAspGlyGlnIleGlyLeuGlyTrpGly	592
QQ	1637	-:	1678
δλ	593	SerAspThrGlyThrArgLeuValThrLysPheGluHisAsnLeuIle	809
qa	1679	ACAGAGAGTGGTATTAGTTATCAAGCAAGTGTTAAACAAGATAATTTCTTGGGAACAGG	1738
δy	609	AsnArgAspGlyTyrGlnAlaGlyAlaGluLeuArgLeu	621
QQ	1739	GCGGCAGTAAGTATAGCTGGTACGAAAAATGATTATGGTACGAGTGTCAATTTGGGTTAT	1798
ογ	622	SerGluAspLysLysGlyValLysLeuTyrAlaThrLysProLeuSerHis	638
qq	1799		1858

2068 TACGATAACTCTAAAAGTGATACATCCTCTAACTATAAGCGTACGACTTACGGAAGTAAT 1918 GITACTITAGGITICCCTGTAAATGAAATAACTCCTATIATGTAGGATTAGGTCATACC 1978 2092 ::::::

AAAGGGGTTAAAGCAAGTCTTGGTGGACGAGTTACTATTCCAGGTTCTGATAACAAATAC 2188 2227 2407 2521 TATAATAAAATTAGTAACTTTGCTCTAGAA------TATAACCGTAATTTATATT 2029 GGTACTGGTACTTTTAAGAAGATAAGTTCTGAT-----GTGATTGGTGGTAATGCAATC 2461 GATAAAAATGGATTAGAGAGCGATGTATTAAAAAGATTGCCTGATTATGGCAAATCAAGC 2641 2642 CGTATTCGCGCCTCTACAGGTGTCGGATTCCAATGGCAATCTCCTATTGGGCCATTGGTA 2701 TTCTCTTATGCCAAACCAATTAAAAATATGAAAATGATGTGGAACAGTTCCAATTT 2761 892 842 875 913 671 TyrSerLeuArgTyrArgLeuAspLysLeuLysThrGlnAlaProProGluThrTrpGln 706 AlaValHisLysThrValAlaAspAsnLeuValAsnProMetArgGlyTyrArgGlnArg 746 747 TyrSerLeuGluValGlySerSerGlyLeuVal------SerAspAlaAsnMet 762 AlalleAlaArgAlaGlyIleSerGlyValTyrSerPheGlyAspAsnAlaTyrGlySer 782 AsnArgAlaHis-----GlnMetThrGlyGlyIleGlnAlaGlyTyrIleTrpSerAsp 800 829 ||||::||||:: |||||: |GGTTTTGCTTATGGTAGTATTGGACCTAACGCAATTTATGCCGAATATGGTAATGGTAGT ------IleSerAspLysGlyTyrLeuThrGlyGlyGlydlLeu AspThrLyslleGlyAlaGlyValGlyValArgTrpAlaSerProValGlyGlnValArg ProLeuAsnAspGlnLeuArgAlaThrLeuGlyTyrGlnGlnGluValPheGlyHisSer --AspLysGlyPheThrAsn ValAspValAlaThrGlyValLys-----GluGluGlyAsnProIleLysLeuHisPhe ---ThrAsnGlyPheAspLeuSerThrArgThr------LeuGluHis---AlaValGlyThrAlaGlu-----TyrAsnTyrGluPheMetLysAsp---------LeuArgLeuAlaValPheGlyAspIleGlyAsnAlaTyr------AspLeuProValAspPheValAsnGlyLysProSerGlnGluAlaLeuLeuAlaGlyVal -----GACTTTGATTTTCTTTTGGTTGG------------AACTATAACAGCCTTAATAGAGGCTATTTCCCAACT -----GluIleSerArgSerIleIleGlnAsnGlyGlyTrpAsnArgThr----TACAAACTAAGTGCAGATGTACAGGGTTTCTACCCATTA------CAATCAATGAAATTTAAAGGTAATGGCATTAAAACAAAT-----GlyTyrAlaHisAspSerLeuSerPro------111111 2762 AGTATTGGAGGTTCTTTC 2779 PhelleGlyThrProPhe 919 1859 1979 2030 2228 2348 2408 2522 2582 1919 2129 2288 843 639 672 2069 727 2093 292 2189 783 801 821 830 2462 857 870 629 707 Dp QY Db Qy Db Qy Db 0y 0y 0b Qy Db οy Oy Ob QY Db QY Db Oy Db QQ οy QQ Ω Ω Qγ qq οy q ò qq ολ

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179 LysValProArgLeuLysAlaLysPheTyrGlnSerGlnSerGlyGluThrSerAla 198
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           Sequence 55, Application US/09135166
Patent No. 6083743
GENERAL INFORMATION:
APPLICANT: THOMAS, Wayne
APPLICANT: THOMAS, Wayne
APPLICANT: YANG, Yan Ping
APPLICANT: SIA, Dwo Yuan Charles
APPLICANT: KLEIN, Michel
TILLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2987
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/135,166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
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NAME: STEWART, Michael I
REGISTATION NUMBER: 24,938
REGISTATION NUMBER: 1038-829 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1155
SEQUENCE CHARACTERISTICS:
LENGTH: 2987 base pairs
STRANBDNESS: Single
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6TH Floor, 330 University Avenue
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APPLICATION NUMBER: 08/433,522
FILING DATE: 12-SEP-1995
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COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disopper.
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35.21%
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                           Toronto
                                                                                                                                                                                                           ADDRESSEE:
US-09-135-166-55
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US-09-135-166-55
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Ile-----GlyGluVal---ASpValIleIleHisAspLeuGlyGluProValTyrIle 275
                                   581 TTCGTAAGTGGTTCGATGATGTGAAAGCGCATCAAGAAGGCGATGTGTTGTT 640
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                                                                                                              641 AGCGTTGTGGCTAAATCGATCATTTCAGATGTTAAAATCAAAGGTAACTCTGTTATTCCC 700
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                                                                                                                                                                                                           757
                                                                                                                                                                                                                                  309 HisGlyLysTyrGluThrLysLysAsnLeuIleGluAsnAlaSerAlaGluHisGlyTyr 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1124 GAAAAAACAAAAGTTAATGTAACCATTGATGTAAATGAAGGTTTACAGTATGACCTTCGT 1183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1184 AGTGCACGCATTATAGGTAATCTGGGAGGTATGTCTGCCGAGCTTGAACCTTTACTTTCA 1243
                                                                                                                                                                                                                                                                                                                                                                                                                               866 CGCGCTGAAATTTTAATTCAAATCAATGAAGATGATAAAGCAAAATTGGCATCATTAACT 925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    366 PhePheThrileAspProLysThrAsnGlnLeuThrThrAspProAspLysLeuProVal 385
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1352 GTACCTGATTTTGATGATGCAAATAAAGATTAGCGATAACCCTTGTTGTTGATGCTGGA 1411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1295 ---AATGCAATTAAAGCAAAACTTGGAGAACGCGGTTACGGTAGGGCAACGGTAAATTCA 1351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           466 ThrValGluLeuThrAspGly1le----LeuMetAspIleSerProlleGluPheSerAla 484
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                                                                                                                                                     289 AspLysAlaPheThrThrValAlaAspGluValProLeuLeuIleGlyAspValPheHis
                                                                                   ValGluValArgGlyGluGlyAla---Asp
                                                                                                                                                                                          701 ACTGAAGCACTTAAAACATAAGATGCTAACGGGTTTAAAGTTGGCGATGTTTAA---
                                                                                                                                                                                                                                                                                                               329 PheAspGlyArgTrpLeuAspArgSerValAspVallle------LeuProAspAsn
                                                                                                                                                                                                                                                                         ------ATTCGAGAAAATTAAATGAATTTGCCAAAAGTGTAAAAGAGCACTATGCA
                                                                                                                                                                                                                                                                                                                                                  809 AGTGTAGGTCGCTAT---AACGCAACATTGAACCTATTGTCAATACGCTACCAAATAAT
                                                                                                                                                                                                                                                                                                                                                                                         {\tt ThrAlaAspValSerLeuIleTyrAspThrGlyThrGlnTyrArgPheAspGluValVal} \\
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 439 GlnValSerPheGluGlnSerSerSerArgThrGluProAlaGlnValAsp-----
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Db 2522 ACGGTCCGAACCTCCTTATTGTTGATGCGGCAAGTGTTTGGAATACTAAATGGAAATCA 2581 Ov 870	2582 GATAAAAATGGATTAGAGAGCGATGTATTAAAAAGATTGCCTGATTATGGCAAATCAAGC	Oy 876 AspThrLysIleGlyAlaGlyValGryValArgTrpAlaSerProValGlyGlnValArg 895 :::	Qy 896 ValaspValalaThrGlyValLysGluGluGlyAsnProlleLysLeuHisPhe 913	Oy 914 PheileGlyThrProPhe 919  Db 2762 AGTATTGGAGGTTCTTC 2779	RESULT 18 US-08-942-046-55 ; Sequence 55, Application US/08942046 ; Patent No. 6264954	GENERAL IFCKMATION:  APPLICANT: CHOMS, Wayne  APPLICANT: THOMAS, Wayne  APPLICANT: YANG, Yan Ping	APPLICANT: DOCUMER, Sheena ; APPLICANT: RISIN, Michel ; APPLICANT: KLEIN, Michel ; TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN	) NUMBER OF SEQUENCES: 55 ; CORRESCONDENCE ADDRESS: ; ADDRESSEE: Sim & McBurney ; STREET: 6TH Floor, 330 University Avenue	: CITY: TOYONLO ; STATE: Ontario ; COUNTRY: Canada ; ZIP: M5G 1R7	ADABLE FORM: PE: Floppy disk IBM PC compatible SYSTEM: PC-DOS/MS-DOS	SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/942,046 ; FILING DATE:	2 H C	CLASSIFICATION: 435 ; ATTORNEY-AGENT INFORMATION: ; NAME: STEWART, Michael I ; REGISTRATION NUMBER: 24,973	TELECOMMUNICATION: TELECOMMUNICATION: TELEPHONE: (416) 595-1163	; INFORMATION FOR SEQ ID NO: 55: ; SEQUENCE CHARACTERISTICS: ; LENGTH: 2987 base pairs ; TYPE: nucleic acid	STRANDENESS: SINGLE; TOPOLOGY: Linear US-08-942-046-55	Alignment Scores: 2.08e-08 Length: 2987  Pred. No.: 172.00 Matches: 171  Percent Similarity: 35.21% Conservative: 141  Best Local Similarity: 19.30% Mismatches: 344  Query Match: 3.64% Indels: 230	
Qy 563 AlaAspValTyrGlnSerLysLysValProLeuTyr 574 ::: Db 1592 ATCAATGTAATGATGAGGGATGTCGTATATAAAGTCAAA	Qy 575 ValPheValAlaSerAspLysProArgAspGlyGlnIleGlyLeuGlyTrpGly 592 ::::	Qy 593 SeraspThrGlyThrargLeuValThrLysPheGluHisasnLeuIle 608 ::::    ::     Db 1679 ACAGAGAGAGAATAATAACAAAGAAAATATCTTGGGAACAGGG 1738	609AsnArgAspGlyTyrGlnAlaGlyAlaGluLeuArgLeu   1739 GCGCCAGTAAATAGAAAAAAAAAAAAAAAAAAAAAAAAA	622 SerGluAspLysLysGlyValLysLeuTyrAlaThrLysProLeuSerHis :::	Oy 639 ProLeuAsnAspGlnLeuArgAlaThrLeuGlyTyrGlnGlnGluValPheGlyHisSer 658	Oy 659ThrasnGlyPheAspLeuSerThrargThr	Qy 672GluileSerArgSerIleileGlnAsnGlyGlyTrpAsnArgThr 686 	Qy 687 TyrSerLeuargTyrargLeuaspLysLeuLysThrGlnalaProProGluThrTrpGln 706	Qy 707 AspLeuProValAspPheValAsnGlyLysProSerGlnGluAlaLeuLeuAlaGlyVal 726	Oy 727 AlaValHisLysThrValAlaAspAsnLeuValAsnProMetArgGlyTyrArgGlnArg 746	Oy 747 TyrSerLeuGluValGlySerSerGlyLeuValSerAspalaAsnMet 762 :::::	Qy 763 AlaIleAlaArgAlaGlyIleSerGlyValTyrSerPheGlyAspAsnAlaTyrGlySer 782	Qy 783 AsnargalaHisGlnMetThrGlyGlyIleGlnAlaGlyTyrIleTrpSerAsp 800 :::	Oy 801 AsnPheasnHisValProTyrArgLeuArgPhePheAlaGlyGlyaspGlnSerIleArg 820 :::	Qy 821 GlyTyralaHisaspSerLeuSerPro	Qy 830	OY 843 AlaValGlyThrAlaGluTyrAsnTyrGluPheMetLysAsp	

DB:			4	Gaps:	44	
us-0	9-914	-168-2 (1-919)	x US-08-942-046	6-55 (1-2987)		
Q D	377		uLysalaLysPheT) :     SaaaaaaCTTCTaa1	rGlnSerSerGlnSe      cGCAAGTTTATTATT	LysValProArgLeuLysAlaLysPheTyrGlnSerSerGlnSerGlyGluThrSerAla ::::: :::	198 436
Oy Dp	199		sGlnLysThrGluPr     CC	OTyrAlaAsnIleLy  ::: :TTTTGTGGCAAAAGA	IleGlySerSerHisGlnLysThrGluProTyrAlaAsnIleLysAlaAlaLeuGluAsp	218 481
à d	219		rAlaMetAspLeuAs	inGlySerIleProAr	IleThrGlnGluSeralaMetAspLeuAsnGlySerIleProArgLeuArgGlnThrAla :::	238
à	239		ahlaValGlvTvrTv	raccaagrinacer raspileaspleuse	TT DT DAY OB SERVER	523 258
, q <sub>0</sub>	524		SCGTGTGACTGACAA	TGATGTGGCTAA	GTTCGTGCCGGTCACCGTGTGACTGACATGATGTGGCTAATATTGTCCGCTCTTTA	വയ
Oy Op	259		JValAspvalil        \TTCGATGATGTGAA	elleHisAspLeuGl	IleGlyGluValAspValllelleHisAspLeuGlyGluProValTyrIle	275 640
λά	276			-ValGluValArgGl		288
q	641		<b>ATCGATCATTTCAGA</b>	TGTTAAAATCAAAGG	O	700
à é	289		ThrValAlaAspGl	AspLysAlaPheThrThrValAlaAspGluValProLeuLeuIleGlyAspValPheHi. :::   AFFCARCEAGE ASSASSORMED OF THE STATE AFFCARCE  ro.	308	
3 ,	101		CAAAACTTAGATGC	TAACGGGTTTAAAGT		757
<u> </u>	309		ThrLysLysAsnLe      GAAAATTAAATGA	uIleGluAsnAlaSe: ::: ATTTGCCAAAAGTGT/	HisGlyLysTyrGluThrLysLysAsnLeuIleGluAsnAlaSerAlaGluHisGlyTyr ::	328 808
à	329		LeuAspArgSerVa	lAspvalIle	PheAspGlyArgTrpLeuAspArgSerValAspValIleLeuPrOAspAsn	345
g G	808		AACGCAACAGT	TGAACCTATTGTCAA		865
2y 2b	346 866		LeuIleTyrAspTh ::: ATTCAAATCAATGA	rGlyThrGlnTyrArg ::: aGATGATAAAGCAAA	ThralaAspValSerLeuIleTyrAspThrGlyThrGlnTyrArgPheAspGluValVal :	365 925
λ	366	PhePheThrIleAsp	ProLysThrAsnGl	nLeuThrThrAspPro		385
ą	926	   TC	:: AAGGGGAACGA	: ::: ATCTGTTAGTAGO		1967
λč	386	LysArgGluLeuLeu	GluGlnLeuLeuTh	rValAsnMetGlyGlu 	LysArgGluLeuLeuGluGlnLeuLeuThrValAsnMetGlyGluAlaTyr (	402
ð	968	CAAATGGAATTACAA	CCTGATTCTTGGTG	SAAATTATGGGGAAAI		1027
λ̈	403	Asn	LeuGlnAlaValAr	gAlaLeuSerAsnAsp 		418
ą	1028	CAATTCGAGAAAGAT	TTGCAGTCAATTCG			1063
Ϋ́	419	TyrPheAsnMetVal	AsnThrGluIleVa	lPheProGluArgGlu		438
q	1064	TATTTAAATAATGGC	TATGCCAAAGCACA	AATTACTAAAACGGAT		1123
<i>≿</i>	439	GlnValSerPheGlu	GlnSerSerSerse:	rArgThrGluProAla   †		456
ą	1124	GAAAAACAAAGTT	AATGTAACCATTGA	rgtaaatgaaggttta		1183
Δi	457			GluSerThrLeu	GluSerThrLeuGluProValIleGlu 4	465
ą	1184	AGTGCACGCATTATA	GGTAATCTGGGAGG	PATGTCTGCCGAGCTT		1243
<u>⊼</u>	466	ThrValGluLeuThr	AspGlyIleLeu	MetAspileSerPro	ThrValGluLeuThrAspGlyIleLeuMetAspIleSerProIleGluPheSerAla 4	484
ð	1244	GCATTACATTTAAAT	GATACTTTCCGCCG1	GCATTACATTAAATGATACTTTCCGCCGTAGTGATATTGCAGATGTAGAA.		1294
Ϋ́	485	SerAsnLeulleGln	AspLysLeuAsnLeu	ıValAlaAlaLysAla	SerAsnLeuIleGlnAspLysLeuAsnLeuValAlaAlaLysAlaArgHisLeuTyrAsp 5	504

qa	1295AATGCAATT	
Qy	505 MetProAsp	AspargValLeuAlaIleAsnHisAspAspClyValAsn 520
QQ	1352 GTACCTGATTTGAT	ATAAAACATTAGCGATAACCCTTGTTGTTGATGCTGGA 1411
QΥ	521 ArgS	erileLeu
qq	1412 CGAC	TTCGCTTTGAAGGAAATACCGTTTCTGCTGATAGCACT 1471
Oy	Oy 534 ValAlaArgAlalleLeuProAspGluSer	spGluSerGluAsnGluValIleAspLeu 550
οp	1472	AAGAAGGAACTTGGTATAATTCACAATTAGTTGGTTA 1531
Qy	551	ProGluArgThrAlaLeuAlaAsnArgLysThrPro 562
qo	1532	CAGGTTTCTTCGAAACAGTCGAAACCGAATTGATCCT 1591
Οy	563 Ala	ValTyrGlnSerLysLysValProLeuTyr 574
a	Db 1592 ATCAATGGTAGTAATGATGAAGT	TGGATGTCGTATATAAAGTCAAA1636
Οy	575 ValPheValAlaSerAs	roArgAspGlyGlnIleGlyLeuGlyTrpGly 592
qq	1637	::: -GAACGTAACACGGGTAGTATCAACTTTGGTATTGGTTACGGT 1678
Οy	593 SerAspThrGlyThrArg	LeuValThrLysPheGluHisAsnLeuIle 608
ΩP	1679 ACAGAGAGTGGTATTAGTT	ATCAAGCAAGTGTTAAACAAGATAATTTCTTGGGAACAGGG 1738
οy	609	snArgAspGlyTyrGlnAlaGlyAlaGluLeuArgLeu 621
QQ	1739 GCGCCAGTAAGTATAGCTGGT	
QY	2y 622 SerGluAspLysLys	SlyValLysLeuTyrAlaThrLysProLeu
QQ	1799	ATGGTGTAAGTCTTGGTGGAAATGTTTTCTTTGAAAAC 1858
Qy	639 р	roLeuAspGlnLeuArgAlaThrLeuGlyTyrGlnGlnGluValPheGlyHisSer 658
qq	1859 T	CATCCTCTAACTATAAGCGTACGACTTACGGAAGTAAT 1918
δλ	2y 659ThrAsnGlyPheAspLeuSerThrArgThr	1
qq	1919 GTT	TITE THE STANDARD STA
Óγ	672GlulleSer	ArgSerIleIleGlnAsnGlyGlyTrpAsnArgThr 686
QΩ	1979 TATAATAAATTAGT	CTCTAGAATATAACCGTAATTTATATATT 2029
Óλ	687 Tyrser	AlaPr
qq	2030 CAATCA	ATGAAATTTAAAGGTAATGGCATTAAAACAAAT2068
Qy	707 AspLeuP	ProSerGlnGluAlaLeul
QQ	b 2069GACTTTGATTTTTTTTTTGGTTGG	TTGGTTGG 2092
Qy	727 AlavalHisLysThrValAlaA	spasnLeuValAsnProMetArgGlyTyrArgGlnArg 746
QQ	2093	AACTATAACAGCCTTAATAGAGGCTATTTCCCAACT 2128
Qy	747 TyrSerLeuGluValGlySerS	rGlyLeuValSerAspAlaAsnMet 762
qq	2129 AAAGGGGTTAAAGCAAGTCTTG	GTGGACGAGTTACTATTCCAGGTTCTGATAACAAATAC 2188
Qy	763 AlaileAlaArgAlaGly	IleSerGlyValTyrSerPheGlyAspAsnAlaTyrGlySer 782
qq	2189 TACAAACTAAGTGCAGAT	T'A
δλ	783 AsnArgAlaHis	GlnMetThrGlyGlyIleGlnAlaGlyTyrIleTrpSerAsp 800

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Tue May

996 549 609 610 CAGCTCGCCTTTGCCCAGGCCCTGACCTATAATACCTCGACCCGCATGGAAGGCCTGACC 669 85 ------AspValValAsnPheAspAspGlnSerProIle---SerArgIleGlyGlu 100 729 119 789 120 LeuGluGluLeuPheAlaGlnGluSerThrGluMetGlyIleAsnProAsnAspTyrIle 139 140 ProGluTyrGlnGlyGluGlnProAsnSerGluValValValProProThrLeuGluPro 159 864 160 GluLysProGlyLeuIleLysArgLeuTyrAlaArgLeuPheAsnAspGlyValAsnLys 179 180 ValProArgLeuLysAlaLysPheTyrGlnSerSerGlnSerGlyGluThrSerAlaIle 199 889 -------GCAGGTTACCAGCAGCTTAACGGGGCCGTCTTGCCGCAGCC 930 200 GlySerSerHisGlnLysThrGluProTyrAlaAsnIleLysAlaAlaLeuGluAspIle 219 220 ThrGlnGluSerAlaMetAspLeuAsnGlySerIleProArgLeuArgGlnThrAlaLeu 239 68 84 670 CGGCTCAAGGATCTCCCAGTCCTTCCGCAGGCCCCCGGTCGAGGCGCCGCCGCGGCG 69 ArgLeu-----AsnAlaAlaGlyLeuAsnAlaLysProGlnSerGlnAlaLeu---GlnSerProProLeuGlyLeuAsp---MetSerVallleGluGluThrThrProLeuSer 820 ------ACGCGCTGCGCGAGCATATGCTCCACCCCCCGGTGGTCCGCCG AsnGlnAlaLysAlaGlyAsnProProValLeuLeuThr---ProGluGlnIleGlnAla 931 GAGCAGTCTTTCCAG-------3957 201 131 360 357 51 -----TCGGCGTTGCAGATCAATTCC------Matches: Conservative: Mismatches: Indels: US-09-914-168-2 (1-919) x US-07-689-008-5 (1-3957) Length: 865 GACAAGGCCGGGCTTGCGCGCCAG-----US 496,236 NAME: Murphy, Lisabeth Feix REGISTRATION NUMBER: 31547 TELECOMMUNICATION: TELEPHONE: (415) 393-2000 TELEFAX: (415) 393-2286 TELEFAX: 340817 MACPAG SFO INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: 790 GAGCAGIGGCTTTCCGCC-----TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) ProAlaHisAspThrAlaIle---APPLICATION NUMBER: US 49 FILING DATE: 23-MAR-1990 ATTORNEY/AGENT INFORMATION: 8.13e-07 159.50 31.65% 19.16% LENGTH: 3957 base pairs TYPE: NUCLEIC ACID STRANDEDNESS: single PRIOR APPLICATION DATA: Percent Similarity: Best Local Similarity: Alignment Scores: US-07-689-008-5 Query Match: Pred. No.: 946 43 20 101 Score: ò g ολ q ò 엄 ò d ò g δy qq Q g à g à qq δ qq δ q

ValAlaAlaArgAlaValGlyTyrTyrAspIleAspLeuSerIleIleArgAsnSerIle 259 :::            	GlyGluvalAspvalIleIleHisAspLeuGlyGluProvalTyrIleAspTyrArgAla 279     ::: :::      GGTGGCATGGGGCTCGTAAGCATGCGCGAGGGGATACCGCGGAGGCGCGCGCGC 1038	ValGluValArgGlyGluGlyAlaAspAspLysAlaPheThrThrValAlaAspGluVal 299 	319		GluAsnAlaSerAlaGluHisGlyTyrPheAspGlyArgTrp333		LeuAspArgServal 338	CCAGCCCGGCCAGTATACTGGCGCGACCCTCATGCTGGCCGACCTGCAGCGCTCGACCTVGACC		1 m	CAGTIGGCCCICAIGGGGCIGGCCGGGGIAGACAIGGCGCAGGGCAACACGGGGGAAGCA 1374	SerLeulleTyrAspThrGlyThrGlnTyrArgPheAspGluValValPhe 366	CGCCAGCTCCTGTCGCCGCTGTCGCCCCCCCATATGCAAGCCAGGTGGGCGAGATCGAGGTT 1434	PheThrIleAspProLysThrAsnGlnLeuThrThrAspProAspLysLeuProValLys 386	rgggcctgatggcggctgcgtcccagacatcggattcacggcgcagggttccatcctg 1494	ArgGluLeuLeuGluGlnLeuLeuThrValAsnMetGlyGluAla 401	GCGAAGCGATGGCCCCAACGTGACCCCTGGGTGCGCATCAACCTTGCCAATGCG 1554	>-	TGCAGCAGGAGGACGTGGCCGAAGCCGGGGGGGGGGGGG	SerAsnAsp 413		LeulleAlaThrArgTyrPheAsnMetValAsnThrGluIleValPheProGluArgGlu 433	GCGATGACCCGCCAGCTTCTGGCTGGTCTGTCGCGGATTATTCTCCTGCCATCCGT 1734	GInIleGinAsnAspCinValSerPheGluGinSerSerSerArgThrGluProAla 453	CCATCGCCGAGGAAATGGAAATCAAGCAGGATCTGGCCAGCCGCCTGTCCATGGTG 1791	<pre>lnValAspGluSerThrLeuGluProValIleGluThrValGluLeuThrAspGlyIle 473 :::</pre>	TCCAACCCGGTGCCGCTGATCCGCGGGGCCCTGACCCAGCCTGATCCGACCGGCGCGCGC	euMetAsplleSerProlleGluPheSerAlaSerAsnLeulleGlnAspLysLeuAsn 493	GGCGTGGCGGTGACCTGTTCCGCCAGCGTGGCATGGTGCTTGCCCGCATGGCA 1911	LeuValAlaAlaLysAlaArgHisLeuTyrAspMetProAspAspArgVal 510	TECGTATCGCCTCGACGCGCACCATCGATCGACCCGACCACCAGCGCCTGTCCTATGCC 1971	LeuAlaIleAsnHisAspAspGlyValAsnArgSerIleLeuGlyArgIle 527
a]						1			_									Τy	C.		SCCG	LeuI	GCGA	GlnI	TCCA	GlnVä	TCCA	LeuMe	GGCG	LeuV	CTGC	
24(	260	280	300	1087	320	1147	334	339	<b>S</b>	342	1315	350	1375	36	1435	387	1495	402	1555	411	1615	414	1675	m r	າ ເ	LÓ.	1792	474	1852	494	1912	511
S G	ç q	Qy Dp	Οy	QQ	οy	QQ	δ	g ò	· 6	οy	qq	ογ	qq	δλ	QQ	οy	QQ	٠ ٥٧	q	οy	QQ	Οy	qq	λo d	a ,	λ	g	δy	qa	δλ	QΩ	δ,,

Dp	1972 AC	ACCGAATACATGAAGATCAGCAGGTGGCCGCTGCGGGGCTGCTGGCCCGGTG	2028
οy	528 Se	rAspAlaValSerAlaValAlaArgAlaIleLeuProAspGluSerGlu	544
qq	2029 GG		2088
QY	545	AsnGluValIleAspLeuProGluArgThrAlaLeuAlaAsnArgLysThr	561
QQ	2089 CA	()	21.48
Qy	562 Pr	m	581
qq		GCCTATGATCATCTGGCCCCCGGGGCTGCAGCCGAGCCG	2208
ΟŻ	O	AspGlyGlnIleGlyLeuGlyTrpGly	592
qq	2209 CC	GOGCTCGCGCGCTGTATATGGCCACGCAAGCCGGGCAAGCCGCTCGAG	2268
Qy	593 Se.	ThrArgLeuValThrLysPheGluHisAsnLeulleAsnArgAspGly	612
QQ	2269 AT	.::	2313
οy	613 TY	nerstr	630
QQ	2314 CG	AGCCTTGCCAC@CGCCTT	2373
δγ	Н	TyralaThrLysProLeuSerHisProLeuAsnAspGlnLeuArgAlaThrLeuGlyTyr (	650
Dp	2374 GC(	GTGCCTGGCTGCCATGGCCGTG	2433
Qy	651 Glr	erThrAsnGlyPheAspLeuSerThrArgThrLeuGlu	0.29
QQ	2434 GCT	GACCAGGCCGATGGCCACGGCCAGCGCAGCGCA	2472
Οy	671 His	ص ص	069
Db	2473	TITECGCCCCTATGACCTGCGC	2499
Οy	691 Tyr	Leu	695
QQ	2500 CTG	: : AGCAGGTCGAGGCACGCGGGCCGCGTCTGGCGGGGGGGTGCTGCG	2559
Οy	696 Leu	rGlnAlaProGluThr	202
qq	2560 CTT	GCTCCGCCCTCGACCCGTTCCGCCCGCGTGGCTACGCCACC	2610
Qy	706 Gln	'alAspPheValAsnGlyLy	721
qq	2611 ACG	::    AACTTGGCGCGCCTGTGACCGGTGGCTCCTACAGCGCGAGGCGGCATCGCCCGAT_2	0297
Qy	722	LeuLeuAlaGlyValAlaValHisLysThrValAlaAspAsn	36
QQ	2671 ACG	GTCGGACCAGATGCTCTCCTCCATCGCAGGCCAGATCCGCAGCTGAGAACCTT 2	1730
Οy	737	ValAsnProMetArgGlyTyrArgGlnArgTyrSerLeuGluValGlySer 7	53
qq	2731 GCC	GGTGAGCATGGC 2	2784
δλ	754 Ser	7	89,
qq	2785 ATG	AAGCGAACATTCCCATCGTGGCCGCCTGCCGCTGCACGCTCGT 2	844
Οy	69	ValTyrSerPheGlyAspAsnAlaTyrGlySerAsnArgAlaHisGlnMet 7	88
qq	2845 GCT	CTG 2	928
δλ	789 Thr	hrGlyGlyIleGlnAlaGlyTyrIleTrpSerAspAsnPheAsn	03
qq	- <b>X</b>	ACGGGTTCCGTCTAT 2	916
δy	804 His	ValProTyrArgLeuArgPhePheAlaGlyGlyAspGlnSerIleArgGlyTyr 8:	22

AlaHisAspSerLeuSerProlleSerAspLysGlyTyrLeuThrGlyGly 839
  -  TATACCAACGCGCAGGACCAG 2997
GlnValLeuAlaValGlyThrAlaGluTyrAsnTyrGluPheMetLysAspLeuArgLeu 859     :::                  CAGGGATGGCGGTGGCAGGCGGAG
AlavalPheGlyAspIleGlyAsnAlaTyrAspLysGlyPheThrAsnAspThrLysIle 879 
-AlaGlyValGlyValArgTrpAlaSerProValGlyGlnVal 894 
2.5
Benziman, Moshe VENTION: METHODS AND NUCLEIC ACID SEQUENCES FOR THE
HASE OPERON

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554 GACCAGGCCCGCGCGCGTTGCCGGGGTCGTTGCGTCAAACCCGCAGGATTACCGCGCC 5613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               824 -----ACCGCGCTGCGCGAGCATATGCTCCACCCCCCCGGTGGTCCGCCG 5868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1893 ------GCAGGTTACCAGCTTAACGGGGGCGGCCGTCTTGCCGCAGCC 5934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9971 -------TCGCTT 5988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   200 GlySerSerHisGlnLysThrGluProTyrAlaAsnIleLysAlaAlaLeuGluAspIle 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              260 GlyGluValAspValIleIleHisAspLeuGlyGluProValTyrIleAspTyrArgAla 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         280 ValGluValArgGlyGluGlyAlaAspAspLysAlaPheThrThrValAlaAspGluVal 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 GlnSerProProLeuGlyLeuAsp---MetSerValIleGluGluThrThrProLeuSer 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 LeuGluGluLeuPheAlaGlnGluSerThrGluMetGlyIleAsnProAsnAspTyrIle 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 ProGluTyrGlnGlyGluGlnProAsnSerGluValValValProProThrLeuGluPro 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          160 GluLysProGlyLeuIleLysArgLeuTyrAlaArgLeuPheAsnAspGlyValAsnLys 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 ValProArgLeuLysAlaLysPheTyrGlnSerSerGlnSerGlyGluThrSerAlaIle 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240 ValalaalaargalavalGlyTyrTyrAspIleAspLeuSerIleIleArgasnSerIle 259
                                                                                                                                                                                                                                                                                                                                                                                                                                       89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84
                                                                                                                                                                                                                                                                                                                                                                                                                                       50 AsnGlnAlaLysAlaGlyAsnProProValLeuLeuThr---ProGluGlnIleGlnAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 ArgLeu-----AsnAlaAlaGlyLeuAsnAlaLysProGlnSerGlnAlaLeu---
                                                      join(328..2589, 2594..4999, 5005..8961, 8964 ...9431)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3935 GAGCAGTCTTTCCAG-------
                                                                                                                                                                                                                Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                914-168-2 (1-919) x US-07-689-008-1 (1-9540)
                                                                                                                                                                                                                                                                                                                                                          43 ProAlaHisAspThrAlaIle-------
                                                                                                                                                                        Length:
Matches:
OLECULE TYPE: DNA (genomic)
                                                                                                                                                                  3.78e-06
159.50
31.65%
19.16%
3.37%
                                 NAME/KEY: CDS
LOCATION: join(328
LOCATION: ..9431)
OTHER INFORMATION:
                                                                                                                                                                                                                nt Similarity:
Local Similarity:
Match:
                                                                                                                                                        ent Scores:
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7848 7153 CAGGGGCAGGCCTATGATCATCTGGCCCCCGCGCTGCAGGCCGACCCGGAGGCGACATCG 7212 7213 CCCAAGCTGGCGCTCGCGCGGCTGTATAATGGCCACGGCAAGCCGGGCAAGGCGCTCGAG 7272 7273 ATCGAC-------CTTGCGGTGCTGCGCCACACCCGCAGGACCTTGATGCG 7317 7504 CTGCAGCAGGTCGAGGCCACGCGGCCGCGCGCGCGCGGGGTGCTGCCCAGGAAGATGCG 7563 113 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 7849 GCTTCCGCC-----CTG 7860 7861 ACCTTCTCGATCACGCCAACCATGATCTGGTCGGCCAACCTCAACACGGGTTCCGTCTAT 7920 7318 CGACAGGCTGCGGTGCAGGCGGCGGTCAACAGCGACCACAACAGCCTTGCCACCGGCTT 7377 1675 ACGTCGGACCAGATGCTCTCCTCCATCGCAGGCCAGATCCGCACGCTGGGTGAGAACCTT 7734 7921 GATGTGCCG------CGTTAT-----GCCACGATGATGGGCGTGCAGGCATATAAC 7965 630 069 7615 ACGGAACTTGGCGCGCCTGTGACCGGTGGCTCCTACAGCGCGGCGGCGGCATCGCCCGAT 7674 7966 CAGTACGATAGC---------------TATACCAACGCGGGCAGGACCAG 8001 ------AspGlyGlnIleGlyLeuGlyTrpGly 592 593 SerAspThrGlyThrArgLeuValThrLysPheGluHisAsnLeuIleAsnArgAspGly 612 631 TyralaThrLysProLeuSerHisProLeuAsnAspGlnLeuArgAlaThrLeuGlyTyr 650 -----AspLys 695 696 LeuLysThrGlnAlaProProGluThr---------Trp 705 721 737 -----ValAsnProMetArgGlyTyrArgGlnArgTyrSerLeuGluValGlySer 753 754 SerGlyLeuValSerAspAlaAsnMetAlaIleAla------AryAlaGly 768 769 IleSerGlyValTyrSerPheGlyAspAsnAlaTyrGlySerAsnArgAlaHisGlnMet 788 803 804 HisValProTyrArgLeuArgPhePheAlaGlyGlyAspGlnSerIleArgGlyTyr--- 822 GlnValLeuAlaValGlyThrAlaGluTyrAsnTyrGluPheMetLysAspLeuArgLeu 859 562 ProAlaAspValTyrGlnSerLysLysValProLeuTyrValPheValAlaSerAspLys 581 860 AlaValPheGlyAspIleGlyAsnAlaTyrAspLysGlyPheThrAsnAspThrLysIle 879 613 TyrGlnAlaGlyAlaGluLeuArgLeuSerGluAspLysLysGlyVal.....LysLeu 651 GlnGlnGluValPheGlyHisSerThrAsnGlyPheAspLeuSerThrArgThrLeuGlu 671 HisGluIleSerArgSerIleIleGlnAsnGlyGlyTrpAsnArgThrTyrSerLeuArg 7789 ATGGGCGCCTGACGGAAGCGAACATTCCCATCGTGGGCCGCCTGCCGCTGCAGGCCGGT 722 ------LeuLeuAlaGlyValAlaValHis---LysThrValAlaAspAsnLeu 789 ThrGlyGlyIleGlnAlaGlyTyrIleTrpSerAspAsnPheAsn------8002 CAGCGCATCGCCGCTGGCACGCCGAG------823 AlaHisAspSerLeuSerProlleSerAspLysGlyTyrLeuThrGlyGly-----706 GlnAspLeuProValAspPheValAsnGlyLysProSerGlnGluAla.... 582 ProArg-----691 TyrArgLeu-----q q g g q Q QQ qq QΩ Ω q q ò ô ò ò ò ò g ô ò Ω δ δ ò δ ò qq οy qq q ò ò

Db 8029	qq	3162 CTATATCAATCCGGCAATCTTTCCAAGCACTTTGCGGTTATTGGAACTGCCCGTAGA 3218
11100001011000000000000000000000000000	Qy	AS
OY 880 GIYAIBGIYVALGIYVALARGIYPALBSERPICVALGIYGINVAL 894	qq	3219CCTTGGAGTAAGGAATATTTGAATCTGTAGTTGTCGAGTCCATCCTT 3266
ArgValAspValAlaThrGlyValLys 903	Qy Db	226 AspLeuAsnGlySerIleProArgLeuArgGlnThrAlaLeuValAlaAlaArgAlaVal 245 
SULT 21 -08 -961-527-126	Qy	246 GlyTyrTyrAspileAspLeuSerileIleArgAsnSerileGlyGluValAspValile 265         3312 TTCTACTATCAA
o ≈	Qy	266 IleHisAspLeuGlyGluProValTyrIleAspTyrArgAlaValGluVal 282         ::: ::::::
NTION: Streptococcus pr NUENCES: 391 E ADDRESS:	δò	ArgGlyGluGlyAlaAspAspLysAlaPheThrThrValAlaAspGluValPro
38.85	ob Qy Ob	3384 AATGAAAATAGCAAGCTGAACACAATAAGCTCTTCTTCTTGTCTATGGCACCT 3437 301 LeuLeuIleGlyAspValPheHisHisGlyLySTyrGluThrLySLySAsnLeuIleGlu 320 111 :::
COMPUTER REABLE FORM: COMPUTER REABLE FORM: COMPUTER: HP Vectra 486/33	Qy	AsnAlaSerAlaGluHisGlyTyrPheAspGlyArgTrpLeuAspArgSerValAspVal
OFFINION STATES: MSDOS VERSION 0.2 SOFTWARE: ASCII Text CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/961,527	da .	341 IleLeuProAspAsnThrAlaAspValSerLeuIleTyrAspThrGlyThrGlnTyrArg 360 
FILIN DATE: CLAIN DATE: PRIOR APPLICATION DATA: APPLICATION NUMBER:	Qy Db	361
ATTORING DATE INFORMATION: NAME: Brookes, A. Anders REGISSTRATION UNMERS: 5373	QY	375 GlnLeuThrThrAspProAspLysLeuProValLysArgGluLeuLeuGluGlnLeuLeu 394 :::    ::::::::::::::::::::::::::::::
TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504 TELEPRAX: (301) 309-812 TELEPRAX: (301) 309-812	Qy	395 ThrvalasnMetGlyGluAlaTyrAsnLeuGlnAlaValArgAlaLeuSerAsnAspLeu 414
INFORMATION FOR SEAT ID NO: 120: SEQUENCE CHARACTERISTICS: LENGTH: 13121 base pairs TYPE: nucleic acid STRANDEDNESS: double	Qy Db	415 IlealaThrargTyrPheAsnMetValAsnThrGluIleValPheProGluArĞGluGln 434 
9	Qy	435 IleQlnAsnAspGlnValSerPheGluGlnSerSerSerSerRgThrGluProAlaGln 454 ::::::
0.00177 Length: 137.50 Matches: 7: 35.288 Conservative: 7: 7.1518 Mismatchko:	Qy	455 ValAspGluSerThrLeuGluProValileGluThrValGluLeuThrAspGlyIleLeu 474
2.91% 4 4 IS-08-961-527	Qy Db	475 MetAspileSerProileGluPheSerAlaSerAsnLeulleGlnAspLysLeuAsnLeu 494 
	Qy	495 ValalaAlaLysAlaArgHisLeuTyrAspWetProAspAspArgValLeuAlaIleAsn 514 :::::!
168LeuTyrAlaArgLeuPheAsnAspGlyValAsnLysValProArgLeuLysAlaLys 3138 AGGTCTACCGTTCCGTTTTTTTTTTTTTTTTTTTTTTTT	Qy Dp	515 HisaspaspGlyValasnArgSerIleLeuGlyArgIleSerAspAlaValSerAlaVal 534   1
187 PheTyrGlnSerSerGlnSerGlyGluThrSerAlalleGlySerSerHisGlnLys	QY	535 AlaArgAlaIleLeuProAspGluSerGluAsnGluValIleAspLeuProGluArgThr 554 ::: 3978 TCTTATCGTAGCGAGCCAAAT3998

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...-----TCACTTGATTACCGTACA 4286
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                                                                                                                                                                                                                                                                  GlnAlaGlyAlaGluLeuArgLeuSerGluAspLysLysGlyValLysLeuTyrAlaThr 633
                                                                                                                                                                                                                                                                                                                                                                                                                                              ValPheGlyHisSerThrAsnGlyPheAspLeuSerThrArgThrLeuGluHisGluIle 673
AlaLeuAlaAsnArgLysThrProAlaAspValTyrGlnSerLysLysValProLeuTyr 574
                                                                                   ValPheValAlaSerAspLysProArgAspGlyGlnIleGlyLeuGlyTrpGlySerAsp 594
                                                                                                                                                                                                                                                                                                                                                     LysProLeuSerHisProLeuAsnAspGlnLeuArgAlaThrLeuGlyTyrGlnGlnGlu
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                                                                                                                                                                            ThrGlyThrArgLeuValThrLysPheGluHis---AsnLeuIleAsnArgAspGlyTyr
                                                                                                                                                                                                        4089 ACAGGTAAACGACTGAAAAAAGGAACTCATGTCAACATCGTC-------
                                       -----GTGAATCCAGAATCAACAGCTGAAACCTTTACATCTGGTGCC-----
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ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb
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REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,702B
FILING DATE: 03-Dec-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1248 GAATTTAACTTGGCTCCTAAC------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 50, Application US/09453702B Patent No. 6365723 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Blattner, Frederick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
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23213 GGCTCAGGTGGTGGGAGTGGTTTCGTGGAAACGATATCGGTATGGTGGCGAGGC 23272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23000 AGGCATGATGCCAGGAGCGGTTATTGGCGGTATTGCCGGGGCTGTCTATGGTCTGGGTAA 23059
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53 LysAlaGlyAsnProProVal-LeuLeuThrProGluGlnIleGlnAlaArgLeuAsnAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 aAlaGlyLeuAsnAlaLysProGlnSerGlnAlaLeuAspValValAsnPheAspAspGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22880 CCGTCAGGAGATAGGCGTTCTGATAGGTGAACTGGCCCGCGCGCAATTTAGGTGCCGCTGAG
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183
126
360
286
42
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                                                                                                                                                                                                                                                                                                                                  Conservative
Mismatches:
                                                                                                                                                                                                                                                                                           Length:
                                                                                                                                                                                                                                                                                                                                                                              Indels:
                                                                                                                                                                                                 50:
                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO:
TELEPHONE: (608) 251-5000
TELEFA: (608) 251-9166
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE_CHARACTERISTICS:
                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                       0.015
136.50
32.36%
19.16%
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                                                                                         LENGTH: 38584
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Best Local Similarity:
                                                                                                                                                                                                                        US-09-453-702B-50
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>-	272	oValTyrIleAspTyrArgAlaValGluValArgGlyGluGlyAlaAspAspLys	290
۵	23402	7990	23461
> Q	291	-AlaPheThrThrValAlaAspGluValProLeuLeuIleGlyAspValPheHisHisGl	310
>	310	yLysTyrGluThrLysLysAsnLeulleGluAsnAlaSerAlaGluHisGlyTyrPheAs	330
۵	23511	:: GATAATAACCTCAATGCGCTTGGCAGTACGCTGAÄGTATCTGTC	23554
>-	330	pGlyArgTrpLeuAs	335
Ω	23555	TGATTTCTGGAGTCGTTTCTGGGATGCGGCCATGAATATTGGTCGTGAAGACTCGCTGGA	23614
<b>&gt;</b> .	335	pArgSerValAspValIle	346
Ω	15	TGAACAGATTGCCGCTTTTACAGGAGAAAGTGTCGCGGGCGAAAAGACTCCCCTGGACGGC	23674
~ Δ	346	rAlaAspValSerLeuIleTyrAspThrGlyThrGlnTyrArgPheAspGluValValPh   ::	366
>	36	GlnLeuTh	98
Ω	23718	:::	CC.
>-	386	SArgGluLeuLeuGluGluGlu	396
a	23771	GCGGAATTATCAGGAGCAACAGAAACGCCGTAATGCTGAAAAATGCTGCACTGAACGGGAT	23830
>-	396	IASDMetGlyGluAlaTyrAsnLeuGlnAlaValArgAlaLeuSerAsnAspLeuIleAl 	16
Ω	<b>-</b> -		23881
<b>&gt;</b> 1	416	ProGluArgGlu	36
,	700	AIAC	າ
ء ہ	436	nAsnAspGinValSerPheGluGlnSerSerSerSerArgThrGluProAl   ::: ::: ::: ::: ::: ::: ::: ::: ::: :	453
		COLOR TARREST COLOR TARREST COLOR TO THE TOTAL TO THE TOTAL TARREST COLOR TO THE TOTAL TOTAL TOTAL TOTAL TOTAL TARREST COLOR TO THE TOTAL	5
۰ ۵	453	acinvalasboluserini :::	461 24043
>-	461	uProVallleGluThrValGluLeuThrAspGlyIleLeuMetAspIleSerProIleGl	481
۵	24044		24080
>-	481	uPheSerAlaSerAsnLeuIleGlnAspLysLeuAsnLeuValAlaAlaLysAlaArgHi	501
Ω	24081	GCCACGGAAAGGATGACAGAGCGCGTAAACAGCTTCTGGCTCTGCAGCAGCGC	24134
>-	501	SLeuTyrAspWetProAspAspArgValLeuAlaIleAsnHisAspAspGlyValAsnAr	521
Ω	24135	GAA	24175
>-	521	rgAlail	541
Ω	24176	GAGTGTGCTGGCCCGTAAAGATGAACTGATTCAGGCACTGACGCTGCTGGA	24226
> 4	541	pGluSerGluAsnGluValIleAspLeuProGluArgThrAlaLeuAlaAsnArgLysTh	61
			C/747
<u>ہ</u> ۔	24276	IPTOALBASPVALTYFGINSerLysLysValProLeuTyrValPheValAlaSerAspLy 	581
2	21717		7431D

δ	581	sProArgAspGlyGlnIleGlyLeuGlyTrpGlySe	593
qq	24317	-	24365
Qy	59	Æ	3
QQ	24366	GGTGATCAGCGACAGCGATATCAGGTACAACTGAGTCTTCGGCAGAAATA	24418
Qy	613	rGlnAlaGlyAlaGluLeuArgLeuSerGluAspLysLysGlyValLysLeuTyr	631
δλ	632	AlaThrLysProLeuSerHisProLeuAsnAspGlnLeuAr	645
QQ	24473	CACGGATGACTACAGAAAGGCCGAGGGGCGCTGACGGAGAGCCTGAACCGACAACTGAA	24532
δλ	645	gAlaThrLeuGlyTyrGlnGlnGluValPheGlyHisSerThrAsnGlyPheAspLeuSe	665
qq	24533	-	24560
ΟŊ	665	rThrArgThrLeuGluHisGluIleSerArgSerIleIleGlnAsnGlyGlyTrpAsnAr	685
QQ	24561	GAAGITGTACAGAA	24583
δλ	685	gThrTyrSerLeuArgTyrArgLeuAspLysLeuLysThrGlnAlaProProGluThrTr	705
QQ	24584		24604
60	70	pGlnAspLeuProValAspPheValAsnGlyLysProSerGlnGluAlaLeuLeuAlaGl	5
Q C	24605	TCAGGATTTTTACCGTGGATGCAGATAATACGGCAGAAACAGCAGAA	24650
δy	72	yValAlaValHisLysThrValAlaAspAsnLeuValAsnProMetArgGlyTyrArgGl :::     :::  ::	745
Op	24651	CAGGTGTTCTCGTCAGCCTTCAGCAACATGGGAAATGGCCTGGCAACTTTTGTCAC	24706
δÿ		nArgTyrSerLeuGluValGlySerSerGlyLeuValSerAspAlaAsnMetAl	763
qq	24707	TACCGGCAAACTCAATTTCAAATCCTTCACCTCTTCTGTGCTGTCAGATATGGCGAAAAT	24766
Óγ	763	alleAlaArgAla	176
οp	24767	CCTGGCGCAGGCAACCATGATGAAATCGATAAAAGGGATTGGCAGTGTACTGGGATTTGA	24826
δy	776	yAspAsnAlaTyrGlySerAsnArgAlaHisGlnMetThrGlyGlyIleGlnAlaGlyTy	962
qq	24827	AT	24874
ογ	196	rIleTrpSerAspAsnPheAsnHisValProTyrArgLeuArgPhePheAla	813
qq	24875	TGATTTGAGTCGTTACAGTGGCACGGTGGTTAACCGTCCGACGTTTTTTGCTTTTGCAAA	24934
δ	814		823
Dp	24935	AGGCGCGCGTGTGTGGGGGAAGCGGGACCTGAAGCCATTCTGCCATTGCGTCGTGCTGCTGCT	24994
Qy	823	aHisAspSerLeuSerProlleSerAspLysGlyTyrLeuThrGlyGlyGlnValLeuAl	843
qq	24995	TGACGGTAAGCTGGGGGTTGTCGCGGATATTGGGGGTTCAGGTATGCG	25042
δy	843	avalGlyThrAlaGluTyrAsnTyrGluPheMetLysAspLeuArgLeuAlaValPheGl	863
QQ	25043	GATGTTTTCCCCGCAGTACAACATCGAGATCAATAACGATGGCACGAACGG	25093
ΟŸ	863	yAspileGlyAsnAlaTyrAspLysGly 872	
qq	25094	GCAGATAGGTCCGGCTGCAAGGCGGTTTATGACCTCGGG 25136	
RES US-	ULT 23 08-621 equenc atent	-944A-2 e 2, Application US/08621944A No. 6440425	

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1357 CCATATTGGATAAAAACAACTTAAAGTGGGTAGTGTTGCAATTACCATAGACAATGGC 1416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1417 ATTGATGCAGGTAATAAAAAGATCAGTAATCTTGCCAAAGGTAGCAGTGCTAACGATGCG 1476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||||
|1537 GTCACACCTACTGAAATATCAGTTGATGCTAAGAGTGGCAATGTTACGGCCCCAACTTAC 1596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1597 AACATTGGCGTGAAAACCACGGAGCTTAACAGTGATGGCACTAGTGATAAATTTAGTGTT 1656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97 ArgileGlyGluGlnSerProProLeuGlyLeuAsp-------MetSerVal 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112 IleGluGluThrThrProLeuSerLeu-----GluGluLeuPheAlaGlnGluSerThr 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 ProLeuMetThrSerGlnAlaLeuAlaGlnGlnAsnAsnProAlaAsnIleIleAsnHis 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ValProAlaHisAspThrAlaIle---AsnGlnAlaLysAlaGlyAsnProProValLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuThrProGluGlnIleGlnAla....ArgLeuAsnAla..-AlaGlyLeuAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77 AlaLysProGlnSerGlnAlaLeuAspValValAsnPheAspAspGlnSerProlleSer
                            APPLICANT: LOOSMONE, Sheena M.
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER
TITLE OF INVENTION: MEMBRANE PROTEIN OF MORAXELLA
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5976
191
128
351
298
49
                                                                                                                                                                                                                                            COMPUTER REARABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/621,944A
FILING DATE: 26-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-914-168-2 (1-919) x US-08-621-944A-2 (1-5976)
                                                                                                                                           3: Sim & McBurney
Suite 701, 330 University Avenue
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/478,370
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTURNALL ANGUER ANGUER STEWATL, MICHAELI I REGISTRATION NUMBER: 24,973
REFRENCE/DOCKET NUMBER: 1038-TELECOMMUICATION INCOMMATION:
TELEPHONE: (416) 595-1163
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5976 base pairs
TYPE: nucleic acid
SASAKI, Ken
HARKNESS, Robin E.
LOOSMORE, Sheena M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.000655
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32.95%
19.73%
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ZIP: M5G 1R7
                                                                                                                                                                             CITY: Toronto
STATE: Ontario
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Best Local Similarity:
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STREET: Su
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1717 GAAGTCAATCGAACGGCTGACAGTGCTCTACAAAGCTTTACCGTTAAAGAAGAAGAACAT 1776 1819 -----TTAAAACTCAAA 1851 1852 GGTAAAAACGGTCTAACGGTTGCTACCAAAAAGATGGTACGGTTACCTTTGGUCTTAGC 1911 1963 ACTGTTAAAGATACCAACGAACAAATT. 111
1963 ACTGTTAAAGATACCAACAAACAAATT. 2019 2112 GluMetGlyIleAsnProAsnAsp------TyrIleProGluTyrGlnGly 144 145 GluGlnProAsnSerGluValValValProProThrLeuGluProGluLysProGlyLeu 164 185 AlaLys------PheTyrGlnSer 190 SerGlnSerGlyGluThrSerAlalleGlySerSerHisGlnLysThrGluProTyrAla 210 2158 AATGTTAAGATTACCAACACTGGCATTAACGCAGGTGGTAAAGGCCATCACAGGGCTGTCC 2217 226 AspLeuAsnGlySerIlePro-----ArgLeuArgGlnThralaLeuValAlaArg 243 244 AlavalGlyTyrTyrAsplleAspLeuSerIleIleArgAsnSerIleGlyGluValAsp 263 264 ValileIleHisAspLeuGlyGluProValTyrIleAspTyrArgAlaValGluVal--- 282 283 .....-ArgGlyGluGlyAlaAspAspLysAlaPheThrThrValAla 296 2218 CCAACACTGCCTAGCATTGCCGATCAAAGTAGCCGCAACATAGAACTGGGCAATACAATC 2277 2278 CAAGACAAAGACAAATCCAAGGCTGCCAGCATTAATGATATATTAAATACAGGCTTTAAG 2337 2374 ------ACTTATGACATTGTTGACTTTGCCAATGGCAATGCCACACGCGC 2418 2419 ACAGTAACCCATGATACCGCTAAC-----AAAACCAGTAAAGTGGTATATGATGTGAAT 2472 303 -----Lys 311 312 TyrGluThrLysLysAsnLeuIleGluAsnAlaSerAlaGluHisGlyTyrPheAspGly 331 332 ArgTrpLeuAspArgSerValAspValIle-----LeuProAspAsnThrAlaAspVal 349 387 ArgGluLeuLeuGluGlnLeuLeuThrvalAsnMetGlyGluAlaTyrAsnLeuGlnAla 406 407 ValArgAlaLeuSerAsnAspLeuIleAlaThrArgTyr---PheAsnMetValAsnThr 425 165 IleLysArgLeuTyrAlaArgLeuPheAsnAspGlyValAsnLysValProArgLeuLys 2113 ------GATACAAACAAACT---TATCTTGATCAAGACAAGCTAGAGTTGGC 369 IleAspProLysThrAsnGlnLeu-----ThrThrAspProAspLysLeuProValLys 350 SerLeuIleTyrAspThrGlyThrGlnTyrArgPheAspGluValValPhe---PheThr 1777 GATGACGCCAACGCTATCACCGTGGCTAAAGATACGACAAAA-----2080 AAAATTGGCTTTGCTGGTTCTGATGGTGCAGTT-----= 297 AspGluValProLeuLeu------2533 ACCACCAAACTGAAC-----= 130 191 q δò qq a δý ò q ò qq ò ò q qq δ δ qq δ qq QQ òγ ò qq δy q ò Op οqα ò qq ŏ

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g		ATTGATGCAGGTAATAAAAAGATCAGTAATCTTGCCAAAGGTAGCAGTGCTAACGATGCG 1	
ž ą	61		
⋩	7.7	96	
ą	1537		
ζ	97	7 ArgileGlyGluGinSerProProLeuGlyLeuAsp	
q	1597		
<i>≿</i> .	112	IleGluGluThrThrProLeuSerLeuGluGluLeuPheAlaGlnGluSerThr 129	
Q.	7591		
<u>&gt;</u> 4	130	GluMetGlylleAsnProAsnAspTyrIleProGluTyrGlnGly 144	
9 ;	1/1/	GAAGTCAATCGAACGGCTGACAGTGCTCTACAAAGCTTTACCGTTAAAGAAGAAGATTACGGTTAAAGAAGAAGAAGATTACAATTAAAAGAAGAAGAAGATTAAAAGAAGAAGAAGAATTAAAAGAAG	
يہ بح	L40	GIUGINFTOASNSERGLUVALVALVALPROPROTHILEUGLUPROGLULYSPROGLYLEU 164	
Ω	1///	GATGAC	
<u>≯</u> .	165	IleLy	
ā	1819		
<u>&gt;</u> -	185	AlaLys	
۵	1852	GGTAAAAACGGTCTAACGGTTGCTACCAAAAAAGATGGTACGGTTAC	
>-	191		
Q	1912	CAAGATAGCGGTCTGACCATTGGCAAAAGCACCCTAAACAACGATGGCTTG 1962	
7	211		
Q	1963	ACTGTTAAAGATACCAACGAACAAATCCAAGTCGGTGCTAATGGCATTAAATTTACT 2019	
λ.	226		
q	2020		
>-	244		
۵	2080	AAAATGGCTTTGCTGGTTCTGATGGTGCAGTT	
>-	264	ValIl	
۵	2113		
>-	283		
۵	2158	AATGTTAAGATTACCAACACTGGCATTAACGCAGGTGGTAAAGCCATCACAGGGGTGTCC 2217	
>-	297	AspGluValProLeuLeu 302	
0	2218	CCAACACTGCCTAGCATTGCCCGATCAAGTAGCCGCAACATAGAACTGGGCAATACAATC 2277	
_	303	Lys 311	
0	2278	CAAGACAAAGACAAATCCAACGCTGCCAGCATTAATGATATATAAATACAGGCTTTAAC 2337	
_	312	TyrGluThrLysLysAsnLeulleGluAsnAlaSerAlaGluHisGly∏yrPheAspGly 331	
	2338	CTAAAAAATAATAACAACCCCATTGACTTTGTCTCC	

Qy	332	rgTrpLeuAspArgSerValAspValIleLeuProAspAsnThrAlaAspVal 34
QO	2374	ACCECC 2
yo g	350	rrgPheAspGluValValPhePheThr 368
} ;		FGAAT 24
දි දි	2473	TEASPITOLYSITTASRCIDLEUThrinaspProAspLysLeuProVallys 386 
Οy	387	lnAla 406
QQ	2533	25
Οy	407	snThr 4
qq	2548	:: ATGAA 26
Οy	426	GluIleValPheProGluArgGluGlnIleGlnAsnAspGlnValSerPheGluGln 444
qq	Ŋ	2
Οy	445	SerSerSerArgThrGluProAlaGlnValAspGluSerThrLeuGluPr@Vallle 464
qq	2665	CACACCACAAAGGCACAGCAGACACCGCCCTACAAACCTTTACCGTTAAAAAGGTAGAT 2724
Οy	465	GluThrValGluLeuThrAspGlyIleLeuMetAspIleSerProlleGluPheSerAla 484
DP	2725	
Qy	485	SerAsnLeulleGlnAspLysLeuAsnLeuValAlaAlaLysAlaArgHisLeuTyrAsp 504
qq	2779	AATAATCAAGTCAACACCCTAACACTCAAAGGTGAAAACGGTCTTAAT 2826
Qy	505	MetProAspAspArgValLeuAlaIleAsnHisAspAspGlyValAsn 520
qq	2827	 ATTAAAACCGACAAAAATGGTACGGTTACCTTTGGCATTAACACCACAAGGGGTCTTAAA 2886
٥y	521	ArgSerIleLeuGlyArgIleSerAspAlaValSerAlaValAlaArgAlaIleLeuPro 540
qq	2887	.:::::
Qy	541 /	AspGluSerGluAsnGluValIleAspLeuProGluArgThrAlaLeuAlaAsnArgLys 560
QQ	2908 (	
Qy	561	ThrProAlaAspValTyrGlnSerLysLysValProLeuTyrValPheValAlaSerAsp 580
qa	2956 (	STCGGTGCTGATGGCGTGAAGTTTGCCAAGGTT
Qy	581 1	sProArgAspGlyGlnIleGlyLeuGlyTrpGlySerAspThrGlyThrArgLeuVal 60
QQ	2989	
Qy	601 7	ThrLysPheGluHisAsnLeuIleAsnArgAspGlyTyrGlnAlaGlyAlaGluLeuArg 620
qq	3037 #	30
Qy	621 1	LeuSerGluAspLysLysGlyValLysLeuTyrAlaThrLysProLeuSerHisProLeu 640
qa	3073	
Ολ	641 4	AsnAspGlnLeuArgAlaThrLeuGlyTyrGlnGlnGluValPheGlyHisSerThr 659
Op	3094 -	111   111
δλ	660 A	AsnGlyPheAspLeuSerThrArgThrLeuGluHisGluIleSerArgSerIleIleGln 679
qq	90	CGCAGGTGGTAAAAAGATTACCAACATTCAATCAGGTGAGATTGCCCAA
δy	680 A	Asn

116   111		ATT	TEL ;	; INFOR		; US-08-47	Alignmen	Score: Percent	Best Loc	DB:	0y	Db 206	Oy 4	Db 212	Oy 6	Db 218	Qy 7	Db 224	6 оу	Db 230	Oy 11	Db 236	Qy 13	Db 242	Qy 14	Db 248	Oy 16	Dp 523	Qy 18	Db 255	Oy 19	Db 261	Oy 21	-
O O O O O O O O O O O O O O O O O O O		694 AspLysLeuLysThrGlnAlaProProGluThrTrpGlnAspLeuProValAspPheVal	714 AsnGlyLysProSerGlnGluAlaLeuLeuAlaGlyValAlaValHisLysThrVal	3223AACAAAATCAGCAGTACTGCCAAAACAGCACAAAACTCATTACACGAATTCTCAGTA 327	/33 Alabap	747 TyrSerLeuGluValGlySerSerGlyLeuValSerAspAlaAsnMet	3340 AAGACCTCTGATGTCATCACCTTTGCAGGTGAAAACGGCATTACCACCAAGGTAAATAAA	763 AlaileAlaArgAlaGlyIleSerGlyValTyrSerPheGlyAspAsnAlaTyrGlySer	3400 GGTGTGGTGGTGTGGGCATTGACCAAACCAAAGGCTTA	783 ASDARGALAHISGIDMETTNRGIYGIYILGGIDALAGIYTYRILGTRFSGRASPASDPDE 802 3439 ACCACGCCTAAGCTGACCGTGGGTAATAATAATAGCCAAAGGCATTGTCATTGACAGCCAA 349	803 AsnHisValProTyrArgLeuArgPhePheAlaGlyGlyAspGlnSerIleArgGlyTyr 822	   11        ::	823 AlaHisAspSerLeuSerProIleSerAspLysGlyTyrLeuThrGlyGlyGlyGluValLeu	3526 AGCAACACTCTAGCTAATGTTACCAATGATAAAGGT	843 AlaValGlyThrAlaGluTyrAsnTyrGluPheMetLysAspLeuArgLeu 8 :::	3562 AGCGTACGCACACAGAACAGGGCAATATAATCAAAGACGAAGACAAAACCCGTGCC	860 AlaValPheGlyAspIleGlyAsnAlaTyr	3619 GCCAGCATTGTTGATGTGCTAAGCGCAGGCTTTAACTTGCAAGGCAATGGTGAAGCGGTT 367	870 AspLysGlyPheThrAsnAspThr	3679 GACTTTGTCTCCACTTATGACACC	RESULT 25 US-08-478-370-1	c	GENERAL INFORMATION: APPLICANT SASAKI Ken	APPLICANT: HARKESS, Robin E.	ìΞ		CONTENT OF SECURITIES 4	Suite 70	CITI: OLIGICO STATE: Ontario COUNTRY Canada	ZIP: M5G 1R:	CONTOILS REMOVABLE FORM:  FORDIUM TYPE: Floppd disk  COMMUTTER: TAM DC Commatible	COMPLETE C PC-DOS/MS-DOS In Release #1 0 Version #1	LICATION DATA	מוני בורנטיונו מכוירני ככל כל יו כ

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64 CCATATTTGGATAAAAAAAACAACTTAAAGTGGGTAGTGTTGCAATTACCATAGACAATGGC 2123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       *::[1] ||||||:::::|||
84 GTTACCATCGAACAGCTCAAAGCCGCAAGCCTACTTTAAACGCAGGCGCTGGCATCAGT 2243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04 AACATIGGCGTGAAAACCACCGAGCTTAACAGTGATGGCACTAGTGATAAATTTAGTGTT 2363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 GAAGTCAATCGAACGGCTGACAGTGCTCTACAAAGCTTTACCGTTAAAGAAGAAGAAGACGAT 2483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 GGTAAAAACGGTCTAACGGTTGCTACCAAAAAGATGGTACGGTTACCTTTGGGCTTAGC 2618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 CAAGATAGCGTCTGACC-----ATTGGCAAAAGCACCCTAAACAACGATGGC---TTG 2669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 IleGluGluThrThrProLeuSerLeu-----GluGluLeuPheAlaGlnGluSerThr 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 GluMetGlyIleAsnProAsnAsp-----TyrIleProGluTyrGlnGly 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45 GluGlnProAsnSerGluValValValProProThrLeuGluProGluLysProGlyLeu 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 IleLysArgLeuTyrAlaArgLeuPheAsnAspGlyValAsnLysValProArgLeuLys 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 AsnIleLysAlaAlaLeuGluAspIleThrGlnGluSerAla------Met 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 LeuThrProGluGlnIleGlnAla-----ArgLeuAsnAla---AlaGlyLeuAsn 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77 AlaLysProGlnSerGlnAlaLeuAspValValAsnPheAspAspGlnSerProIleSer 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 ProLeuMetThrSerGlnAlaLeuAlaGlnGlnAsnAsnProAlaAsnIleIleAsnHis 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42 ValProAlaHisAspThrAlaIle -- - AsnGlnAlaLysAlaGlyAsnProProValLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 GATGACGCCAACGCTATCACCGTGGCTAAAGATACGACAAAAA --------
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128
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298
49
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Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
RECISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-502
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEPHONE: (416) 595-1155
TELEPHONE: (416) 595-1163
NFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6973 base pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                       0.000858
136.00
32.95$
19.73$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85 AlaLys------
                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear 78-370-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                        c Similarity:
ccal Similarity:
datch:
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2726 243 2786 263 2819 282 282	296 2924 302 2984	3 3 0	349 3125 368 3179	386 3239 406 3254	425 3311 444 3371	464 3431 484 3485	504 3533 520 3593 540
ACTGTTAAAGATACCAACGAACAAATCCAAGTCGGTGCTAATGGCATTAAATTTACT ASPLeuAsnGlySerileProArgLeuArgGlnThrAlaLeuValAlaAlaArg :::::!		CAAGACAAAGACAAATCCAACGCTGCCAGCATTAATGATATTAAATAACAGCTTTAACTTGATATTAAATAATAAAGACTTTAATGATATTAAATAATAAAGATTTAAACTTTAATAATAAATA	ArgTrpLeuAspArgSerValAspValIleLeuProAspAsnThrAlaAspVal :::    :::::	IleAspProLysThrAsnGlnLeuThrThrAspProAspLysLeuProValLys ::	ValargalaLeuSerasnaspLeuIlealaThrargTyrPheAsnMetValasnThr :::	SerSerSerArgThrGluProAlaGlnValAspGluSerThrLeuGluProVallle ::::::	SerAsnLeulleGlnAspLysLeuAsnLeuValAlaAlaLysAlaArgHisLeuTyrAsp :::    :::    :::    :::    AATAATCAAGTCAACACCCTAACACTCAAAGGTGAAAACGGTCTTAAT MetProAspAspArgValLeuAlaIleAsnHisAspAspGIYValAsn :::   ::: ATTAAAACCGACAAAAATGGTACGTTACCTTTGCCATTAACACCACAAGCGGTCTTAAA ArgSerlleLeuGlyArgIleSerAspAlaValSerAlaValAlaArgAlaIleLeuPro ArgScrlleLeuGlyArgIleSerAspAlaValSerAlaValAlaArgAlaIleLeuPro
2670 226 2727 244 2787 264 2820	2865 2865 297 2925	303 2985 312 3045	332 3081 350 3126	369 3180 387 3240	407 3255 426 3312	445 3372 465 3432	485 3486 505 3534 521 3594
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3779 3695 3615 GACGGTGGC------TTGTCTATTAAAAACCCCACTGGTAGCGAACAAATCCAA 3662 ---AATAATAATGGTGTGTTGTAGGTGCTGGC-----ATTGATGGCACAACTCGCATT 3743 3813 GACGGCATTAACGCAGGTGGTAAAAAGATTACCAACATTCAATCAGGTGAGATTGCCCAA 3872 3873 AACAGCCATGATGCTGTGACAGGCGGC-----AAGATTTATGATTTAAAAACCGAACTT 3926 3987 GCAGATGAACAAGGTAATAACTTTACGGTTAGTAACCCTTACTCCAGTTATGACACCTCA 4046 4146 ACCACGCCTAAGCTGACCGTGGGTAATAATAATGGCAAAGGCATTGTCATTGACAGCCAA 4205 4206 AAT-----GTCAAAATACCATCACAGACTA 4232 ThrLysPheGluHisAsnLeuIleAsnArgAspGlyTyrGlnAlaGlyAlaGluLeuArg 620 LeuSerGluAspLysLysGlyValLysLeuTyrAlaThrLysProLeuSerHisProLeu 640 641 AsnAspGlnLeuArgAlaThrLeuGlyTyrGlnGlnGluValPheGlyHis---SerThr 659 660 AsnGlyPheAspLeuSerThrArgThrLeuGluHisGluIleSerArgSerIleIleGln 679 693 694 AspLysLeuLysThrGlnAlaProProGluThrTrpGlnAspLeuProValAspPheVal 713 714 AsnGlyLysProSerGlnGluAlaLeuLeuAlaGlyValAlaValHisLys---ThrVal 732 733 AlaAsp-----AsnLeuValAsnProMetArgGlyTyrArgGlnArg 746 747 TyrSerLeuGluVal-----GlySerSerGlyLeuValSerAspAlaAsnMet 762 823 AlaHisAspSerLeuSerProIleSerAspLysGlyTyrLeuThrGlyGlyGlnValLeu 842 541 AspGluSerGluAsnGluValIleAspLeuProGluArgThrAlaLeuAlaAsnArgLys 560 561 ThrProAlaAspValTyrGlnSerLysLysValProLeuTyrValPheValAlaSerAsp 580 763 AlaIleAlaArgAlaGlyIleSerGlyValTyrSerPheGlyAspAsnAlaTyrGlySer 782 783 AsnArgAlaHisGlnMetThrGlyGlyIleGlnAlaGlyTyrIleTrpSerAspAsnPhe 802 843 AlaValGlyThrAlaGluTyrAsnTyrGluPheMetLysAsp------LeuArgLeu 859 860 AlaValPheGlyAspile------GlyAsnAlaTyr 869 3663 GTCGGTGCTGATGCCGTGAAGTTTGCCAAGGTT-----LysProArgAspGlyGlnIleGlyLeuGlyTrpGlySerAspThrGlyThrArgLeuVal -----CACCTAAGCAAA Asn.......GlyGlyTrpAsnArgThrTyrSerLeuArgTyrArgLeu 803 AsnHisValProTyrArgLeuArgPhePheAlaGlyGlyAspGlnSerIleArgGlyTyr 3780 ---TCACTTGATAAA-----------AGCAAACCC------3927 GAA-----3744 ACCAGAGATGAAATTGGCTTTACTGGGACTAATGGC-------621 089 601 3801 qq ò qq Ω g ο̈́ Op ολ Db Ωý Db Ωý qq Ωý qq ò qq ολ рþ οy οp Οy qq δy QQ ò QQ οy Ω ò qq οy Db ò

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GENERAL INFORMATION:
APPLICANT: Sasaki, Ken
APPLICANT: Sasaki, Ken
APPLICANT: Harkness, Robin E.
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: LOOSMORE, Sheena M.
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE PROTEIN OF
TITLE OF INVENTION: MORAXELLA
FILE REFERENCE: 1038-503 MIS
CURRENT APPLICATION NUMBER: US/08/483,855C
CURRENT FILING DATE: 1995-06-07
PRIOR PILING DATE: 1995-05-01
NUMBER OF SEO ID NOS: 4
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 6973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2064 CCATATTTGGATAAAAAACAACTTAAAGTGGGTAGTGTTGCAATTACCATAGACAATGGC 2123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2424 GAAGTCAATCGAACGGCTGACAGTGCTCTACAAAGCTTTACCGTTAAAGAAGAAGAAGAT 2483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2484 GATGACGCCAACGCTATCACCGTGGCTAAAGATACGACAAAA---------2525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2244 GTCACACCTACTGAAATATCAGTTGATGCTAAGAGTGGCAATGTTACCGCCCCAACTTAC 2303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2304 AACATTGGCGTGAAAACCACCGAGCTTAACAGTGATGGCACTAGTGATAAATTTAGTGTT 2363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2124 ATTGATGCAGGTAATAAAAGATCAGTAATCTTGCCAAAGGTAGCAGTGCTAACGATGCG 2183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112 IleGluGluThrThrProLeuSerLeu-----GluGluLeuPheAlaGlnGluSerThr 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 GluMetGlyIleAsnProAsnAsp-----TyrIleProGluTyrGlnGly 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    165 IleLysArgLeuTyrAlaArgLeuPheAsnAspGlyValAsnLysValProArgLeuLys 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 GluGlnProAsnSerGluValValValProProThrLeuGluProGluLysProGlyLeu 164
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Matches:
Conservative:
Mismatches:
Indels:
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                              4386 GACTTTGTCTCCACTTATGACACC 4409
870 AspLysGlyPheThrAsnAspThr 877
                                                                                                          Sequence 1, Application US/08483855C Patent No. 6440424
                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Moraxella catarrhalis
US-08-483-855C-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.000858
136.00
32.95%
. 19.73%
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                       RESULT 26
US-08-483-855C-1
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QY	185		190
QQ	2559	Ö	2618
0y	191	luThrSerAlalleGlySerSerHisGlnLysThrGluProTyrAl	- '
an i	7 .	TGACCATTGGCAAAAGCACCCTAAACAACGATGGCT	، و
à a	211	AsnitelysAlaAlaLeuGluAspilefhrGinGluSerAlaMet :::i	225
Oy	22	eProArgLeuArgGlnThrAlaLeuvalAlaAlaAr	
Db	2727	::: ATCCAGGTACTGGCATTGCAAATACCGCTCGCATTACCAGAGA	2786
Qγ	244	Ilear	263
QΩ	2787		2819
δy	264	alileileHisAspLeuGlyGluProVa	282
Dp	2820	TTATCTTGAGACAAGCTACAAGTTG	2864
Qy	283	pAspLysAlaPheThrThrValAl	296
Op	2865	AATGTTAAGATTACCAACACTGGCATTAACGCAGGTGGTAAAGCCCATCACAGGGCTGTCC	2924
Qy	297	alProLeuLeu	302
Dp	2925	CCAACACTGCCTAGCATTGCCGATCAAAGTAGCCGCAACATAGAACTGGGCAATACAATC	2984
Οý	303	eG1y	311
Db	2985	::: ::       ATGATATTAAATACAGGCTTTAA	3044
Qy	312	uThrLysLysAsnLeuIleGluAsnAlaSerAlaGluHisGl	331
qq	3045	::: TAAAAAATAACAACCCCATTGACTTTGTCTCC	3080
ΟŸ	332	ArgTrpLeuAspArgSerValAspVallleLeuProAspAsnThrAlaAspVal	349
Dp	3081	::::	3125
οy	350	SerLeulleTyrAspThrGlyThrGlnTyrArgPheAspGluValValPhePheThr	368
Op	3126	AAC	3179
ΟŊ	369	leAspProLysThrAsnGlnLeu	386
op .	3180	:     GATGATACAACCATTCATCTAACAGGCACTGATGACAATAAAAACTTC	3239
οy	387	ArgGluLeuLeuGluGlnLeuLeuThrValAsnMetGlyGluAlaTyrAsnLeuGlnAla	406
qq	3240	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	3254
Οy	407	ValArgAlaLeuSerAsnAspLeuIleAlaThrArgTyrPheAsnMetValAsnThr	425
qq	3255	TAATACAGCAACTAACTTTAATGTTAACTCT	3311
ΟŊ	426	luIleValPheProGluArgGluGlnIleGlnAsnAspGlnValSerF	444
Db	3312	STTAACGCCAAAGACATCGCCGAAAATCTAAACACCCT	3371
ΟŊ	445	SerSerSerSerArgThrGluProAlaGlnValAspGluSerThrLeuGluProVallle	464
Dp	3372	CCACCAAAGGCACAGCAGACGCCCTACAAACCTTTAC	3431
ΟŸ	465	GluThrValGluLeuThrAspGlyIleLeuMetAspIleSerProIleGluPheSerAla	484
ď	3432		3485

Db	:::::: :::::: ::::::::::::::::::::::::
Οy	843 AlaValGlyThrAlaGluTyrAsnTyrGluPheMetLysAspLeuArgLeu 859
QQ	4269 AGCGTACGCACCACAGAACAGGCCAATATAATCAAAGACGAAGACAAAAACCGGTGCC 4325
٥y	860 AlaValPheGlyAspIle
QQ	4326 GCCAGCATTGTTGATGTGCTAAGCGCAGGCTTTAACTTGCAAGGCAATGGTGAAGCGGTT 4385
ζς d	870 AspLysGlyPheThrAsnAspThr 877 
2	#ESULT 2/ US-08-621-944A-1 ; Sequence 1, Application US/08621944A ; Sequence 1, Application US/08621944A ; Patent No. 64440425 ; GENERAL INFORMATION:     APPLICANT: ARKINESS, Robin E.     APPLICANT: KLEIN, Michel H.     TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER     TITLE OF INVENTION: MEMBRANE PROTEIN OF MORAXELLA     NUMBER OF SEQUENCES: 10
	CORRESPONDENCE ADDRESS: ADDRESSEE: Sim & McBurney STREET: Suite 701, 330 University Avenue
	STATE: Ontario COUNTRY: Canada
	COMPUTER READBALE FORM:
	: ()
	C : 1 # 110Te 15
	FILING DATE: 26-MAR-1996 CLASSIFICATION:
	PRIOR APPLICATION DATA: APPLICATION UNDER: BITING DATE: 07-INA_100E
	CLASSIFICATION: ATTORNEY/AGENT INFORMATION:
	NAME: Stewart, Minher 1 REGISTRATION NUMBER: 24 973
	REFERENCE/DOCKETTON TO 1038-587
	IELECCMMUNICATION INFORMATION: PELEDOND: (416) 552-1155 PETERONO. (416) 552-1155
	INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
	LENGTH: 6973 base pairs
	TYPE: nucleic acid STRANDEDNESS: single
	TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
S	20 20 20 20 20 20 20 20 20 20 20 20 20 2
Alic Prec Scor Perc Best Quer DB:	Alignment Scores: 0.000858 Length: 6973 Pred. No.: 136.00 Matches: 191 Score: 32.95% Conservative: 128 Best Local Similarity: 19.73% Mismatches: 351 Ouery Match: 4.88% Gaps: 49

00-51	- 914	-168-2 /1-9191	
9	#T6	(0/60-I) I V#46-I70-00-C0 V (6I6-I) 7-001	
<u></u>	22	ProLeuMetThrSerGinAlaLeuAlaGinGinAsnAsnProAlaAsnIlelleAsnHis 41	
q	7004	CCATATTTGGATAAAAACAACTTAAAGTGGGTAGTGTTGCAATTACCATAGACAATGGC 2123	
<u>ک</u> ج	2124	ValProAlaHisAspThrAlaIleAsnGlnAlaLysAlaGlyAsnProProValLeu 60	
}			
<b>≿</b> 8	61 2184	LeuThrProGluGlnIleGlnAlaArgleuAsnAlaAlaGlyLeuAsn 76 :::          ::::::    GTTACCATCGAACAGCTCAAGCCCCACTTTAAACGCAGCGCTGGCATCAGT 2243	
ķ	77		
ą	2244	::::::	
λ	97	ArgiledlyGluGlnSerProProLeuGlyLeuAsp	
ą	2304		
<i></i>	112	IleGluGluThrThrProLeuSerLeuGluGluLeuPheAlaGlnGluSerThr 129	
q	2364	AAGGGTAGTACGAACAATAGCTTAGTTACCGC	
λ	130	GlumetGlyIleAsnProAsnAspTyrIleProGluTyrGlnGly 144	
q	2424	GAAGTCAATCGAACGGCTGACAGTGCTCTACAAAGCTTTACCGTTAAAGAAGAAGAAGAT 2483	
λ̈	145		
q	2484	GATGACGCCAACGCTATCACCGTGGCTAAAGATACGACAAAA2525	
λ	165	IleLysArgLeuTyrAlaArgLeuPheAsnAspGlyValAsnLysValProArgLeuLys 184	
ą	2526		
λ	185	AlaLys	
ą	2559	GGTAAAAAACGGTCTAACGGTTGCTACCAAAAAAGATGGTACGGTTACCTTTGGGCTTAGC 2618	
à	191		
q	2619	CAAGATAGCGGTCTGACCATTGGCAAAAGCACCCTAAACAACGACGTTTG 2669	
ζ	211	AsnIleLysAlaAlaLeuGluAspIleThrGlnGluSerAlaMet 225	
ð	2670		
Σγ	226		
qc	2727	ANTGTGAATGGTAGTAATCCAGGTACTGGCATTGCAAATACCGCTCGCATTACCAGAGAT 2786	
λζ	244		
ą	2787		
λ	264		
ą	2820		
λά	283		
qo	2865		
λά	297	AspGluValProLeuL	
qq	2925	CCAACA	
δý	303		

3081 ------ACTTATGACATTGTTACCAATGCCAATGCCACCACCGCC 3125 :::::: :::||||||||| :::
3126 ACAGTAACCCATGATACCGCTAAC-----AAAACCAGTAAAGTGGTATATGATGTGAAT 3179 3255 ---AAAACAAGTGCTAATGGTAATACAGCAACTAACTTTAATGTTAACTCTAGTGATGAA 3311 :::||| :::||| :::|| | :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| ::::|| ::::|| ::::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| --CACCTAAGCAAA 3812 3312 GATGCCCTTGTTAACGCCAAAGACATCGCCGAAAATCTAAACACCCTAGCCAAGGAAATT 3371 3432 GAAAATAATAATGCTGATGACGCCAACGCCATCACCGTGGGT-----CAAAAGAACGCA 3485 3534 ATTAAAACCGACAAAAATGGTACGGTTACCTTTGGCATTAACACCACAAGCGGTCTTAAA 3593 3615 GACGGTGGC------TTGTCTATTAAAACCCCCACTGGTAGCGAACAAATCCAA 3662 --- 3254 3372 CACACCACAAAGGCACAGCAGCACCGCCCTACAAAACCTTTACCGTTAAAAAGGTAGAT 3431 --GCCGGCAAAGCACCCTAAAC 3614 2985 CAAGACAAAGACAAATCCAACGCTGCCAGCATTAATGATATTAAATACAGGCTTTAAC 3044 561 ThrProAlaAspValTyrGlnSerLysLysValProLeuTyrValPheValAlaSerAsp 580 LeuSerGluAspLysLysGlyValLysLeuTyrAlaThrLysProLeuSerHisProLeu 640 332 ArgTrpLeuAspArgSerValAspValIle-----LeuProAspAsnThrAlaAspVal 349 369 IleAspProLysThrAsnGlnLeu-----ThrThrAspProAspLysLeuProValLys 386 387 ArgGluLeuLeuGluGlnLeuLeuThrValAsnMetGlyGluAlaTyrAsnLeyGlnAla 406 407 ValArgAlaLeuSerAsnAspLeuIleAlaThrArgTyr---PheAsnMetValAsnThr 425 426 GluIleValPheProGluArgCluGlnIleGlnAsn---AspGlnValSerPheGluGln 444 505 MetProAspAspArg------ValLeuAlaIleAsnHisAspAspGlyValAsn 520 521 ArgSerIleLeuGlyArgIleSerAspAlaValSerAlaValAlaArgAlaIleLeuPro 540 541 AspGluSerGluAsnGluValIleAspLeuProGluArgThrAlaLeuAlaAsnArgLys 560 LysProArgAspGlyGlnIleGlyLeuGlyTrpGlySerAspThrGlyThrArgLeuVal 600 ThrLysPheGluHisAsnLeuIleAsnArgAspGlyTyrGlnAlaGlyAlaGluLeuArg 620 641 AsnAspGlnLeuArgAlaThrLeuGlyTyrGlnGlnGluValPheGlyHis---SerThr 659 445 SerSerSerArgThrGluProAlaGlnValAspGluSerThrLeuGluProValIle 464 465 GluThrValGluLeuThrAspGlyIleLeuMetAspIleSerProIleGluPheSerAla 484 SerAsnLeuIleGlnAspLysLeuAsnLeuValAlaAlaLysAlaArgHisLeuTyrAsp 504 TyrGluThrLysLysAsnLeuIleGluAsnAlaSerAlaGluHisGlyTyrPheAspGly 331 350 SerLeuIleTyrAspThrGlyThrGlnTyrArgPheAspGluValValPhe---PheThr -----AGCAAACCC-----3663 GTCGGTGCTGATGGCGTGAAGTTTGCCAAGGTT-----|||::: ||| 3744 ACCAGAGATGAANTIGGCTTTACTGGGACTAATGGC-----3045 CTAAAAAATAATAACAACCCCATTGACTTTGTCTCC 3240 ACCACCAAACTGAAC-------TCACTTGATAAA----3594 ----312 485 581 601 3801 q qq QQ οy qq ò qq qq qq ò g q Qγ QQ ò οp δλ Ω ò QQ ò Q δ δ ΩŸ qq 0y 0y 0y δy ò οy οχ g á

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2064 CCATATTTGGATAAAAAACAACTTAAAGTGGGTAGTGTTGCAATTACCATAGACAATGGC 2123
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Matches:
Conservative:
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Gaps:
PRIOR FILING DATE: 1996-03-26
PRIOR PAPLICATION NUMBER: PCT/CA96/00264
PRIOR FILING DATE: 1996-04-29
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 1
LENGTH: 6973
                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Moraxella catarrhalis
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32.95%
19.73%
2.88%
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; LOCATION: (708)...(6683)
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q	2727 AATGTGAATGGTAGTAATCCAGGTACTGGCATTGCAAATACCGCTCGCATTACCAGAGAT 2786
oy Ob	244 AlavalGlyTyrTyrAspIleAspLeuSerIleIleArgAsnSerIleGlyGluValAsp 263 2787 AAAATTGGCTTTGCTGGTTCTGATGGTTT
O.Y	264 ValileileHisAspLeuGlyGluProValTyrileAspTyrArgAlaValGluVal 282 111
Qy Dp	
οy	AspGluValProLeuLeu
Op	2925 CCAACACTGCCTAGCATTTAAAGTAGCCGCAACATAGAACTGGGCAATACAATC 2984
Qy Dp	303Lys 311 2985 CAAGACAAAGACAAATCCAACGCTGCCAGCATTAATGATATTAAATACAGGCTTTAAC 3044
Qy	312 TyrGluThrLysLysAsnLeuIleGluAsnAlaSerAlaGluHisGlyTyrPheAspGly 331 :::
οy	ArgTrpLeuAspAr
οp	3081ACTTATGACATTGTTGACTTTGCCAATGGCAATGCCACCGCC 3125
oy Db	350 SerLeulleTyrAspThrGlyThrGlnTyrArgPheAspGluValValPhePheThr 368 ::::: :::
Sy Op	369 IleaspProLysThrAsnGlnLeuThrThrAspProAspLysLeuProValLys 386 
δy	387 ArgGluLeuLeuGluGlnLeuLeuThrValAsnMetGlyGluAlaTyrAsnLeuGlnAla 406
Q	3240 ACCACCAAACTGAAC 3254
Qy Dp	407 ValargalaLeuSerasnaspLeuileAlaThrargTyrPheasnMetValasnThr 425 
Qy Db	426 GlulleValPheProGluargGluGlnIleGlnAsnAspGlnValSerPheGluGln 444 ::: ::: ::: :::       3312 GATGCCCTTGTTAACGCCAAAGACTCGAAAATCTAAACCCTAGCCAAGGAAATT 3371
Qy Dp	445 SerSerSerArgThrGluProAlaGlnValAspGluSerThrLeuGluProValIle 464 ::::::
O.y Db	465 GluthrValGluLeuthrAspGlyIleLeuMetAspIleSerProIleGluPheSerAla 484
Q. Db	485 SerasnLeuIleGlnAspLysLeuAsnLeuValAlaalaLysAlaargHisLeuTyrAsp 504 
Oy Dp	505 MetProAspAspArgValLeuAlalleAsnHisAspAspGlyValAsn 520 
λo d	521 ArgSerIleLeuGlyArgIleSerAspAlaValSerAlaValAlaArgAlaIleLeuPro 540
δ	AspCluSerGluAsnGluVallleAspLeuProGluArgThrAlaLeuAlaAsnArgLys

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                                    Sequence 1, Application US/08431718C
Patent No. 6335018
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Robin, Harkness E.
APPLICANT: LOSSMORTE, Sheena M.
APPLICANT: LOSSMORTE, Sheena M.
APPLICANT: HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE PROTEIN OF TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE PROTEIN OF TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE PROTEIN OF TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE PROTEIN OF TITLE OF INVENTION: 1995-05-01
NUMBER OF SEO ID NOS: 4
SOFTWARE: PATENTI VET: 2.1
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Moraxella catarrhalis
US-08-431-718C-1
                                                                                                                                                                                                                                                                                                                                                                                                                        0.000859
136.00
32.95%
19.73%
2.88%
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score:
Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
                      US-08-431-718C-1
                                                                                                                                                                                                                                                                                                              LENGTH: 6975
                                                                                                                                                                                                                                                                                               SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
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QQ	_	CAAGATAGCGGTCTGACCATTGGCAAAAGCACCCTAAACAACGA	2669
οу	211	AsnileLysAlaAlaLeuGluAspileThrGlnGluSerA	225
qq	2670	ACTGTTAAAGATACCAACGAACAAATC	2726
Qγ	226	AspLeuAsnGlySerIleProArgLeuArgGlnThrAlaLe	243
qq	2727	AATGTGAATGGTAGTAATCCAGGTACTGGCATTGCAAATACCGCT	2786
Οy	244	AlaValGlyTyrTyrAspIleAspLeuSerIleIleArgAsnSerIl	263
QQ	2787	AAAATTGGCTTTGCTGGTTCTGATGGTGCAGTT	2819
Qy	264	ValileileHisAspLeuGlyGluProValTyrileAspTyrArgAlaValGluVa	282
ρp	2820		2864
٥y	283		296
Db	2865	AATGTTAAGATTACCAACACGCATTAACGCAGGTGGTAAAGCCATCACAGGG	2924
Oγ	297	AspGluvalProLeuLeu	302
qq	2925	CCAACACTGCCTAGCATTGCCG	2984
Qy	303	IleGlyAspvalPh	3.1.1
qq	2985	CAAGACAAAGACAAATCCAACGTGCCAGCATTAATGATATATTAAATACAGGGTTT	3044
ΟŸ	312	TyrGluThrLysLysAsnLeulleGluAsnAlaSerAlaGluHis	331
QQ	3045	CTAAAAAATAATAACAACCCCATTGACTTTGTCTCC	3080
οy	332	ArgTrpLeuAspArgSerValAspVallleLeuProAspAsnThrAlaAspVal	349
Dp	3081	ACTTTGCCAATGGCAATGCCACCGCC	3125
οy	350	rLeulleTyrAspThrGlyThrGlnTyrArgPheAspGluValValPhePheThr	368
qq	3126	.CATGATACGCTAACAAAACCAGTAAAGTGGTATATGATGAAT	3179
ολ	36	IleAspProLysThrAsnGlnLeuThrThrAspProAspLysLeuProValLys	386
DP	3180	TCATCTAACAGGCACTGATGACAATAAAAAACTTGGCGTCAAA	3239
δλ	38	LeuLeuThrValAsnMetGlyGluAlaTyrAsnLeuGlnAla	406
Dp	3240		3254
δλ	407	alArgAlaLeuSerAsnAspLeuIleAlaThrArgTyrPheAsnMetValAsnThr	425
QQ	3255	ACCAAGTGCTAATGGTAATACAGCAACTAACTTTAATGTTAACTCTAGTGAAAAAAAA	3311
ΟŊ	426	lulleValPheProGluArgGluGlnIleGlnAsnAspGlnValSerPheGluGln	444
qq	3312	CTTGTTAACGCCAAAGACATCGCCGAAAATCTAAACACCCTAGCCAAGGAAATT	3371
δy	445	SerSerSerArgThrGluProAlaGlnValAspGluSerThrLeuGluProVallle	464
qq	3372	AAAGGCACAGCAGCACCCCTACAAACCTTTACCGTTAAA	3431
ΟŊ	465	<b>~</b>	484
QQ	3432	AAAATAATAATGCTGATGACGCCAACGCCATCACCGTGGGTCAAAAGAACG	1485
ΟŻ	485	SerAsnLeulleGlnAspLysLeuAsnLeuValAlaAlaLysAlaArgHisLeuTyrAsp 5	04
QQ	3486	FAATCAAGTCAACACCTAACACTCAAAGGTGAAAACGGTCTTAA	533
Qy	505	MetProAspAspArgValLeuAlalleAspHisAspAspGlvValAsn 5	000

Page 49

3534 ATTAAAACCGACAAAAATGGTACGTTACCTTTGGCATTAACACCACAAGCGGTCTTAAA 3593	Db 4269 AGCGTACGCACCACAGAACAGGGCAATATAATCAAAGACGAAGACAAAAACCCGTGCC 4325
ArgSerIleLeuGlyArgIleSerAspAlaValSerAlaValAlaArgAlaIleLeuPro	Oy 860 AlavalPheGlyAspIle
3594	870 AspLysGlyPheThrAsnAspThr
   GACGGTGGCTTGTCTATTAAAAACCCCACTGGTAGCGAACAAATCCAA	Db 4386 GACTTTGTCTCCACTTATGACACC 4409 RESULT 30
561 ThrProAlaAspValTyrGlnSerLysLysValProLeuTyrValPheValAlaSerAsp 580         :: 3663 GTCGGTGCTGATGGCGAGTTTGCCAAGGTT	US-09-103-840A-2/c; Sequence 2, Application US/09103840A; Patent No. 529428
581 LysproargaspGlyGlnIleGlyLeuGlyTrpGlySeraspThrGlyThrargLeuVal 600 :::    :::	; GENERAL INFORMATION: ; APPLICANT: FLEISCHANN, Robert D. ; APPLICANT: WHITE, Owen R. ; APPLICANT: FRASER, Claire M.
601 ThrLysPheGluHisAsnLeuIleAsnArgAspGlyTyrGlnAlaGlyAlaGluLeuArg 620 	; APPLICANT: VENTER, JOHN C.; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM; TITLE OF INVENTION: TUBERCULOSIS; FILE REFERENCE: 24366-20007.00
621 LeuSerGluAspLysLysGlyValLysLeuTyrAlaThrLysProLeuSerHisProLeu 640 	; CURRENT APPLICATION NUMBER: US/09/103,840A; CURRENT FILING DATE: 1998-06-24; NUMBER OF SEQ ID NOS: 2 ; SOFTWARE: Patentin Ver. 2.1
641 AsnAspGlnLeuArgAlaThrLeuGlyTyrGlnGluValPheGlyHisSerThr 659           3801CACCTAAGCAAA 3812	; SEQ ID NO 2; LENGTH: 4403765; TYPE: DNA; TYPE: DNA; ORGANISM: Mycobacterium tuberculosis
660 AsnGlyPheAspLeuSerThrArgThrLeuGluHisGluIleSerArgSerIleIleGln 679 :::    :::	
680 Asn	-103-840A-2 ment Scores: No.: 66.9 Length:
694 AspLysLeuLysThrGlnAlaProProGluThrTrpGlnAspLeuProValAspPheVal 713 ::: 3927 GAA 3929	ore: 136.00 rect Similarity: 33.98% recort Similarity: 21.78% ery Match: 2.88%
714 AsnGlyLysProSerGlnGlualaLeuLeuAlaGlyValAlaValHisLysThrVal 732 	Gaps:  -103-840A-2 (1-4403765)
AlaAsp	Qy 8 AlaAsnArgSerPheMetProValAlaLeuAlaAlaTyrLeuProLeuMet 24
TyrSerLeuGluValGlySerSerGlyLeuValSerAspAlaAsnMetGlySerSerGlyLeuValSerAspAlaAsnMet	Oy 25
	Qy 36 AlaAsnIleIleAsnHisValPro
ASNARGARIAN SELECTION OF THE STANDARD SELECTION OF THE SE	Oy 44AlaHisAspThrAlaIleAsnGlnAlaLysAlaGlyAsnProPro 58
AsnHisValProTyrArgLeuArgPhePheAlaGlyGlyAspGlnSerlleArgGlyTyr	Qy 59 Val
AlahisaspSerLeuSerProlleSerAspLysGlyTyrLeuThrGlyGlyGlnVa   ::::::   AGCARCACTCTAACTAARGTAAAGGT	QY 63 68  III :::::   Db 461939 CTACTGGAGGCTGTCGGTGTCGCCCCCACCGCGCGCGCAAACCCAGCGGCTGCTC 461880
	Oy 69ArgLeuAsnAlaAlaGlyLeuAsnAlaLysProGln

οy			
QQ	461819		
O O	96	SerArgileGlyGluGlnSerProProLeuGlyLeuAspMetSerValile 112   SerArgileGlyGluGlnSerProProLeuGlyLeu	
O.Y	113	GluGluThrThrProLeuSerLeuGluGluLeuPheAlaGlnGlu 127 ::: AAGCTGTTGACGGCGCAAGGGCGCTAAGGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAA	
ò		Sermhra lumatal viladen broden avati obeset i messoli soli oli oli oli oli oli oli oli oli oli	
g 2	461		
à	148		
g	461594	TACTCCACCGACCTGACCGCCCGCGCGCGAAGGCAAACTCGACCCGGGTCATCGGCCGC 461535	
ò a	158	GluProGluLysProGlyLeuIleLysArgLeuTyrAlaArgLeuPheAsnAsp 175 :::	
ò			
Q	461474		
δ	184	LysAlaLysPheTyrGlnSerSerGlnSerGlyGluThr196	
QQ	461414	   GTGGCGGCGACGTGCCGGAGAGCTTGCGCGACAAGACCATCGTCGCGCTCGATCTCGGC 461355	
δy			
g ,	461		
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g	461294	GACGACATCAAGAACTCGGCCGGCCAAATCATCACGTTCATCGACGAGCTGCACCATC 461235	
ŏ		ThrGlnGluSerAlaMetAspLeuAsnGlySerIleProArg 233	
QQ	461234	GTCGGCGCCGCGCGACGGGGCGATGGACGCCGGCAACATGATCAAGCCGATG 461175	
δy		LeuArgGlnThrAlaLeuVal	
Dρ	461		
à	254	IleIleArgAsnSerIleGlyGluValAspValIleIleHisAspLeuGlyGluProVal 273	
QQ	461129	GAATACCGCAAGCACATCGAGAAGGACGCCGCGCTCGAGCGCCGTTTCCAACAGGTG 461073	
à	274	TyrileAspTyrArgAlaValGluValArgGlyGluGlyAlaAspAspLysAlaPheThr 293    ::	
q	461072	TACGTCGCCGAGCCGTCGGTGGAG	
ά	294	ThrvalalaaspGluValProLeuLeuIleGlyAspValPheHisHis 309	
g	461048	GACACCATCGGCATCCTGCGCGGCTCAAAGACCGCTACGAGGTGCACCAC 460998	
ά	310	GlyLysTyrGluThrLysLysAsnLeulleGluAsnAlaSerAlaGluHisGlyTyrPhe 329	
Q	ob 460997	GGGGTGCGCATCACCGACTCGGCGCTGGTGGCAGCTGCCACTTTGAGCGACCGGTATATC 460938	
S G	330 460937	AspGlyArgTrpLeuAspArgSerValAspVallleLeuProAspAsnThrAlaAspVal 349    :::   ACCGCCCGCTTC	
à	350	SerLeulleTyrAspThrGlyThrGlnTyrArgPheAspGlnValValDhePhePheTile 369	
9	ob 460904		

0	370	AspProf.vsThrAsnGlnLenThrasnBrokeplwstenBrowsllwsArmClus	200
qq	46086	GACTCGCGGCCGTCGAGATC-	
Οy	390	LeuGluGlnLeuLeuThrValAsnMetGlyGluAlaTyrAsnLeuGlnAlaValArgAl	409
QC	460808		460752
Οy	41	LeuSerAsnAspLeu	420
qq	4607	CTGCGCTCCGAGCTGGCCGACCAGAAAGAGAAGTTGGCCGAGCTCACCACCGCTGGCAG	460692
Οy	42	AsnMetValAsnThrGluIleValPheProGluArgGluGInIleGlnAsnAspGln	439
ద	460691	AACGAGAAGAACGCGATCGAAATCGTCCGCGACCTCAAGGAGCAGCTGGAA	460641
δy	44	ValSerPheGluGlnSerSerSerArgThrGluProAlaGlnValAspGluSerThr	459
Ω	460640	GCCCTGCGCGGGAATCCGAGCGGGCCGAAGCCCTGCGCGGAATCCGAGCGGGCCGAA	460611
ΟY	460	LeuGluProValIleGluThrValGluLeuThrAspGlyIleLeuMetAspIleSerPro	479
QQ	460610	::: CCCGACGGCCAAGGCCGACGAGGCCGAGGCCGAGGCCGAAGGCCAAGGCCGAAGGCCAAGGCCAAGGCCAAGGCCGAAGGCCAAGGCAAAGGCCAAAGCCAAAGGCCAAAGGCCAAAGGCCAAAGGCCAAAGGCCAAAGGCCAAAGGCCAAAGGCCAAAGGCAAAGGCCAAAGGCCAAAGGCCAAAGGCCAAAGGCCAAAGGCCAAAGGCCAAAGGCCAAAGGCCAAAGGCCAAAGGCCAAAGGCCAAAGGCCAAAGGCCAAAGGCCAAAGGCCAAAAGCAAAGAAAAAA	460581
δ	48	IleGluPheSerAlaSerAsnLeulleGlnAspLysLeuAsnLeuValAlaAla	497
DP	460580	CTGCGCTACGGACGCATCCCCGAGGTGGAGAAGAAGCTCGACGCGGCGTTGCCCGCAGGCG	460521
Qy	4 9	LysAlaArgHisLeuTyrAspMet	508
QQ	460520	CAGGCCCGGGAGCAGGTGATGCTCAAGGAGGAGGTCGGTC	460461
QY	509	Ala	512
qq	460460	GTGTCGGCGTGGACCGGCATCCCGGCCGGTCGGCTGCTGCTGGAGGCGAGACCGCCAAGCTG	460401
Qy	513	IleAsnHisAspAspGlyValAsnArgSerIleLeuGlyArgIleSerAspAlaValSer	532
qq	460400	CTGCGCATGGAAGACGAGCTGGCGAAGCGGGTCATCGGGCCACAAGGCCGCGTTACC	460344
ογ	533	AlaValAlaArgAlaIleLeuProAspGluSerGluAsnGluValIleAspLeuProGlu	552
qq	460343	GCAGTCTCTGATGCGGTGCGGCGCAGCCGGGCCGG	460299
Qy	553	ArgThrAlaLeuAlaAsnArgLysThrProAlaAspValTyrGlnSerLysLysValPro	572
qq	460298		460278
Qy	573	LeuTyrValPheValAlaSerAspLysProArgAspGlyGln1leGlyLeuGlyTrpGly	592
ΩD	460277	TTCATGTTCTTGGCCC-GACCGGTGTCGCCAAGACCGAGCTGGCCCAAGGCGCTGGC	460222
Óλ	593	rAs	611
g	460221		460177
QY	611		611
Dp	460176	GAGCGAGTACGGCGAGAGCACACCGTGGCTCGGTTGATCGGCGCCCCGGCCTATGT	460117
ΟŊ	612	-GlyTyrGlnAlaGlyAlaGluLeuArgLeuSerGluAspLysLysGlyValLy	629
qq	460116	GGGATACGAGGCGGGCGGGCGGCGGCGCGCGCGCGCGTCCMTACACGGGGG	460057
Οy	629	sLeuTyrAlaThrLysProLeuSerHisProLeuAsnAspGlnLeuArgAlaThrLeuGl    :::    :::	649
qq	460056	GAGAAGGCGCACCCG	460003
δy	649	rGlnGlnGluValPhe 	699
q	CI.	GGTCCTCGACGAGGGCCGGCTCACCGACGGCCACGGCCGCACGGT-CGACTTCC	459950
Οy	699 .	uGluHisGluIleSerArgSerIleIleGlnAsnGlyGlyTrpAsnArg 685	

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114 GluThrThrProLeuSerLeuGluGluLeuPheAlaGlnGluSerThrGluMetGlyIle 133
                                                     3109 ACCCTCACG----
                                                                                                                                                                                                                      153 ValProPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AACTGGAATGCTCCACTGCAATCGCATATTTATAACATTGAGGCAAACCAGAATAAGGCT 3170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCGCGAATTATCCGGCCTATAAGCAAGGGACTGCACTAAGGGCACAACTTAGCCTTCAC 3230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProlleSerArglleGlyGluGlnSerProProLeuGlyLeuAspMetSerVallleGlu 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 AlaClyAsnProProValLeuLeuThrProGluGlnIleGlnAlaArgLeuAsnAlaAla 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlyLeuAsnAlaLysProGlnSerGlnAlaLeuAspValValAsnPheAspAspGlnSer 93
                                                                                                                                                                                                                                                                                                                                                    coli 0157
Db 459949 GCAACACCATTGATCCTGACGTCCAACCTGGGGTGGGGGGGCAGCGC 459901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: US
2.IP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5629
205
157
365
428
51
                                                                                                                                                                                                                                                                                                                                                    <u>ы</u>
                                                                                                                                                                                                                                                                                                                   Welch, Rod
TITLE OF INVENTION: No. 6365723el Sequences of
NUMBER OF SEQUENCES: 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-914-168-2 (1-919) x US-09-453-702B-243 (1-5629)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEPHONE: (608) 251-9166
INFORMATION FOR SEO ID NO: 243:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,7028
FILING DATE: 03-Dec-1999
CLASSIFICATION: <union-color color co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA (genomic)
DESCRIPTION: SEQ ID NO: 243:
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                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                               Valerie
                                                                                                  US-09-453-702B-243/C
; Sequence 243, Application US/09453702B
; Patent No. 6365/23
; GENERAL INFORMATION:
                                                                                                                                                                                                                APPLICANT: Blattner, Frederick
                                                                                                                                                                                                                                                                      Nicole T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                     Guy
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17.75%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                            Plunkett,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.868
                                                                                                                                                                                                                                               Burland,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE : US-09-453-702B-243
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No
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                                                                            RESULT 31
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--ATCAACGTCACTGATGAGAGTGAT 3077
                                                                                              2896 GCGAAATTCGTTAGCGAT----TCGAGTACGCCA------AAATTCAAACAA 2855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2854 CIGGIIGCCGAICCAGAIACCAITAIIGCIGGCAACAGCCAGGGCAGIACICIGACCGCC 2795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2794 ATCATCACAGACTTTCATAACAACCCGTTAAAAGATATGAAAGTGAATTTTGTGGCACCT 2735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2734 GGTGGCTCGCAACTGGACAACACGACC-----GCCACAACAGACCAGTCCGGTATTGTG 2681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2533 GCGATCGCTAACAATACAAATATCGTTACCCTGACTGCCAGTGTGAAAGATGTTATGGA 2474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2239 ACTGCCTCATTAAATTCCATTGTTGCGGGTAACAGTACGGGGAGTACCCTGACGGCAACG 2180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    170 AlaArgLeuPheAsnAspGlyValAsnLysValProArgLeuLysAlaLysPheTyrGln 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         304 GlyAspValPheHisHisGlyLysTyrGluThrLysLysAsnLeuIleGluAsnAlaSer 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          324 AlaGluHisGlyTyr-----PheAspGly-------ArgTrpLeu 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               367
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                                                                                                                                                                                                                                                   3016 GAACCGCCGCAGCAAAATACGGATGCATATGGTGTTGCCACAATAAACATGGTAAGTCAG
                                                                                                                                                                                                                                                                                                                    -------ThrLeuGluProGluLysPro---GlyLeuIleLysArgLeuTyr
                                                                                                                                                                                                                                                                                                                                                                                 2956 GTTGCGGAAGAAATACGATTAGCGCCACGCTGCCAAATGGTTTTTCACAACGGATAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  190 SerSerGlnSerGlyGluThrSerAlaIleGlySerSerHisGlnLysThr-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            214 -----AlaAlaLeuGluAspIleThrGlnGluSerAlaMetAspLeuAsnGlySerIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      232 ProArgLeuArgGlnThrAlaLeuValAlaAlaArgAlaValGlyTyrTyrAspIleAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   252 LeuSerIleIleArgAsnSerIleGlyGluValAspValIleIleHisAspLeuGlyGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 272 ProValTyrIleAspTyrArgAlaValGluVal------ArgGlyGluGlyAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2593 ATCACCGTGGTCCCAAACAGGGAACAATCGGTAATGACCTTGAATGCCGGGTCGGGCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2473 CACCCGTTGCCGGATGAGGATGTGAAATTTACCTTGCCAGCCTCCATGACCGGGAACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134 AsnPro---AsnAspTyrIleProGluTyrGlnGlyGluGlnProAsnSerGluValVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------AspAspLysAlaPheThrThrValAla-----
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QQ	2119 GTCA	GTCACTCTAAGCGAAACAGAAGTCACCACCAATACGCTGGGTCAGGCGGACGGTAACAATG 206	09
ò	368	Thr1leAsp 370	0
QΩ	2059 ACC	ACCAGCAATATTGCCGGACAACATAACGTCGTGGTGAGCCGGAAAGCGCAAGCTTCCGAT 20	2000
Οy		ProLysThrAsnGlnLeuThrThrAspProAspLysLeuProValLysArgGluLeu 389	389
qq	1999 AAT		0
ογ		LeuGluGlnLeuLeuThrValAsnMetGlyGluAlaTyrAsnLeuGlnAlaValArg 408	86
QQ	1939 ACC		1880
ô	409 Alal		8
qq	1879 GAC	GACGCGTTTAACAATGTAATCGCGGGTCAACGCGTCAGATTAAGTGCGCAGCCAACAACT 18	1820
δy	419		22
QQ	1819 AAC	AACATTACGATAGGCGATACGGCTTACACCGATAATAACGGTTATGCGTACGTTAACCTT 17	1760
ογ	423 Val	alPheProGluArgGluGlnIleGlnAsnA	12
qq	1759 CTC	CTCAGCACCCAACCTGGGGTTTATCAGGTGACGGCAACGCTG 17	1718
οy	443 Glu		451
qq	1717 GAC	GTTGACGTGAATGTGGCAAATGGCAAACTCGAGTTAACA	1658
٥y	451	45	451
qq	1657 TCA	TCATCGAAACCAGAAACTACGGTCCATAATAGTGAGGGTATTACGCTGACCGCAACGGCG 15	1598
ò	452		463
QQ	1597 AGA	AGAAATGCGCGGGGTGAATTGATGCCAGGGCAAATTATACACCTTTAGCGTAACGCTTAA 15	1538
δλ	464 Ile		483
qq	1537 GGT	ACTGACCAGTCAGGTCAGGCC	1484
οy	484 Ala	AlaSerAsnLeuIleGlnAspLysLeuAsnLeuValAlaAlaLysAlaArgHisLeuTyr 5(	503
qq	1483 AAA		1424
δy	504 Asp		516
QQ	1423 GAT	GATGTTCCCGTTCAGAGCCAGGTAACGGTTGCGGTTAAGGCAGATGCTAAAACGGCACAT 1.	1364
Qγ	517	5	522
qq	1363 GTT		1304
οy	523 Ile	IleLeuGlyArgIleSerAspAlaValSerAlaValAlaArgAlaIle 5	538
QQ	1303 ATC	SATTACGGATTCCCGGTTGAAGGTGTCGATATTAGTCAT	1244
٥y	539 Let		551
qq	1243 GGG	GCTTAGACACCAAAGGCAGCCCGGTAGTTAATATTCCAACTACGCGTACCGATCAGTCC 1	1184
οy	552	GluArgThrAlaLeuAlaAsnArgLys 5	560
qq	1183 GG	GGGCAAGTCACGGCGACAATAACCAGTACATTGGCAGAAACCTTAACAGTCAATGTGCAA 1	1124
δy	561 Th		580
qq	1123 GT	GTTCCTGGCACAGCCAACCAATCCGCAACCATTACATTGGTTGCCGGCACGGCCGATGAA 1	1064
Qy	581 LY:	LysProArgAspGlyGlnIleGlyLeuGlyTrpGlySerAspThrGlyThrArgLeuVal 6	009

QQ	ob 1063	AGTAAGTCAATT 1052
οy	601 ThrLysPheGluHis	lyTyrGlnAlaGlyAlaGluLeuArg 6
QQ	1051 TTGAAATCCGATGTT	TACCAGCAGAGCGCAAAACTTACG 99
رم درم	2y 621 LeuSerGluAspLysLysGlyVa     :: ::          	yValLysLeuTyrAlaThrLysProLeu 636 
g &	637SerHis	euArgAlaThrLeuGlyTyrGlnGlnGluVal 6
o d	 934 CAGTCAGGCCCTTC	::: ::::::::::::::::::::::::::::::::
Oy	655 P	9
QQ	874 TA	AAAGAGGAACAGCGACACTCATTCCC 81
Οy	9	LeuGluHisGluIleSerArgSerIle 67'
qq	814 ATGC	ATATCGCTGAATCTCATCCAATCGATA 75
Qy	678 IleG	TyrArgLeu 69
Db	754 AAAG	T 70
Oy	694 As	rpGlnAspLeuProValAspPheVal 71 ::
Dp	703AAATTCCCGAGCGAAGG	ATTACACACTC
Qy	714 AsnGlyLysProSerGlnGl	BLeuLeuAlaGlyValAlaValHisLySThrValAla 73
Dp	661AACAATGA	CTTTGAAGCGGGTAAAACCGTTGAT 620
δλ	734 AspAsnLeuValAsnProMe	rgTyrSerLeuGluValGlySer 75
QQ	625 GATTATATGTTTTCAAGTTC	TGGGTGTCTGTCGATGCT
Qy	Qy 754 SerGlyLeuValSerAspAlaAsnMet	AlaileAlaArgAlaGlyileSerGlyValTyr 77
qq	580 TCGGGTAAAGTT	55
Qy	774 SerPheG	ySerAsnArgAlaHisGlnMetThrGlyGly 79
QQ	553GGCG	CACAATAAGCGCTGTTCCCCGACAAGGAGGTACAACC 5
Οy	792 -	IleTrpSerAspAsnPheAsnHisValProTyr
qq	499 TACCAGACCTT	TGGTGGGTGAATAATGGAAATCATACCAATATC 44
Qy	808 ArgLeuArgPhePheAlaGlyG	yAspGlnSerIleArgGlyTyrAlaHisAspSerLeu         ::::::::::
QQ	439 TGGCTA	GCTGCCAATGCGCTC 41
δλ	828 SerProlleSerAspLysGlyT	
qq	418 TGTCATGCTAAAAATGATGGAT	TAATCTTCCTGGCATCACATTTGACGTCTGGCGAA 35
Qy	841 ValLeuAlaValGlyThrAlaG	luTyrAsnTyrGluPheMetLysAspLeuArgLeuAla 86
qq	358	AACAAACGCACGCAGGGATC
οy	861 ValPheGlyAspIleGlyAsn	spLysGlyPheThr
qq	337 CTGTATGGTGAATGGGGGAAC	GGAGCGTTTTCCAGT
Οy	881 AlaGlyValGlyValArgTrpA	laSerProvalGlyGlnValArgVal
QQ	283 CCGGGAGCTTACTGG	CAAGT
Οy	901 GlyvalLysGl	uGluGlyAsnProlleLysLeuHisPhePhelle 915
Ę	262	CACTACTATGTG 23

Qy         205 LysThrCluProTyrAlaAsnIleLysAlaAlaLeuGluAspIleThrClnGluSerAla         224           Db         8629 GTGATTGATAATGGGGATGCTACAACTCAAGAAATTCTTCTGAAAAATCT         8679           Qy         225 MetAspLeuAsnGlySerIleProArgLeuArgGlnThrAlaLeuValAlaArgAla 244         246           Db         8680        AAAGTAGAGCAAGCAATGCAAGCTTTAACTAATGCTAAA         8718           Qy         245 ValGlyTyTyTASpIleAspLeuSerIleIleArgAsnSerIleGlyGluValAspVal         264           Db         8719	QY         305 AspValPheHisHisGlyLysTyGluThrLysLysAsn 317           Db         8776 AACGTATCTACCAATGGTAAAAAACCGGCGAGTATACGTCAATACGAAACAGCCAAAGCC         8835           QY         318 LeuIleGluAsnAlaSerAlaGluHisGlyTyrPheAspGlyArgTrpLeuAsp 335         315           Db         8836 AGAATACAAATTAATGATGCTAAAATGAAGCGGAGCGAATTTAGGTAATGAT         8895           QY         336	QY         358 GINTYRARGPHEASPGIUVAIVAIPHEPHETHLIEASPPROLYSTHRASNGINLEUTHR 377           Db         9016 AAAACAGACTTGAAAATGCAGTAAATGATACAGATCCAACACACGGTATGACT 9069           QY         378 ThrAsp	Oy 415IleAlaThrArgTyrPheAsnMet
RESULT 32  US-09-134-001C-322  US-09-134-001C-322  Sequence 322, Application US/09134001C  Sequence 322, Application US/09134001C  GENERAL INFORMATION:  APPLICANT DOUGCETE-Stamm et al  APPLICANT LYND DOUGCETE-Stamm et al  TITLE OF INVENTION: DEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  TITLE OF INVENTION: DEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  TITLE OF INVENTION: DEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  CURRENT APPLICANTON NUMBER: US/09/134,001C  CURRENT FILING DATE: 1998-08-13  PRIOR FILING DATE: 1997-11-08  PRIOR PLICATION NUMBER: US 60/055,779  PRIOR PLICATION DATE: 1997-08-14  SEQ ID NO 322  LENGTH: 3049  TYPE: DNA	Staphylococcus epidermidis C-322 res: 0.0146	46 8143 66 8197 86 8254 8254 8314	0y 113 GluGluThrThrProLeuSerLeuGluGluLeuPhealaGlnGluSerThrGluMetGly 132

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                                                                                                                                                  9589 ATTAATAATTACACAACAAAAGGTAGAGAAGCACAAAATATAGCAAGTTCTGCTGACACT 9648
                                                                                                                                                                                                                                                                                     9529 GAAAAATTAGATCAAGCGATTAATAGTCAACCATCACTAAATGGTATGACTCAAGAATCT 9588
                                                                                                                                                                                                                                                                                                                                                                                                                                                            9709 GAGGCAACTAATGCACTTAACGAAGCAAAAACAACATTTAACGGCAGATACACTTCTTTA 9768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----AGTGCTTATAACAATACTATTCGTTCGCTACAATCTGAAATTACACAGACTGAA 9885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9886 AATAGAGCAAATACTATCATC-----AATAAGCCTATTCGTTCTGTTGAAGAAGTAAAT 9939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9940 AATGCATTGCATGAAGTAAACCAATTGAACCCAACGCTTAACAGATACAATTAACTTATTA 9999
                                                                                                                                                                                                                                512 AlaileAsnHisAspAspGlyValAsnArgSerIleLeuGly-----ArglleSer 528
                                                                             LeuAsnLeuValAlaAlaLysAlaArgHisLeuTyrAspMetProAspAspArgValLeu 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 544 GluAsnGluValIleAspLeuProGluArgThrAlaLeuAlaAsnArgLysThrProAla 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    564 AspValTyrGlnSerLysLysValProLeuTyrValPheValAlaSerAspLysProArg 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               584 AspGlyGlnIleGlyLeuGlyTrpGlySerAspThrGlyThrArgLeuValThrLysPhe 603
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                                                                                                                                                                                                                                                                                                                                                                                      529 AspAlaValSerAlaValAlaArgAla------IleLeuProAspGluSer----
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Sequence 1002, Application US/09221017B

Patent No. 6444799

Patent No. 644799

Patent No. 6444799

Patent No. 644799

Patent No. 64479

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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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ZIP: 94304-1018
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2585 GTTACACCGGGAGCTTTTTCTGCGAGGATGATGTGGAACGCTCTTATATCAACCTGAAT 2526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2642 TACTATGGGAGTAGGGACGTTATATCCGGGCA---TCGGCTCTCACGCGGTCGGTGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----SerIleLeuGlyArgIleSerAspAlaValSerAlaValAlaArgAlaIle---
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                   for Windows Version 2.0b
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Indels:
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Matches:
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ORIGINAL SOURCE:
ORGANISM: PORYPHYROMONAS GINGIVALIS
                                          US/09/221,017B
23-DEC-1998
                                                                                                                                                                                                                                                                                                                         PCT/AU98/01023
                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1546
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP2911
                                                                                                                                                                                                                                                                                                                                                                                                          32,430
                                                                                                                                                                                                                                                                                                                                                                              NAME: MODICOY, GLADYS H
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
Windows
                                                                                                                                                                                                                                                                               FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/F
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 706141
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 9377 base pairs
              SOFTWARE: FastSEQ for CURRENT APPLICATION DATA:
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34.00%
21.39%
2.85%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
EDNESS: double
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                                                       APPLICATION NUMBER:
FILING DATE: 23-DEC
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nuclei
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GATTATTTCCTTGTGCGGCTGGAT-----GCCGGACTGAAAGCCTACGATCCTCAGCAG 1260
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1430 GCCGGCAATGTCTGGACGATAAAGGAGTATGAGAAATCAGGAGGACGGTCTCTTTCGTTTC 1371
                                                                                                                                                                                                                                                                                                                                                 Sequence 117, Application US/08961083
Patent No. 6159469
GENERAL INFORMATION:
APPLICANT: Chai et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
                                   AspLysGlyPheThrAsnAspThrLysIleGlyAlaGlyValGlyValArgTrpAlaSer
                                                                                                                                                                          ...-----GluGluGlyAsnProlleLysLeuHis
                                                                                                    890 ProValGlyGlnValArgValAspValAlaThrGlyValLys-----
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190
124
318
348
53
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COMPUTER READABLE FORM:
MEDIUW TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-914-168-2 (1-919) x US-08-961-083-117 (1-3121)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: PB340P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                   1199 ATTGCAGTAGGCTATCCGTTC 1179
                                                                                                                                                                                                                                             913 PhePheIleGlyThrProPhe 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 117:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 3121 base pairs
TYPE: nucleic acid
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32.04%
19.39%
2.83%
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                    RESULT 34
US-08-961-083-117
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|GACTGGCTTTCCCTTAT-----GGCAATGCTCGCCATATACCCTTTGAGTTACGT 1611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGAATGTCGAATACAGGACAAAGCTGTTCTGGAAGTTTCGCGCAGCAGCTTTTGTCGAT 1431
                                                                                                                                                                                                                            2249 CACAGCTTCATGGAATATGGGGTGGAAAGCTCGCTCCGTTTCCCTCGTCTCCTCTTCCCA 2190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1940 ACGGAGCAGTTTATCCTCGGCTCGGCATATATACTGAACTATACCACGGCTTCGTCCATG 1881
                                                                                                                                                                                                                                                                                                                                  674
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2429 TATATTCTTACCGTTCCGGCCAAGAGCAAATCGTTCGAAGCCGGAAGTCCTCGGCACAAT
                                                                                                                                                                                                                                                                                                                                                                    -------GAGTTTAGTAGACACGTCCG------GAGTTTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2045 CTGCGTCATACGATCCGCCTGCTGGATGTCGAT------TATCTCCATCTC
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                                                                        -----ArgAspGlyTyrGlnAlaGlyAlaGluLeuArg
                                                                                                                                                                                                                                                                                                                                 655 PheGlyHisSerThrAsnGlyPheAspLeuSerThrArgThrLeuGluHisGluIleSer
                                                                                                                                                                                                                                                                                                                                                                                                                                          2102 CGGGTGATTCTCTCCGCTCAACTCAATTATTCATGG----CAGACCTACCTGCACAATCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuArgTyrArgLeuAspLysLeuLysThrGlnAlaProProGluThrTrpGlnAspLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProVal-----AspPheValAsnGlyLysProSerGlnGluAlaLeu-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------ValAsnProMetArgGlyTyrArgGlnArgTyrSerLeuGluValGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           845 GlyThrAlaGluTyrAsnTyrGluPheMetLysAspLeuArgLeuAlaValPheGlyAsp
                                                  TrpGlySerAspThrGlyThrArgLeuValThrLysPhe---GluHisAsnLeuIleAsn
                                                                                                                                                      2309 GGGGCGGAGATGTTCAATATCAAACTCAAGGGTGCTTACGAAGCCATTCGCAAGGGTTCG
                                                                                                                                                                                         LeuSerGluAspLysLysGlyValLysLeuTyrAlaThrLysPro-------
                                                                                                                                                                                                                                                              ---LeuSerHisProLeuAsnAspGlnLeuArgAlaThrLeuGlyTyrGlnGlnVal
                                                                                                                                                                                                                                                                                                                                                                                                       675 ArgSerIleIleGln-----AsnGlyGlyTrpAsnArgThrTyr----Ser
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                                                                                                                                                                                                                                                                                                 2189 TTCATTTCTGACGAAACGCGCCGGCGGCTACGGGCATCCACGGAATGGAAG-----
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214 24 MetThrSerGlnAlaLeuAlaGlnGlnAsnAsnProAlaAsnIle-----IleAsnHis 41 qq us-09-914-168-2.rni

Qy	9	leAspProLysThrAsnGlnLeuThrThrAspProAspLysLeuProValLysArgGlu 38
qa	1007	:::    :::CCTTATACAACAGAAATTCAGGATCCAACACTTCTGAAAAATGGTGTAAG 1060
Qy	389	uLeuGluGlnLeuLeuThrValAsnMetGlyGluAlaTyrAsnLe
qa	1061	
Qy	409	aLeuSerAsnAspLeuIleAlaThrArgTyrPheAsn
qa	1082	
Qy	425	1SerPheGluGln 4
qq	1121	GAAACT 1
Qy	445	rSerSerSerArgThrGluProAlaGlnValAspGluSerThrLeu 4
qq	1139	
ΟŸ	461	JThrValGluLeuThrAspGlyIleLeuMetAspIleSerProIle 4
QQ	1199	CTTAACAAAGTT 1
Qy	481	luPheSerAlaSerAsnLeulleGlnAspLysLeuAsnLeuVal
qq	1244	TATAACTGTAAGTTATAACTTAATAGACACTACCTCAGCATATGTT 1
δλ	496	laalaLysAlaArgHisLeuTyrAspWetProAspAspArgValLeuAlaIleAsnHis ::       :::
qq		GCAAAAACGCAAGTTTTCCAT 13
QY	516	lSerAlaValAla 53
qa	1328	ACAAGCTAGTT
Qy	536	AlalleLeuProAspGluSerGluAsnGluVallleAspLeuProGluArgThr
QQ	1346	GGATATAGAAAATCCTGCCAAAGAGCAAGTAATA
Qy	556	AlaAsnArgLysThrProAlaAspValTyrGlnSerLysLysValProLeuTyrVa
qq	1385	ACACACCGTATACAGTTAAAACACACCTA 14
Qy	576	eValAlaSerAspLysProArgAspGlyGlnIleGlyLeuGlyTrpGlySerAs
qa	1430	CTTATAATTTGGGTGAAAATAATGAGGAA
Οy	296	ArgLeuValThrLysPheGluHisAsnLeuIleAsnArgAspr
qa	1460	TACTGAAACATCAACTTTCCAATTAGAGTATAAGAAAAAAAA
Qy	613	SlnAlaGlyAlaGluLeuArgLeuSerGluAspLysLysGlyValLysLeuTyr
qa	1511	::
Qy	633	roLeuSerHisProLeuAsnAspGlnLeuArgAlaThrLeuGlyTyrGLnGln 6
QQ	1544	AATGATCGTTATCGTAGATATTAAGTCTAAGT 15
Qy	653	heGlyHisSerThrAsnGlyPheAspLeuSerThrArgThrLeuGluHisG
QQ	1583	GAAGCGCCGACTGATACGCTAAA 16
οy	673	leSerArgSerIleIleGlnAsnGlyGlyTrpAsnArgThrTyrSerLeuArgTyrArg 69
qq	1607	TIL ::::::
Qγ	693	luThrTrpGlnAspLeuProValAspPhe 71
qq	1625	GCTTCAAAGAAATGTAC
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Alignment Scores:
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1949 GATGGAACAAAATCGTATGCCATTTATGATTTGAAGAAACCATTATTTGATACATTAAAT 2008
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                                                                                              1721 GAAGAAGGT-----ACAGACGGTTACAAAGATGATTACACATTTACTGTAGCT 1768
                                                                                                                                                                                                                                                       1829 CAAAGCAATCTGTCTGGTGTCTATACATTGGCTTCAGATATGACCGCAGATGAGGTGAGC 1888
                                                                                                                                                                                                                                                                                                                                   1889 TTAGGCGATAAGCAGACAAGTTATCTCACAGGTGCATTTACAGGGAGCTTGATCGGTTCT 1948
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2189 AACAGCTCGTTTACAGGGAAACTT--------ATCGCAAATCACCAG 2227
                                                                                                                                                                                                                766 ArgAlaGlyIleSerGlyValTyrSerPheGlyAspAsn------Ala 779
                                                                                                                                                                                                                                                                                                                                                                          AspAsnPhe---AsnHisValProTyrArgLeuArg-------PhePheAla 813
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             850 AsnTyrGluPheMetLysAspLeuArgLeuAlaValPheGlyAspIleGlyAsnAlaTyr
                                                       733 AlaAspAsnLeuValAsnProMetArgGlyTyrArgGlnArgTyrSerLeuGluValGly
                                                                                                                                   753 SerSer-----GlyLeuValSerAspAlaAsnMetAlaIleAla-----
                                                                                                                                                                                                                                                                                            TyrGlySerAsnArgAlaHisGlnMetThrGlyGlyIleGlnAlaGlyTyrIleTrpSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----LeuSerProlleSerAspLysGlyTyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      814 GlyGly------AspGlnSerIleArgGlyTyrAlaHisAspSer------
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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1185 Avenue of the Americas
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Patent No. 5849564
GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Bohenzky, Roy A.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: POLYPEPTIDES FR.
TITLE OF INVENTION: HERPESVIRUS, DUNDBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuThrGlyGlyGlnValLeu-----
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ADDRESSEE: COOPER &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New York
: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 GlnGluSerThrGluMetGlyIleAsnProAsnAspTyrIleProGluTyrGlnGlyGlu 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlnProAsnSerGluValValValProProThrLeuGluProGluLysProGlyLeuIle 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SerGlnAlaLeuAlaGlnGlnAsnAsnProAlaAsnIleIleAsnHisValProAlaHis 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 LeuPheAlaAsnArgSerPheMetProValAlaLeuAlaAlaTyrLeuProLeuMetThr 25
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167
118
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches:
APPLICATION NUMBER: US/08/770,379
                                                            ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 52342
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 391-0525
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 32207 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                       DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132.50
33.29%
19.51%
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                                                                                                                                                                                                                                                                                                                                                                Linear
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Best Local Similarity:
Query Match:
                      FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: lin
MOLECULE TYPE:
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٥y	206 ThrGluProTyrAlaAsnIleLysAlaAalaLeuGluAspIleThrGlnGluSerAlaMet 225		
qq	1997 ATGGAGGAATGGAAGCAGAAAGTACTGGCTCTTGACAATGCGTCTCCGGAACGTGTCGCC 2056	975	Gluval I leAcoLouDr
δ i	AspLeuAsnGlySerIleProArgLeuArgGlnThralaLeuValAlaAlaArg	2909	GAGTCGCTCGAGAGCGA
2 2	205/ ALCUIC	Qу 566 Туг	TyrGlnSerLys
S G	ALAVALOTYITYINAPILEOSPINALALIILE 111   11   11   11   11   11   11   11	Db 2969 ACC	ACCCAGCGCAAAATGGC
δ		576	PheValAlaSerAspLy
qq	2159 CCAACGCCGATGGAATACAGCGCCCGCCCCCCGGACCCAAGGATATAGACAGA 2215	3029	TCGGGGCG
Qy	279 AlaValGluValArgGlyGluGlyAlaAspAspLys	Qy 596 GIy	GlyThrArgLeuValTh
q	2216 GCTACATCCATCCACGGGGAACAGGCGTGGAAGATACAGCAGGCGTTCAAGGATTTC 2275	3008	ol valacini in in in in in in in in in in in in
δλ		3119	GAC
වූ	AACTTCGCCGTCCTGCGGCCCGCTGACTGGGATGCCCTGGCAGCGGAGTACCAACGCCGT	Qy 633	ThrLysProLe
o y	298GluValProLeuLeuIldGlyAspValPheHisHisGlyLysTyrGluThrLys 315 1	Db 3179 GTA	 GTAGAGGAGAAGCAAAG
3 8	LvsAsnLeulleGluAsnAlaSerAlaGluHisGlvTvrPheAspGlvArgTroLeuAsp	Qy 648 Leu	LeuGlyTyrGlnGlnGl
. අ	CTAGGGACGCTGAACGACATCTACATGGAT	Db 3239 ACT	ACTGAGACCGCTCTCGA
ογ	336 ArgSerValAspValIleLeuProAspAsnThrAlaAspValSerLeuIleTyrAspThr 355	Qy 668 Thr	ThrLeuGluHisGluIl
D D	:::	3293	CTCCTGCAGCGAGCGGT
οy	356 GlyThrGlnTyrArgPheAspGluValValPhePheThrileAspProLysThr 373	Qy 686 Thr	ThrTyrSerLeuArgTy 
QQ	2480 CTAACGCCGTATCAGGACCAAGTCAGCTTTTTGTTGCGCACCATAGGG 2527	2055	
ò	374 AsnGlnLeuThrThrAspProAspLysLeuProValLysArgGluLeuLeuGluGlnLeu 393	3398	eurn or anordeu
QQ	greceaecece		ValAlaValHi
QY	394 LeuThrValAsnMetGlyGluAlaTyrAsnLeu	3419	
qq	2561 AGCGTGCAGGCACTGAGGCTTAGCCACGCGCTCCAGTCCGGCGATTTGCAGCAGGCCACG 2620	7 1	
δγ	408 ArgAlaLeuSerAsnAspLeuIleAlaThrArgTyrPheAsnMetValAsnThrGlu 426		Argennagiyi serbe
qq	CCT		
ογ	427 IleValPheProGluArgGluGlnIleGlnAsnAspGlnValSerPheGluGlnSer 445	40 /	::: ::: :::
qq	2681 TCCGTGTTCAACGACCACGGACTTCAGGTGCGATCAGAGGTCGCGGATTATGTGGAGGCC 2740		ATATCACCATCCACACT
ò	446 SerSerArgThrGluProAlaGlnValAspGluSerThrLeuGluProValIleGlu 465	RESULT 36 US-08-757-669A-20	A-20
qq	111 2741 CAACGAGGCGACGCACACGCCACACGTCCCAAAGATACAGGCACCAAAGACT 2800		Sequence 20, Application Patent No. 6183751
δy	466 ThrvalGluLeuThrAspGlyIleLeuMetAspIleSerProIleGluPheSerAlaSer 485	GENERAL INFO	₹
QQ	2801 CTGATTCCACATCCGGACGCAATCGTCGCGGACGACTACCCGCCTTTCTTAAGACG 2857	APPLICANT: APPLICANT: APPLICANT:	T: Bonenzky, T: Russo, Jam m: Edolman T
δλ	486 AsnLeulleGlnAspLysLeuAsnLeuValAlaAlaLysAlaArgHisLeuTyrAspMet 505		T: EUELMAN, I
qq	2858 TCCCTACTGCAGCAAGGGCCAAACTTCTGGCGCTACAG		TILLE OF INVENTION: STITLE OF INVENTION: S
δy	506 ProAspAspArgValLeuAlaIleAsnHisAspAspGlyValAsnArgSerIleLeuGly 525		CORRESPONDENCE ADDRESS ADDRESSEE: Cooper &
qq	2896 2896	STREET:	118
ò,	526 ArgileSerAspAlaValSerAlaValAlaArgAlaIleLeuProAspGluSerGluAsn 545	STATE	New York

SCCATCATATACGACAAGGTCCTGGAGCGCGAATCCTACGAGACG 3118 3352 ----- CGGGCGGACTTC 2908 SACATGCGCGCCGCAGAGCCCCAGAGAAAGCATCGCGCGAGGAA 2968 SCACACGCCATCACTCTTACAGCAGCACCCAGTGCGATC 3028 AGAAAATCCAAACCCTGAAATCCCTGGTA-----3397 ATAGACACGGTGGCC---- 3448 -------3466 HisLysThrValAlaAspAsnLeuValAsnProMetArgGlyTyr 743 ProGluArgThrAlaLeuAlaAsnArgLysThrProAlaAspVal 565 -----LysValProLeuTyrVal 575 LysProArgAspGlyGlnIleGlyLeuGlyTrpGlySerAspThr 595 LeuArgLeuSerGluAspLysLysGlyValLysLeuTyrAla··· 632 JeuSerHisProLeuAsnAspGlnLeu-----ArgAlaThr 647 lleSerArg----SerIleIleGlnAsnGlyGlyTrpAsnArg 685 AspPheValAsnGlyLysProSerGlnGluAlaLeuLeuAlaGly 725 hrLysPheGluHisAsnLeuIleAsnArgAspGlyTyrGlnAla 615 TyrArgLeuAspLysLeuLysThrGlnAlaProProGluThrTrp 705 JeuGluValGlySerSerGlyLeuValSerAspAlaAsnMetAla 763 atrick S.

atrick S.

undue Associated Kaposi's Sarcoma Virus
sequences and uses Thereof ::: ||||:::|||| CTCCAGGGACTGTACCAACAGGACAGGAGGCC 3514 [leSerGlyValTyrSerPheGlyAspAsnAla 779 & Dunham LLP Le of the Americas n US/08757669A Roy A.

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167
118
300
271
39
                                                                                 OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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FILING DATE:
CLASSIFICATION: 424
ATTORREY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 45185-F
REFERENCE/DOCKET NUMBER: 45185-F
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEPHONE: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                 ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                         DNA (genomic)
                                                                                                                                                                                                                                                                                                                                    LENGTH: 32207 base pairs
TYPE: nucleic acid
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132.50
33.29%
19.51%
2.80%
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U.S.A.
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2422 2479 2158 CCAACGCCGATGGAATACAGCGCCAGCCCTCCCGGACCCAAAGGATATAGAC---AGA 2215 GCTACATCCATCCACGGGGAACAGGCGTGGAAGAAGATACAGCAGGCGTTCAAGGATTTC 2275 2527 2336 GGTTCGCCCCTTCCGCCGCCGCCGTCCACCGCTC---TCAGGGTTCCTGGAGACGATC 2392 1895 ACTCTGGCCACGACGCCATCGAGACGGCTACGAAACGGAAACTATACAGATGATGATCAA 1954 955 AGGGACCTCAAAGAGGCTCAAAAACACGAGACC-------AATCGGGCC 1996 290 AGCGTGCAGGCACTGAGGCTTAGCCACGCGTCCAGTCCGGCGATTTGCAGCAGGCCACG 2620 243 ArgSerValAspValIleLeuProAspAsnThrAlaAspValSerLeuIleTyFAspThr 355 298 -----GluValProLeuLeuIleGlyAspValPheHisHisGlyLysTyrGluThrLys 315 316 LysAsnLeuIleGluAsnAlaSerAlaGluHisGlyTyrPheAspGlyArgTrpLeuAsp 335 374 AsnGlnLeuThrThrAspProAspLysLeuProValLysArgGluLeuLeuGluGlnLeu 393 407 ArgAlaLeuSerAsnAspLeuIleAlaThrArgTyrPheAsnMetVal---AsnThrGlu 426 SerSerSerArgThrGluProAlaGlnValAspGluSerThrLeuGluProValIleGlu 465 AsnLeulleGlnAspLysLeuAsnLeuValAlaAlaLysAlaArgHisLeuTyrAspMet 505 ThrGluProTyrAlaAsnIleLysAlaAlaLeuGluAspIleThrGlnGluSerAlaMet 1997 ATGGAGGAATGGAAGCAGAAAGTACTGGCTCTTGACAATGCGTCTCCGGAACGTGTCGCC AlaValGluValArgGlyGluGlyAlaAspAspLys-------------GlnSerSerGlnSerGlyGluThrSerAlaIleGlySerSerHisGlnLys 259 IleGlyGluValAspValIleIleHisAspLeuGlyGluProValTyrIleAspTyrArg 291 -----AlaPheThrThrValAlaAsp------2276 AACTTCGCCGTCCTGCGGCCCGCTGACTGGGATGCCCTGGCAGCGGGAGTACCAACGCCGT 2423 ---AAGCTCCGCTCCTTTCTGCCCGACGCGCAGCCTTTTCAGGCGCCCCCTTCGACTGG 356 GlyThrGlnTyrArgPheAspGluValValPhePhe-----ThrIleAspProLysThr 394 LeuThrValAsnMetGlyGluAlaTyrAsnLeu---------GlnAlaVal 427 IlevalPheProGluArgGlu---GlnIleGlnAsnAspGlnValSerPheGluGlnSer 2741 CAACGAGCCGACGCACACGCCACACGTCCCACGTCCAAAGATACAGGCACCAAAGACT CTGATTCCACATCCGGACGCAATCGTCGCGGACGGACTACCC---GCCTTTCTTAAGACG AspLeuAsnGlySerIleProArgLeuArgGlnThrAlaLeuValAlaAlaArg----------IleArgAsnSer 2393 CTAGGGACGCTGAACGACATC------TACATGGAT-------GTGGGCACGCCCTGGAGCTCCCTGCCACAGAGTACGCGCGCATCGCCTCCAACATGAAG ThrValGluLeuThrAspGlyIleLeuMetAspIleSerProIleGluPheSerAlaSer --LysPheTyr---244 AlaValGlyTyrTyrAspIleAspLeuSerIle-----2099 2216 206 2159 408 446 2801 189 2621 486 186 ōλ qq g qq g g qq g qq g qq g qq δ a ò ò ò δ δ ò q ٥y ò δ οy δ ŏ δ δ δy ò

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                                    506 ProAspAspArgValLeuAlaIleAsnHisAspAspGlyValAsnArgSerIleLeuGly
                                                                                      526 ArgIleSerAspAlaValSerAlaValAlaArgAlaIleLeuProAspGluSerGluAsn
                                                                                                                                         546 GluValIleAspLeuProGluArgThrAlaLeuAlaAsnArgLysThrProAlaAspVal
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TCCCTACTGCAGCAAGGCCAAACTTCTGGCGCTACAG-
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Patent No. 6348586
GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A
APPLICANT: Russo, James J
APPLICANT: Redlman, Isidore S
APPLICANT: Moore, Patrick S
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TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND TITLE OF INVENTION: USES THEREOF FILE REFERENCE: 45185-G-PCT-W. CURRENT ELING DATE: 1999-11-17 CURRENT FILING DATE: 1999-11-17 PRIOR APPLICATION NUMBER: PCT/US97/13346 PRIOR FILING DATE: 1997-07-22 NUMBER OF SEQ ID NOS: 30 SOFFWARE: Patentin Ver. 2.0 SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1637 ---TCCGTGAGACAGTCCCTTTCCACCTGCAGACCCTGCTGCAGATGCCCTGGAC 1693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1715 ------GCCCTTCTTGGTGAGGGACCACGTTGGGGAGACACTCCTAGGA 1762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86 ValValAsnPheAspAspGlnSerProIleSerArg11eGlyGluGlnSerProProLeu 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106 GlyLeuAspMetSerVallleGluGluThrThrProLeuSerLeuGluGluLeuPheAla 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 GlnGluSerThrGluMetGlyIleAsnProAsnAspTyrIleProGluTyrGlnGlyGlu 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----ATAATATCCAGCCTTGTGGGCATCCAAAA-----TTAGTC 1834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1835 AGGGACCAGGGCGCGGACAAGTGGGCCACTGCCGTGACAAGGCTAACTGACTCAATTA 1894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1895 ACTCTGGCCACGACGCCATCGAGACGGCTACGAAACGGAAACTATACAGATTGATCCAA 1954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1997 ATGGAGGAATGGAAGCAGAAAGTACTGGCTCTTGACAATGCGTCTCCGGAACGTGTCGCC 2056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   146 GlnProAsnSerGluValValValProProThrLeuGluProGluLysProGlyLeulle 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   166 LysArgLeuTyrAlaArgLeuPheAsnAspGlyValAsnLysValProArgleuLysAla 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 LeuPheAlaAsnArgSerPheMetProValAlaLeuAlaAlaTyrLeuProLeuMetThr 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AspThrAlaIleAsnGlnAlaLysAlaGlyAsnProProValLeuLeuThrProGluGln 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           206 ThrGluProTyrAlaAsnIleLysAlaAlaLeuGluAspIleThrGlnGluSerAlaMet 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 SerGlnAlaLeuAlaGlnGlnAsnAsnProAlaAsnIleIleAsnHisValProAlaHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1589 -----AAACTTGGTGAGGGGTTCACCGGGGGCCCGCACCTCCTGACAAGCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 IleGlnAlaArgLeuAsnAlaAlaGlyLeuAsnAlaLysProGlnSerGlnAlaLeuAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1550 -----CACAGTACAAACCTTGGAAACCTAGTTACCAACGTACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1763 TACGGGTCGGTGCAG-------GACTACAAGGAGGAGGGTACAG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ...-LysPheTyr-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32207
167
118
300
271
39
                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Kaposi's sarcoma-associated herpesvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-914-168-2 (1-919) x US-09-230-371A-20 (1-32207)
                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1955 AGGGACCTCAAAGGGCTCAAAAACACGAGACC-----
                                                                                                                                                                                                                                                                                                                                                                                                                         Matches:
                                                                                                                                                                                                                                                                                                                                                                                               Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels:
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132.50
33.29%
19.51%
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                            32207
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                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match:
                                                                                                                                                                                                                                            LENGTH:
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δŏ	AsnGlySerIleProArgLeuArgGlnThrAlaLeuValAlaAlaArg	Db 2909 GAGTGCTCGAGAGCGACATGCGCCGC
QQ	ACCCTC	Qy 566 TyrGlnSerLys
ò a	244 AlaValGlyTyrTyrAspileAspLeuSerIleIleArgAsnSer 258 2099 GCAGAGAGAGAGTTCAAAATACTCCCCGTACCGCGACGCCCGTTCAAAGATACTACTACTACCCCGTACCGCGACGCCCTCCAAGAGACGTTCAAAAAAAA	2969
Qy		Qy 576 PheValAlaSeraspLysProArgAspGl   11   111   Db 3029TCGGGGGGGCGCCGCTATCCTT
g :		Qy 596 GlyThrArgLeuValThrLysPheGluHi
g g	2/9 mayalsiuvalaigolysiuulayalahspablus 2/10 mayalsii:	3068CTCGA
δý	291AlapheThrThrValAlaAsp	Qy 616 GlyAlaGluLeuArgLeuSerGl
QQ	AACTTCGCCGTCCTGCGGCCCGCTGACTGGGATGCCCTGGCAGGGGGAGTACCAACGCCGT	633
yo d	298GluValProLeuLeuIleGlyAspValPheHisHisGlyLySTyrGluThrLys 315	
ò		648
qq	2393 CTAGGGACGCTGAACGACATCTACATGGAT2422	Db 3239 ACTGAGACGGCTCTCGAGCTAGAGGCGGC
οy	ArgSerValAspValIleLeuProAspAsnThrAlaAspValSerLeuIleTyrAspThr :::	
QQ	TTTCAGGCGCCGCCTTCGACTGG	Qy 686 ThrTyrSerLeuArgTyrArgLeuAspLy
6 6	356 GlyThrGlnTyrArgPheAspGluValPhePheThrIleAspProLysThr 373  2480 CTAAGGCGTATCAGGACCAAGTCAGCTTTTCTTGCGCACCATAGG 2527	3353
δ	spProAspLysLeuProValLysArgGluLeuLeuGluGlnLeu	
qq	2528	3398
δ	394 LeuThrValAsnMetGlyGluAlaTyrAsnLeuGlnAlaVal 407	
Op	2561 AGCGTGCAGGCACTAAGCCACGCGTCCAGTCCGGCGATTTGCAGCAGGCCACG 2620	3419
ò i	408 ArgAlaLeuSerAsnAspLeuIleAlaThrArgTyrPheAsnMetValAsnThrGlu 426	VY /44 AtgornatgrytserLeugitagratorYse
QQ	2621 GTGGGCACGCCCTGGAGCTCCCTGCCACAGAGTACGCGCGCATCGCCTCCAACATGAAG 2680	Ov 764 IleAlaArqAlaGlyIleSerGlyValTv
Qy Bp	427 IleValPheProGluArgGluGlnIleGlnAsnAspGlnValSerPheGluGlnSer 445                 ::           ::::::::::	3467
٥y	446 SerSerArgThrGluProAlaGlnValAspGluSerThrLeuGluProValIleGlu 465	RESULT 38 US-09-103-840A-1
QQ	2741 CAACGAGCGACGCACACGCCCACGTCCCACGTCCAAAGATACAGGCACCAAAGACT 2800	; Sequence 1, Application US/U91U384UA; Patent No. 6294338.
δλ	466 ThrValGluLeuThrAspGlyIleLeuMetAspIleSerProIleGluPheSerAlaSer 485	; APPLICANT: FLEISCHMAN, Robert D APPLICANT: GLITTE OF THE CAME OF THE CA
qq	2801 CTGATTCCACATCGGACGCAATCGTCGCGGACGGACTACCCGCCTTTCTTAAGACG 2857	, APPLICANT: WILLS, CWELL N. ; APPLICANT: FRASER, Claire M. · APPLICANT: VENTER, John C
ر ا	486 AsnLeulleGlnAspLysLeuAsnLeuValAlaAlaLysAlaArgHisLeuTyrAspMet 505	TITLE OF INVENTION: DNA SEQUENCES FO
3 8		; FILE REFERENCE: 24350-2000.00 ; CURRENT APPLICATION NUMBER: US/09/10 · CIRPENT FILING DATE: 1998-06-24
අ		
οy	526 ArglieSerAspAlaValSerAlaValAlaArgAlaIleLeuProAspGluSerGluAsn 545	; SEQ ID NO 1 ; LENGTH: 4411529
q	2897	) ORGANISM: Mycobacterium tuberculosi
٥y	546 GluValIleAspLeuProGluArgThrAlaLeuAlaAsnArgLysThrProAlaAspVal 565	; OTHER INFORMATION: H3/RV US-09-103-840A-1

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SASnLeulleAsnArgAspGlyTyrGlnAla 615
:::::: |||::: |||:::
CAAGGTCCTGGAGGGGGATCCTA&GAGAGG 3118
                                                                                                                                                                                                                                                   uAspLysLysGlyValLysLeuTyrala--- 632
: ||| :: :::|||||||
iGACCATCAAGTCCATCACGGTATACGCTCC 3178
                                                                                                                                                                                                                                                                                                                   udsnaspaspGlnLeu-----argalaThr 647
| |||||||
|GCTGGACGAGGTGAAAAGCAGCGAGCAAC 3238
                                                                                                                                                                                                                                                                                                                                                                                      IsSerThrasnGlyPheaspLeuSerThrarg 667
:::||||::||| || ||
:GGCTACGCACGCGACGAC-----GCTAGA 3292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :::
ACCGTTGCGCGTTAAGGGGGGGAAGGCCGCG 3352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLeuLysThrGlnAlaProProGluThrTrp 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCAGCTCTTACAGCAGGCACCCAGTGCGATC 3028
                                                                                                                                        | | | | :::|||:::
| ACAGGACCCGGTGGCTTC----- 3067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------GGCCAGGCCAGGAGACC 3466
                                               yGlnIleGlyLeuGlyTrpGlySerAspThr 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                       -SerIleIleGlnAsnGlyGlyTrpAsnArg 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aAspAsnLeuValAsnProMetArgGlyTyr 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rSerGlyLeuValSerAspAlaAsnMetAla 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R STRAIN ANALYSIS IN MYCOBACTERIUM
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Scores:  211 Length: 4411529  milarity: 33.21% Conservative: 165 Similarity: 20.52% Mismatches: 276 h: 2.78% Indels: 262 h: 4.099) x US-09-103-840A-1 (1-4411529) ValAlaLeualaAlaTyrLeuProLeuMetThrSerClnAlaLeuAlaGlnGlnAsnAsn 34	ACGGGGGGGGGGGGGGCTACAGTTGCTGG ValProAlaHisAspThrAlaIleAsnGlnAlaLysAla 	GCGCAGGCTGTCTTGGACCACGACGACGACGAGCTCACCTTTG 3497095	MetGlyIleAsnProAsnAspTyrIleProGluTyrGlnGlyGluGl 146	17 C 3 19 T 3 Z1 Z1	edsturspiteIntGinGinSeralaMetAspLeuAsnGlySerIleProArgLeuArgG 236
ment (No.: No.: Int Sir Local Matcl	35 E 35 E 96935   55 C 56977	97037 70 - 97096 87 v 87 s 106 y	126 nGluserThrGluMe :: 97244CTGGCAC: 146 nProAsnSerGluVa. :	162ProGlyLeu ::: 97417 CGGCTACCCCCAGAV 178 nLysValProArgLeu 97477 ACCGACGCCAGGG 198 lalleGlySe 97528 ACTGCGACACGCGC 216 euGluAsnTlemhrol	Α .
Alignmee Pred. N Score: Percent Best Loc Query M UB: US-09-91	Db 349 Db 349 Db 349	34 34	09 09 09 09 09 09	<ul><li>Δγ</li><li>Db 349</li><li>Qγ</li><li>Qγ</li><li>Db 349</li><li>Oγ</li><li>Oγ</li></ul>	34

ה ממ	49/045
Oy Db 3	275 eAspTyrArgAlaValGluValArgGlyGluGlyAlaAspAspAsAlaPheThrThrVa 295 
Qy Db 3	295 lalaAspCluValProLeuLeuIleGlyAspValPheHisHisGlyLysTyrGluThrLy 315          497756 TGCTGACCGCTTCCCG
Qy Db 3,	335 A 34
οy	355
Dp 3	497828 CGAATTGAACGC 3497839
0y Db 34	355 rGlyThrGlnTyrArgPheAspGluValValPhePheThrIleAspProLysThrAsnGl 375
Оу Db 34	euGluGlnLeuLe 394 
Oy Db 34	4 .
•	,
U.Y Db 34	414 UlleAläThrArgTyrPheAsnMetValAsnThrGluIleValPheProGluArgGluG1 434 
Qy Db 34	434 nIleGlnAsnAspGlnValSerPheGluGlnSerSerSerSerserar 449 ::: :::::::   :97993 GTTGCTGCACTTCAGGATTACGTTCGTGCGGACAGCCACCCTGCAAAGCCAGGCCAATCG 3498052
Oy Db 34	449 gThrGluProAlaGlnValAspGluSerThrLeuGluProValIleGluThrValGluLe 469 
Qy Db 34	469 uThrAspGlyIleLeuMetAspIleSerProIleGluPheSerAlaSerAsnLeulleGl 489 ::::       :::          ::
δy	503
Db 34	98146 TGGCCAATTGCCAAGCCAGGGGGGGGGGGGGAACGCGGGCAATGTTGGAGGTTGTT 3
Oy Db 34	504 AspMetProAspAspArgValLeuAlaIleAsnHisAsp 516
0y 23	517 -AspGlyValAsnArgSerIleLeuGlyArgIleSerAspAlaValSerAlaValAlaAr 536
	98200 LIUIGGUUUGUAGGGAAACAGCAGCAGCAGCTGGGTGGGCGAGTTGGTCCAGGCTTT
34	326 326
Oy Db 34	554 rAlaLeuAlaAsnArgLysThrPro
Oy 40	rLysLysValProLeuTyrValPheValAlaSerAspLysProArgAspGlyGlnIL 587
<b>,</b>	מייים וכשכנשפנאפרו כנונים ביייים בייים ביייים בייים ביייים בייים ביייים בייים ביים ביים בייים בייים ביים
UY Db 345	58/ eGlyLeuGlyTrpGlySerAspThrGlyThrArgLeuValThrLysPheGluHisAsnLe 607 98462

Qy         101 GlnSerProProLeuGlyLeuAspWetSerValIleGluGluThrThrProLeuSer 119           Db         6340 AATCAAGATGCAACTACTGAAGAGAAAAACAAAGAAAAAACAAAGAAAAAACAAAGAAACAAGCAATACATCT         6384           Qy         120 LeuGluGluLeuPheAlaGlnGluSerThrGluMetGlyIleAsnProAsnAspTyr 138           Cy         120 LeuGluGluLeuPheAlaGlnGluSerThrGluMetGlyIleAsnProAsnAspTyr 138           Cy         139 IleProGluTyrGlnGlyGluGlnProAsnSerGluValValValPro 154           Cy         139 IleProGluTyrGlnGlyGluGlnProAsnSerGluValValValPro 154           Cy         155           Cy         155	OY 171 ArgLeuPheAsnAspGlyValAsnLysValProArgLeuLysAlaLysPheTyrGlnSer 190  Db 6625 GAAACAAATGGAGTCAATGATAGAATACAAGCAGCTTTAGCAAATCAA 6672  OY 191 SerGlnSerGlyGluThrSerAlaIleGlySerSerHisGlnLysThrGluProTyrAla 210  191 SerGlnSerGlyGluThrSerAlaIleGlySerSerHisGlnLysThrGluProTyrAla 210  191 SarGTTAGCAGACAAAATAATATAGAACAATAGAAATGTTGAACCTATTGTA 6732  OY 211 AsnIleLysAlaAlaLeuGluAspIleThrGlnGluSerAlaMetAsp 226  11	Oy 227 Leuasn	Oy 267	Db 7087 GCTAAAATTGATGCTATTAACTAATTGCTACAACTACACAATTGTTTATGTT 7146  Qy 322 AlaSerAlaGluHisGlyTyrPheAspGlyArgTrpLeuAspArgSerValAspValle 341
	3498684 3498719 703 uThrTrpGlnAspLeuProValAspPheValAsnGlyLysProSerGlnGluAlaLeuLe 723 3498720GAACGGTTGCCGTTGGTCTTGTCAGTACGTCGTCGACGATTGT 3498772 723 uAla 724 3498773 CGCG 3498776 SULT 39 -09-134-001C-2243	Sequence 2143, Application US/09134001C Patent No. 6380370  APPLICANT: Lynn Doucette-Stamm et al TITLE DF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS FILE REFERENCE: GTC-007 CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT PAPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR APPLICATION NUMBER: US 60/055,779		ative: hes: (1-11091 Lysalagl         AAAGCA AlaGlyLe ATTAATGC SerProll

q	7354	:::         :::         :::           :::	
λ	422	MetValAsnThrGluIleValPheProGluArgGluGlnIleGlnAsnAspGlnValSer 441	
ą	7408	  GCTGTTCAAGTTGAAGTTATCAAGAAACAAAACGTTAAAAACCAATTAAATCAA 7461	
ž q	442	PheGluGinSerSerSerArgThrGluProAlaGinValAspGluSerThrLeuGlu 461      :::::::         TTCATTGATAATCAAAAGAAAATTATTGAAAATACGCCTGATGCAAAACACTAGAA 7515	
3 2	462	07 L	
. A	7516		
à	480	IleGluPheSerAlaSerAsnLeuIleGlnAspLysLeuAsnLeuValAlaAlaLysAla 499	
q	7576	GCTAATGTAGATCATAACAACGAGGTTGATCAAGCTTTAGATAAAGCTAGACCAAAAATC 7635	
ζ	200	ArgHisLeuTyrAspMetProAspAspArgValLeuAlaIleAsnHisAspAspGlyVal 519	
q	7636	GAGGAAATTGTACCACAAGTTAGTAAGAAA	
<u></u>	520	AsnargSerileLeuGlyArgileSerAspAlaValSerAlaValAlaArgAlaileLeu 539	
3	000		
දු ද	540	ProAspGluSerGluAsnGluVallleAspLeuProGluArgThrAlaLeuAlaAsnArg 559         ::: CAAGAGAACCAAGAAGCTACGAATGAAGAAAAACTGAAGCATTAAATAAA	
à	260		
. <u>8</u>	7771		
λ	572	ProLeuTyrValPheValAlaSerAspLysProArgAspGlyGlnIleGlyLeuGlyTrp 591	
q	7828		•
λά	592	GlySerAspThrGlyThrArgLeuValThrLySPheGluHisAsnLeuIleAsnArgAsp 611	
q	7846	ACACGIAGTATICAAGAIAIAGAGCAAATICAACCACAICCA 7887	
λά	612	GlyTyrGlnAlaGlyAlaGluLeuArgLeuSerGluAspLysLysGlyValLysLeuTyr 631	
q	7888	CAAACAAAAGCAACCGGGGGTCACAGATTAAATGAAAAAGCTAACCAACAACAA 7941	
λά g	632	AlaThrLysProLeuSerHisProLeuAsnAspGlnLeuArgAlaThrLeuGlyTyrGln 651 :::	
ΣŽ	652	GlnGluValPheGlyHisSerThrAsnGlyPheAspLeuSerThrArgThrLeuGluHis 671	
g	7984		
γά	672	GluIleSerArgSerIleIleGlnAsnGlyGlyTrpAsnArgThrTyrSerLeuArgTyr 691	
QQ	8011	GTTCTTAAAAAGCCATAGCT	
λά	692	ArgLeuAspLysLeuLysThrGlnAlaProProGluThrTrpGlnAspLeuProValAsp 711	*
Q	8032	AAAATAGATAAAGGTCAAACCAATGATGATGTGATG	
δλ	712	PheValAsnGlyLysProSerGlnGluAlaLeuLeuAlaGlyValAlaValHisLysThr 731	
q	8074	GTAGTAAACGGAATAGCTGAAATTGAAAATATTACCTGCTACTACA 8121	
δλ	732	ValAlaAspAsnLeuValAsnProMetArgGlyTyrArgGlnArgTyrSerLeuGluVal 751 	
g	8122		
δy	752	<pre>GlySerSerGlyLeuValSerAspAlaAsnMetAlaIleAlaArgAlaGlyIleSerGly 771 !!!::</pre>	

Sequence 1, Application US/09147236A

Patent No. 6316251

GENERAL INFORMATION:
APPLICANT: TOUGHIDA, Takayasu
APPLICANT: TAHARA, Naoto
APPLICANT: TAHARA, Naoti
APPLICANT: TAHARA, Naoti
APPLICANT: TAHARA, Naoti
APPLICANT: HAYASHI, Takahisa
APPLICANT: HAYASHI, Takahisa
FILE OF INVENTION: NOVEL GENE, GROUP OF GENES, AND NOVEL BETA-GLUCOSIDASE
FILE REFERENCE: 6537-011-0PCT
CURRENT APPLICATION NUMBER: US/09/147,236A
CURRENT FILING DATE: 1999-04-08
EARLIER APPLICATION NUMBER: PCT/JP97/03633
EARLIER FILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1 8223 .---- 8223 772 ValTyrSerPheGlyAspAsnAlaTyrGlySerAsnArgAlaHisGlnMetThrGlyGly 791 47 ThrAlaIleAsnGlnAlaLysAlaGlyAsnProProValLeuLeuThr---ProGluGln 65 ; OTHER INFORMATION: n at positions 15741 and 15767 may be a, g, t, or ; OTHER INFORMATION: c US-09-147-236-1 16836 198 146 367 307 51 792 IleGlnAlaGlyTyrIleTrpSerAspAsnPheAsnHisVal 805 8182 AATAGTAATGATGAAGCAACGACTGAAGAAAATTAGTTGCT---Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: US-09-914-168-2 (1-919) x US-09-147-236-1 (1-16836) TYPE: DNA ORGANISM: Acetobacter xylinum NAME/KEY: CDS LOCATION: (3101)...(5368) FEATURE: NAME/KEY: CDS LOCATION: (5373)...(7778) FEATURE: NAME/KEY: CDS LOCATION: (7784)...(11761) FEATURE: NAME/KEY: CDS LOCATION: (11764)...(12231) FEATURE: NAME/KEY: CDS LOCATION: (12448)...(14652) FEATURE: 0.0162 130.50 33.82% 19.47% 2.76% NAME/KEY: CDS LOCATION: (869)..(1891) Percent Similarity:
Best Local Similarity:
Query Match:
DB: LENGTH: 16836 Alignment Scores: RESULT 40 US-09-147-236-1 8223 -----FEATURE: q δŏ q à

	400	luGlnLeuLeuThrValAsnMetGlyGlu		δ
	380	PheaspGluValValPhePheThrIleAspProLysThrAsnGlnLeuThrThrAspPro   11	0	Oy Db
	9301		σ	op op
	360	341 IleLeuProAspAsnThrAlaAspValSerLeuIleTvrAspThrGlvThrGlnTvrArg		ò
	340 9244	321 AsnalaSerAlaGluHisGlyTyrPheAspGlyArgTrpLeuAspArgSerValAspVal         233 GCAGCGTCGCAG	6	Oy Dp
	9232	AGCCAGGTCGGGGAAATCGAGGTTTCCGCC	9194	Ωp
	320	303IleGlyAspValPheHisHisGlyLysTyrGluThrLysLysAsnLeulleGlu		δ
	9193		9134	OP
	302	spGluValPro		õ
	9133	:::	9074	Dp
•	290	280 ValGluValArg		ò
	279 9073	260 GlyGluValAspValIleIleHisAspLeuGlyGluProValTyrIleAspTyrArgAla   111:::	δ	8 6
	9037		æ	. a
	8977	TTGATTGCCGCCCATCAGTATACCGAGGCCAAGCAGAAGCTTGCCACGCTGGCC	80	g
	242	237 ThralaLeuValAlaAla		Q
	236 8923	SeralaMetAspLeuAsnGlySerIleProArgLeuArgGln :::    :::    :::     :::	80	Q Dp
	8863	acceccaaccccaattttgaagagecgatgccccccaagacteccaa	8804	Ω
	222			ò
	204 8803	GINSerGlyGluThrSerAlaIleGlySerSerHisGln	<b>∞</b>	9 P
	8743		6698 0	οp
	191	177 ValAsnLysValProArgLeuLysAlaLysPheTyrGlnSerSer		õ
	176 8698	LeuGluBrodluLysProGlyLeulIeLysArgLeuTyrAlaArgLeuPheAshAspGly	σ.	8 6
	8638	GATGCGGGGCTGCGCGAACACATGCTTCACCCCCCGGC	0098 0	ďΩ
	156	137 AspTyrIleProGluTyrGlnGlyGluGlnProAsnSerGluValValValProProThr		οy
	136 8599	ProLeuSerLeuGluGluLeuPheAlaGlnGluSerThrGluMetGlyIleAsnProAsn 	, 117 5 8564	Qy Dp
	8563		ω	QΩ
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10001 GCGCTCGCGCGCTGTATAACGCCCACGCCAAGCCGGCAAGGCGCTCGAGATCGACCTT 10060 10174 GGAAAGCCCGATGGATGCCCGCGCCTGGCTGGCCATGGCCGTAGCTGACCAGGCCGATGG 10233 10333 TGAAGAAGCGTTGCCCCGCCATCGACCATCGTTC-----CAGTCGCGTGCGTACGG 10386 9941 GCCTACGATCATCTGGCGCCCGCCCTGCAGGCCGACCCGGAGGCGACATCGCCCAAGCTG 10000 10234 CCATGGTCAGCGCACCATCGAGGACCTGCGCCGCGCCTATGACCTGCGCCTGCAGGT 10293 CGCCAGCTTCTGGCCGGTCTGTCGCCCGCGGATTATTCCCCCCGCGATCCGTTCCATTGCC 9526 GTGCCGCTGATCCGCGAGGCCCTTTCCCAGCCTGATCCGACCGGCGCGCGTGGCGTGGCG 9643 9644 GTGGCCGACCTGTTCCGCCAGCGTGGCGACATGGTGCATGCGCGCATGGCGCTGCGTATC 9703 9881 cgcangggcancrogragggggagnccancracrcaaccagcgragggancaggggag 9940 -----SerLysLysValProLeuTyrVal 575 617 rGlnGlnGluValPheGlyHisSerThrAsnGlyPheAspLeuSerThrArgThrLeuGl 670 618 ------GluLeuArgLeuSerGluAspLysLysGlyValLysLe 630 630 uTyrAlaThrLysProLeuSerHisProLeuAsnAspGlnLeuArgAlaThrLeuGlyTy 650 417 ThrargTyrPheAsnMetValAsnThrGluIleValPheProGluArgGluGlnIleGln 436 GluSerThrLeuGluProValIleGluThrValGluLeuThrAspGlyIleLeuMetAsp 476 IleSerProIleGluPheSerAlaSerAsnLeuIleGlnAspLysLeuAsnLeuValAla 496 576 PheValAlaSerAspLysProArgAspGlyGlnIleGlyLeuGlyTrpGlySerAspThr 595 AlaTyrAsnLeuGlnAla------ValArgAlaLeuSerAsnAspLeuIleAla 416 AsnAspGlnValSerPheGluGlnSerSerSerArgThrGluProAlaGlnValAsp 456 AsnGluValIleAspLeuProGluArgThrAlaLeuAlaAsnArgLysThrProAlaAsp 564 LeuAlaIleAsnHisAspAspGlyValAsnArgSerIleLeuGlyArgIleSerAspAla 616 Gly-Ala-----268 -----650 401 9467 9584 457 545 437 477 497 Op Q q g qq δλ 엄 Ω qq ò Ob δý Ω οy Db οy QQ QΥ QQ δy Ор οy QQ δý δ òχ δ δy ολ δy δy

670 uHisGlulleSerArgSerIlelleGlnAsnGlyGlyTrpAsnArgThrTyrSerLeuAr 690

3TCCTACAGTGCCGA 10437	ogluThrTrpGlnAspLeuProVa 710	CGATACG10456	LEGUALAGIYVALAIAVA 728	SCTCTCCATTGCTGGCCAGAT 10491	LASnProMetArgGlyTyrArgGl 745	GATGGTGGGCTGGGTTCCGGTC 10548	SerAspAlaAsnMetAlaileA  765	SACGGAAGCGAACATTCCCATCGT 10602	lTyrSerPheGlyAspAsnAlaTy 780	10636	eGlnAlaGlyTyrIleTrpSerAs 800	   CACGCCAACCATGATCTGGTCGGG 10674	rArgLeuArgPhePheAlaGlyGl 815	-CGTTATGGCACGTTCATGGCAAC 10731	uSerProlleSerAspLysGlyTy 835	rggcgggcrrgarrr 10782	YThrAlaGluTyrAsnTyrGluPh 853		eGlyAsnAlaTyrAspLysGlyPh 873		lArgTrp 887	TGGGTGCGCGCTGATGTCTG 10884	aThrGlyValLys 903	GGGGGGTCGAG 10933	
10387 GCATCAGGTGGAACTGGGCGCGCGGTGACCGGTGGC	gTyrArgLeuAspLysLeuLysThrGlnAlaProProGluThrTrpGlnAspLeuProVa	GGCGGCATCGC	lAspPheValAsnGlyLysProSerGlnGluAlaL	TCGGACCAGATGCTCCTCCATTGCTGGCAGATGCTAGATTGCTGGCCAGAT	THISLYSThrValAlaAspAsnLeuValAsnProMetArgGlyTyrArgGl 745	:	nArgTyrSerLeuGluValGlySerSerGlyLeuV	GCGTTCGGCCGAGCATGGCATGGGCCGCC	765 aArgalaGlyIleSerGlyValTyrSerPheGlyAspAsnAlaTy 780	GGGCCGCCTGCGCTGCAGGCCGGTGCTTCCGCC-	rGlySerAsnArgAlaHisGlnMetThrGlyGlyIleGlnAlaGlyTyrIleTrpSerAs	:::III	800 pasnPheasnHisValproTyrargLeuargPhePheAlaGlyGl	CCAGCTCAACACGCTCCGTCTATGATGTGCCG-	815 yAspGlnSerIleArgGlyTyrAlaHisAspSerLeuSerProIleSerAspLysGlyTy	GCAGGCTGCCAACCAGTGCGCGGGCCACAGTTCGT	rLeuThrGlyGlyGlnValLeuAlaValGlyThrAlaGluTyrAsnTyrGluPh	CTGAGCGCCAACCATACCCAGCGCATCGCGGCTG	eMetLysAspLeuArgLeuAlaValPheGlyAspIleGlyAsnAlaTyrAspLysGlyPh		eThrAsnAspThrLysIleGlyAlaGlyValGlyValArgTrp	TGCGCCGGATGTGCATTCGCCAATAGC	-AlaSerProValGlyGlnValArgValAspValAlaThrGlyValLyS	CGCCTCGCCCATCGGCTTCCCCATTACCAACGTGC	
10387	069	10438	710	10457	728	10492	745	10549	765	10603	780	10637	800	10675	815	10732	835	10783	853	10829	873	10837	888	10885	
QQ	Qy	qq	οy	QΩ	ογ	q	ογ	qq	QY	qq	οy	Op	οy	QQ	δλ	qq	οy	qq	Qy	qq	δy	qq	οy	q	

Search completed: May 6, 2003, 03:17:43 Job time : 5587 secs

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Sequence 4760, App Sequence 6, Appli Sequence 117, App Sequence 6, Appli Sequence 6, Appli Sequence 9166, App Sequence 9166, App Sequence 4761, App Sequence 4761, App Sequence 4779, App Sequence 1779, App Sequence 1774, App Sequence 1779, Ap
Sequence 8291, Ap
Sequence 50, Appl
Sequence 7474, Ap
Sequence 236, App
Sequence 243, App
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Seguence 48, Appl
Seguence 1, Appli
Seguence 3499, Ap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/10210296
Publication No. US20030021802A1
GENERAL INFORMATION:
APPLICANT: Pfizer Products Inc.
TITLE OF INVENTION: LAWSONIA INTRACELLULARIS PROTEINS, AND RELATED
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: METHODS
FILE REPERENCE: PC10589A
CURRENT APPLICATION NUMBER: US/10/210,296
CURRENT FILING DATE: 2002-08-01
PRIOR APPLICATION NUMBER: US/09/689,065
PRIOR FILING DATE: 2000-10-12
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US-10-10-114-170-243

US-10-10-1758-7

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US-10-18-242-9168

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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-801-368-363
US-09-789-561-48
US-09-995-749A-1
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SOFTWARE: PatentIn Ver. 2.1
  Lawsonia
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US-10-210-296-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
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-FGAPEXI=7 - YGAPOP=10 - YGAPEXI=0.5 - DELOP=6 - DELOF=7
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Sequence 23, Appl
Sequence 12, Appl
Sequence 4580, Ap
                                                                                                                                                       (without alignments) 6066.535 Million cell updates/sec
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17310
5245
7104
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Ygapop 10.0 ,
Fgapop 6.0 ,
Delop 6.0 ,
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139
137.5
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Perfect score:
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                                                                                              OM protein
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                                                                                                                                   Run on:
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8
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#TC C		
50	AsnGlnAlaLysAlaGlyAsnProProValLeuL	
3764		
70	LeuasnalaalaGlyLeuasnalaLysProGlnSerGlnalaLeuaspvalvalasn 88	
3824		
8	PheAspAspGlnSerProIleSerArgIleGlyGluGlnSerProProLeuGlyLeuAsp 108	
3884	AAGGGA 3889	
109	MetServallleGluGluThrThrProLeuSerLeuGluGluLeuPheAlaGlnGluSer 128	
129	148	
3944		
149	<pre>proProThrLeuGluProGluLysProGlyLeulleLysArgLeu</pre>	
3992	GCTGACTATGTAGTA 4006	
169	TyralaargLeuPheasnAspGlyValAsnLysValProArgLeuLysAlaLysPheTyr 188	
180	100111	
1043	CGTCCAT	
206	ThrGluProTyralaAsnIleLysAlaAlaLeuGluAspIleThrGlnGluSerAlaMet 225	
4103	AAACCAAAATTTAATGAGGTAAATATTGCTGTAACAAAACTTGCTGAACGTATAAGT 4159	
226	AspLeuAsnGlySerIleProArgLeuArgGlnThrAlaLeuValAlaAlaArgAlaVal 245	
4160	AATGGCCTTATAAGAAAAACACTATTGCTGATGTACGTATTCATGGGCTT 4210	
246	<pre>GlyTyrTyrAspileAspLeuSerileileArgAsnSerileGlyGluValAspValile 265        ::</pre>	
4211	AAAGTICTIGAICCIGAIGIAAICCITACACGACTCACIATTAATAAGGGAGAICATACT 4270	
266	uProValTyr 274	
275		
4325	AGGARITINA AND AND AND AND AND AND AND AND AND A	
294	ThrValAlaAspGluValProLeuLeuIleGlyAspValPheHisHisGlyLysTyrGlu 313	
4376	::: TTACTGTACAAGAAAAAGCCTAAAATTACAGATGTTGTTGTTCAAGGCTCAAAAGCTGTA 4435	
314	ThrLysLysAsnLeulleGluAsnAlaSerAlaGluHisGlyTyrPheAspGlyArgTrp 333	
1436	::: AGTATCGATAACATTCTTGCTGCAATGAGTTCTAAAAAGGA4477	
334	LeuAspArgSerValAspVallleLeuProAspAsnThrAlaAspValSerLeu 351	
1478		
352	<pre>1leTyrAspThrGlyThrGlnTyrArgPheAspGluValValPhePheThrIleAspPro 371 :::      </pre>	
4529	CTCTATAGAAAAGAAGGCTACTATCTCGCTGAAGTTAATTATGAAATAAAGAG 4582	
372	LysThrAsnGlnLeuThrThrAspProAspLysLeuProValLysArqGluLeuLeuGlu 391	

Db	4583	
Qy	392	GlnLeuLeuThrValAsnMetGlyGluAlaTyrAsnLeuGlnAlaValArgAlaLeuSer 411
QQ	4607	CTATTGTTAACAGTAAATGAAGGGAAAAACTTTATATTAAAGATGTCCGAATTGAAGGA 4666
δλ	4.1	AsnAspLeulleAlaThrArgTyrPheAsnMetValAsnThrGlu1leValPheProGlu 431
a C	٥	47
δ 4	432	ArgGluGln1leGlnAsn 437
3 6	4 4 3	
G 6	7	ATAGCAATCTCTGCCTATGCCATGATCATGCTATGTAGTT 4
Qy	458	SerThrLeuGluPro
qq	4829	4
$o_{Y}$	470	pGlyIleLeuMet
QQ	4889	
Qy	490	AspLysLeuAsnLeuValAlaAlaLysAlaArgHisLeuTyrAspMetProAspAsg 509
QQ	4949	⊢
Qy	510	lyValAsnArgSerIleLeuGlyArglleSerAs
qq	5009	TCTCTTTCTGTTATGCAAGATGATGTAAAAGCATTAAACAGTTTTTATTCAGAT 5062
Οy	530	AlaValSerAlaValAlaArgAlaIleLeuProAspGluSerGluAsnGlu 546
QQ	5063	TGGTTATGCATTTGCTGAAGTAGATCTT
QY	547	
qq	5120	CTTT
Oy	557	AlaAshArgLysThrProAlaAspValTyr566
Dp	5180	AAGGAAATACTC
Qy	266	999 299
QQ	5240	GGAGATCTTTTAATGGTCAACATCTCCGACGCTCTAATGAATG
Qy	567	GlnSerLysValProLeu 573
QQ	5300	TATTITAACCAAGTAGATACAGATACACTGCCTACAGGGAAGATGATGAAGTTGATCTA 5359
Οy	574	TyrvalPhevalAlaSerAspLysProArgAspGlyGlnIleGlyLeuGlyfrpGlySer 593
Db	5360	5
δy	594	AspThrGlyThrArgLeuValThrLysPheGluHisAsnLeulleAsnArg 610
qq	5414	TCAACACATTCTAAATTTGGTGTTTCAGGAAGTATCTCAGAAAGAA
Qy	611	AspGlyTyrGlnAlaGlyAlaGluLeuArgLeuSerGluAspLysLysClyValLysLeu 630
Dp	5474	GGTTATATTTTAAGTATTGAAGGTTTTATTTCTAGTAAGTCATCTTCTCTTGATCTT 5530
Οy	631	TyrAlaThrLysProLeuSerHisProLeuAspAlnLeuArgAlaThrLeuGlyTyr 650
QQ	5531	
Oy	651	GlnGlnGluValPheGlyHisSerThrAsnGlyPheAspLeu

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US-08-781-986A-23
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Publication No. 0S20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6223
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5708 CTATATGATATICCATCTACAGCACCACGCTCTTATCTTGACTAT---CAAGGGAAAAAT 5764
                                                                                                                                                                                                                                                                                                                                                                                                       -----TCAAGAAGTAAAAACCATATAATACATTGGCGTACACGTGCAGGTGCAGCT 5983
                                                                                                                                                                                                                                                                                                                                                                                                                                                              5984 TATAAGAATAGTAAAAAACCTGTGCCAGTATTTGACCGATTTTTTATTGGTGGTATAGAT 6043
-----TTTGGCTTTAGTAATAACATTTATACGCTACGAGATGAATGGGATGAC 5611
                                                                                                              -----GGAGAATATTCATCTATCTTGTTGGCTATCGAATTGATCAATATCGT 5707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SerIleArgGlyTyrAlaHisAspSerLeuSerProIleSerAspLys---GlyTyrLeu 836
                                                                                                                                           ThrGlnAlaProProGluThrTrpGlnAspLeuProValAspPheValAsnGlyLysPro 717
                                                                                                                                                                                                   SerGlnGluAlaLeuLeuAlaGlyValAlaValHisLysThrValAlaAspAsnLeuVal 737
                                                                                                                                                                                                                                                                                                                    SerAspAlaAsnMetAlaIleAlaArgAlaGlyIleSerGlyValTyrSerPheGlyAsp 777
                                                                                                                                                                                                                                                                                                                                                                            778 AsnAlaTyrGlySerAsnArgAlaHisGlnMetThrGlyGlyIleGlnAlaGlyTyrIle 797
                            ---SerThrArgThrLeuGluHisGluIleSerArgSerIle 677
                                                                                                                                                                                                                                                                                                                                                                                                                                    837 ThrGlyGlyGlnValLeuAlaValGlyThrAlaGluTyrAsnTyrGluPheMetLysAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LeuArgLeuAlaVal-----PheGlyAspIleGlyAsnAlaTyrAspLysGlyPheThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTAGGTCTTGCATTAGTTCCATTCTATGACATAGGATTCCAAACAGATTCTGTACAAACT
                                                                                   678 IleGlnAsnGlyGlyTrpAsnArgThrTyrSerLeuArgTyrArgLeuAspLysLeuLys
                                                                                                                                                                                                                            5765 ATTTCTAGTGTAGTAGTGGTGGTTTTTACTTTTGATTCTACA-----GACAGTCGTGAG
                                                                                                                                                                                                                                                           AsnProMetArgGlyTyrArgGlnArgTyrSerLeuGluValGlySerSerGlyLeuVal
                                                                                                                                                                                                                                                                                                                                      5612 TTCCGTAAAAAACTTATGGAGATACCATACGTCTATTCACCCTATA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ...ureSSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
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6284 ATGGCAGATTTGCGA 6298
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11688 CCCAAAGATTTTATTTATTACCAACACATCTTATCAAATCAATGTGTTGCGACAGCAT 11629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11892 CATCCATTTCAT------CCGACTCCTAAGAGTGCAAGTGGGTTTTCAGAAGCA 11845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12051 CAAAGTGCAGAT------AATCAAACGGCAGTGCAACAACATATGGCG 12010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12111 AAAAGTAAAAAATAACAACTTATAAAGAAGCAATTGCGCGTATTTTGCAACATATGGCT 12052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        245 ValGlyTyrTyrAspIleAspLeuSerIleIleArgAsnSerIleGlyGluValAspVal 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            265 IleIleHisAspLeuGlyGluProValTyrIleAspTyrArgAlaValGluValArgGly 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ThrGlnTyrArgPheAspGluValValPhePheThrIleAspProLysThrAsnGln---
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-914-168-2 (1-919) x US-08-781-986A-23 (1-17310)
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Matches:
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                        US/08/781,986A
                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILLING DATE:
ATTORNEY AGENT INFORMATION:
NAME: BERSON, BOD
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 17310 base pairs
TYPE: NUCLEIC acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140.00
32.16%
18.91%
2.96%
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
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Best Local Similarity:
Query Match:
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ογ	388		qq	10593 TAATCGTG
QQ	11628	. CCACAGTATATGCAATATAGTGAACAAGGTTTAATAAAAGACCTTGGCGTTTCCGGTGAT 11569	C	
δŽ	400		G &	
qq	11568	TCAGTGTACCCGACGTCTTCGGTTAGAACTGTATTTTCAAAAGCATTAAACATTTATTT	3 8	
δλ	411		<u> </u>	
Dp	11508	AAATTACCGATACACGTTAAAATCACTAATTTTATACGTACG	3 6	
ογ	415	IlealaThrarg 418	ši t	634 SProbeus 
q	11448	11448 GAACGGACAATTGATGCCGCGCAAGTTATCGCATCAGTCAAAGATGAGGTTGAAACACCC 11389	a à	653G
οy	419	TyrPheAsnMetValAsnThrGlu	Š Š	,
qq	11388	:::    :::::   CATTTAAATTGATGTTTGAAGGATATCGTGCATTGTTACCGAATCCATTAGGGCAA 11329	an :	10353 GAGAGAGG
δλ	427	IleValPheProGluArgGluGlnIleGlnAsnAspGlnValSerPheGluGlnSer 445	Š č	10001
qq	11328	ACAGTTGAAG	<u> </u>	
ò	445	445	<u> </u>	10263
Ωp	11268	11268 CCGAATTACCATGCTGATAAAGATATTCATGTATTGGCGTCATTATTTGAAACGATGCCT 11209	3 6	
δy	446	SerSerSerArgThrGluProAlaGlnValAspGluSer	<u>`</u>	-
Dp	11208	GATTCACCGATGTCTAAGTTA	2 :	T0203
Οy	459		Š	11/
qq	11148		gg ,	10149
٥y	466		δō	61/
QQ	11088	:::	QD	10089
ογ	474		QY	738
<u>අ</u> .	11028	GACGTATGCTTTGTCAGAGATCTTGAAGGCATTTGTCTATCTA	ga :	10029
οy	490		δo ·	TC/
QC	10968		ga (	9972
Οy	508	AspArgValLeuAlaIleAsnHisAspAspGlyVal	ογ	rGLyv
qq	10920		a i	T 0266
οy	524		δò	
qq	10878	:::   GTAAATCACTTAGGACATTTAGTATCAATATTGGTAAAGCGACT 10834	QQ :	0786
Qy	544		Š í	
qq	10833	::   AGAAATGAAGTTGTGTTATGGCAACTTGTGTCTTTGTGACTTGGAAAAAAAA	<del>а</del>	9827
Οy	562		δλ	
qq	10773		qа	9804 GTCGCCAA
δy	572		δy	847
qq	10713	:::      GCGGCTAAAGCGAATTIGATGATGATGATGTGTGGTGCAAACCCTATTATACA 10654	qa	9765
οy	576		δ i	
QQ	10653	::: ::: ::: ::: ::: ::: ::::::::::::::	ag (	9744
οy	593	SerAspThrGlyThrArgLeuValThrLys-PheGluHisAs 606	λ̄ο —	887 TrpALaSe

QQ	10593	::::::    :::   :::	10534
Qγ	909	nLeulleAsnArgAspGlyTyrGlnAlaGly61	516
qq	10533		10474
Qy	617	-AlaGluLeuArgLeuSerGluAspLysLysGlyValLysLeuTyrAlaThrLy 6:	534
Qy	63	9	52
qq	10413	1	10354
Qy	653	IPheGlyHisSerThrAsnGlyPheAspLeuSerThrAr 6	299
QQ	10353	Н	10294
Qγ	299	ArgSerIleIleGlnAsnGlyGlyTrpAsnArgThrTy 6	587
qq	10293		10264
Qy Db	687 10263	rSerLeuArgTyrArgLeuAspLysLeuLysThrGlnAlaProProGluThrTrpGlnAs 70	707
Oy	707	L	110
qq	10209	   CTATGAATTTTATGCGATGGAAGGGCATCAGTATCATCCAAGTTACAAATCACGTTAGG	10150
oγ	711	7	719
qq	10149		10090
QY	719	LeuAlaGlyvalAlavalHisLysThrvalAlaAspAsnLeuvalAs 7	738
g ,	<b>σ</b>	TOTAGITAA T	20 1
Qy	73	nProMet	5 2
QQ	10029	ACAGCAAAT'	9973
Oy	751	Φ	770
Dp	9972	GAAGCATCTGGCAAACATGTAAATGATGTTGAGATGATACCTGTACACCCA	9921
Οy	7	GlyValTyrSerPheGlyAspAsnAlaTyrGlySerAsnArgAlaHisGlnMetThrGl	062
QQ	9920	sgcagiitiGaacaigicaiccaagiigaiitiggcigaagaaagciiaa 9	1871
Óγ	790	<pre>LnAlaGlyTyrIleTrpSerAspAsnPheAsnHisValProTy :::     </pre>	807
qq	9870	SCACAGTACTATGGTTAGGGGAAAGTGATGAGCTATATCAC9	9828
δλ	807	rgLeuArgPhePheAlaGlyGlyAspGlnSerIleArgGlyTyrAlaHisAspSerLe 8	327
qq	9827	ACGAT 9	802
δλ	827	TyrLeuThrGlyGlyGlnValLeuAlaValGlyThr 8 ::}	346
qq	9804	GGCCAATAGACACGACAAAATATTATTTAAAGGTACC	99/6
δλ	847	pLeuArgLeuAlaValPheGlyAspIleGly 8	998
Dp	9765		9745
οy	867	rAsnAspThrLysIleGlyAlaGlyValGlyValArg 8	986
οp	9744	AACGAAACGAGTGTTGGCGCCTCATACAATTGAAAA 9	6046
Oy	887	TrpAlaSerProValGlyGlnValArgValAspValAlaThr 900	

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|GGT-----TTAGCAAAACTTAATGGTAATGTCACTTTAATAAATCATAGCCAATTTACA 2736
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2737 TTGAGCAACAATGCCACCCAAACAGGCAATATCCAACTTTCAAATCACGCAAATGCAACG 2796
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2384 ATGACGATTGGATCACCCGCACATTTAAAGCTGAAAACTTCCAAATTAAAGGGGGGAAGTG 2443
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                                                                                                         APPLICANT: St. Geme, Joseph W.
TITLE OF INVENTION: HAEMOPHILUS ADHERENCE AND PENETRATION PROTIENS
FILE REFERENCE: A-5941-1/RET/DCF/DHR
CURRENT APPLICATION UNBER: US/10/080,505
CURRENT FILING DATE: 2002-02-2
FRIOR APPLICATION UNBER: US 08/296,791
PRIOR APPLICATION UNBER: US 09/839,996
PRIOR FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin version 3.1
SEQ ID NO 12
LENGTH: 5245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LysAlaGlyAsnProProValLeuLeuThrProGluGlnIleGlnAlaArgLeuAsnAla 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProGlnSerGlnAlaLeuAspValValAsnPheAspAspGlnSerProIleSerArgile 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MetProValAlaLeuAlaAlaTyrLeuProLeuMetThrSerGlnAlaLeuAlaGlnGln 32
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9708 TGCAGCGCAAATTACGGATTGGTTAAAGCAGATACAGCAACA 9667
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                            RESULT 3
US-10-080-505-12
; Sequence 12, Application US/10080505
; Publication No. US20030073166A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                          ORGANISM: Haemophilus influenzae
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Best Local Similarity:
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                                                                                                                                    ----LeuPheAsnAspGlyValAsnLysValProArgLeuLysAla 185
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154 ProProThrLeuGluProGluLysProGlyLeuIleLysArgLeuTyrAlaArg-
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486	AsnLeulleGlnAspLysLeuAsnLeuValAlaAlaLysAlaArgHisLeuTyrAspMet 50 :::::::        :::::       aAGGTATTAGAAGTCAAACTTGAGGTTATTAATGCCCAACAGCAAGTGAAAAAAAAA38	5 46	Ω Ω
506 3847	ProaspaspargValLeualalleasnHisaspaspGlyValAsnargSer 	522 3906	4 🗅
523 3907	IleLeuGlyArgIleSerAspAlaValSerAlaValAlaArgAlaIleLeuProAspGlu	542 3960	
543 3961	SerGluAsnGluValIleAspLeuProGluArgThrAlaLeuAlaAsnArgLysThrPro :::         '   '     TAGATCGTCTTTTGTAGATCAAGCACAATCTGCCGTGTGGAAAT	562 4008	
563 4009	AlaaspValTyrGlnSerLysLysValProLeuTyrValPheValAlaSerAspLysPro 582 ::          :::	2 26	
583 4027	ArgAspGlyGlnIleGlyLeuGlyTrpGlySerAspThrGlyThrArgLeuValThr	601 4077	
602 4078	LysPheGluHisAsnLeuIleAsnArgAspGlyTyrGlnAlaGlyAlaGluLeuArgLeu 	621 4101	
622 4102	SerGluaspLysLysGlyValLysLeuTyrAlaThrLysProLeuSerHisProLeuAsn :::	641 4158	
642 4159	AspGlnLeuargAlaThrLeuGlyTyrGlnGlnGluValPhe :::   :::	655 4218	
656	GlyHisserThrasnGlyPheAsp	671 4278	
672 4279	GlulleSerargSerIleIleGlnasnGlyGlyTrpAsnArgThrTyrSer                 :::              sil   GAACAAAGCCGAAAAATTCATCGAAAGCGATAAATTATGGCGTGAATGCAAGTTATCAG	688 4338	
689	Leuarg	690 4398	
691	TyrArgLeuAspLysLeuLysThrGlnAlaProProGluThrTrpGlnAsp 	707	
708	TATAATGCTGGCATTCGAGTTGATTATACATTTACTCCGACAGATAATATCGCGCATTATACATTATACAGAGATAATATAGGATAATAAGATTAAAG	716	
717	ProSerGlnGluAlaLeuLeuAlaGlyValAlaValHis 	729	
730	LysThrValalaaspAsnLeuValasnProMetArgGlyTyrArgGlnArgTyrSerLeu 	749	
750	GluValGlySerSerGlyLeuValSerAspAlaAsnMetAlaIleAlaArgAlaGlyIle	769 4662	_
770	SerGlyValTyrSerPheGlyAspAsnAlaTyrGlySerAsnArgAlaHisGlnMetThr :::	789 4710	
790	790 GlyGlyIleGlnAlaGlyTyrIleTrp 798	_	

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                                                                                                                                    US-UY-U15-44-458U
US-U3-U0200051569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Application US/09815242
APPLICANT: Translow, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Aramacto, Nobert T.
APPLICANT: Xu, Howard
TITLE OF INVENTION: Defort T.
APPLICANT: Xu, Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Defortyotes
TITLE OF INVENTION: Defortyotes
FILE REFERENCE: ELITRA.011A
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/201, 727
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR PRILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
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PRIOR PELING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR PELING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-23
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Matches:
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4711 GTGGGCGTGAAATTGGGGTATCGTTGG 4737
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Best Local Similarity:
Query Match:
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٩	1675	GAATACAATAAACTTAAACAACAAGCAGACAATATTTTAAATGAAGATGCGAATCATGTT 1734	
ي <u>ج</u>	85	AspvalvalAsnPheAspAspGlnSerProIle	
ج د ج	96		
۾,	1795	GCATTANTIGATAATCAAGCAGCAATIGCIGAATIAGAIGCIAAAGCTCAAGAAAAGGIT	
٠ <u>ځ</u>	116		
۵	1855	   ACAGCAGCACAACAAAAAAAAATTACGCAAGATGAAGTTGCAGCGCTTGTGACTAAA    1914	
Σ.	131		
ā	1915	FIRMCAATGAAAAATAATGCAATCGCAGAAATTAATAAACAAAC	
<b>≻</b> 4	145		
۹	1975	GTTACAACTGAAAAAGGTAACGGTATCGCAGTGTTAGATCAAGATGTGATTACACCAACA 2034	
<u>~</u>	157	LeuGluProGluLysProGlyLeuIleLysArgLeuTyrAlaArg 171	
ڡۣ	2035		
٠,	172		
ڡ	2095	AAAAAGTCAAATGCATCATTACAAGATGAAAAAGA	
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۸.	195	GluThrSerAlaIleGlySerSerHisGlnLysThrGluProTyrAlaAsnIleLys 213	
۾	2215		
Α.	214	AlaAlaLeuGlu 217	
۵	2272		
<u>~</u> ⊊	218	AspileThrGlnGluSerAlaMetAspLeuAsnGlySerIleProArgLeuArg 235	
ڡۣ	2332	AAT	
	236	GlnThrAlaLeuValAlaAlaArgAlaValGlyTyrTyrAspIleAspLeuSer 253	
ā	2383		
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۾	2443	AGAGTTAAAAACGAAGAAATCTCAAAAATTGAAAATATTACTGACTCTACTGAACAAAA 2502	
>	257	257	
ڡۣ	2503	ATGGATGCCTATAATGAAGTTAAACAAGCAGCAACAGCTAGAAAAACTCAAAATGCTACA 2562	
<u>~</u>	258	SerIleGlyGluValAspValIleIleHisAspLeuGly 270	
Q	2563		
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ą	2683	TCAAAAGTATTAGATAAAATCAATGCAATTCAAAGCAAAAGGTAAAAGTTAAACT	
2	303	IleGlyAspValPheHisHisGlvLvsTvrGluThrLvsLysAsnLeuIleGluAsnAla 322	

qq	2737 (		2796
Qy	323	SerAlaGluSerAlaGlu	334
qq	2797	:::    AATGCTTCAACTACAGAAGAAAAAGCTGCATATACAGAATTAGATACTAAAAAGCAA	2856
οу.	35	AspArgSerValAspValIleLeuProAspAsnThrAlaAspValSerLeuIleTyrAsp	54
Q C	2857 (	GAAGCAAGAACAAATCTTGATGCTGCAAATACAAACAGTGATGTAACAACAGCTAAAGAC	2916
δλ	355 7	ThrGlyThrglnTyrargPheAsp	362
qq	2917	aatggtattgctgcaattaatcaagtacaagcggcaacaactaagaaatcggatgctaaa	2976
δy	363	GluValValPhePheThrIleAspProLysThrAsnGlnLeu	376
QQ	2977 (	GCGGAAATCGCTCAAAAAGCAAGTGAACGTAAAACTGCAATTGAAGCAATGAATG	3036
ΟŊ	377	ThrThrAspProAspLysLeuProValLysArgGluLeuLeuGluGlnLeuLeuThrVal	396
QQ	3037 1	ACTACTGAAGAACAACAAGCTGCAAAAGATAAAGTTGATCAAGCAGTAGTTACT	3090
Qy	397	υA	416
qq	3091 (	GCAAACGCTGATATAGATAATGCTGCAGCAAATACTGATGATAAT	3138
ΟY	417	ThrargTyrPheAsnMetValAsnThrGluIleValPheProGlu	431
qq	3139 (	::: GCAAAAACTACTAATGAAGCTACAATCGCAGCCATTACACCTGATGCAAATGTTAAACCA	3198
Οÿ	432	ArgGluGlnIleGlnAsnAspGlnValSerPheGluGlnSer	445
qa	3199 /	ACAGCGAAACAAGCAATTGCTGATAAAGTACAAGCGCAAGAAACAGCAATTGATGCTAAT	3258
٥y	w	SerSerSerArgThrGluProAlaGlnValAspGluSer	458
qq	3259 1	aacggtgcaacaacagaaaaaagcagctgcgaaacaacaagttcaaactgaaaaaaca	3318
Qy	459	ThrLeuGluProValIleGluThrValGluLeuThrAspGlyIleLeu	474
qq	3319 /	ACAGCTGATACAGCAATTGATGGTGCACATACAAATGCAGAAGTTGAAGCGGCTAAAAAT	3378
Qy	475 1	MetAspileSerProlleGluPheSerAlaSer	485
QQ	3379 (	GCAGAAATTGCTAAAATTGAAGCAATTCAGCCAGCAACAACAACTAAAGATAATGCGAAA	3438
Οy	486	AsnLeuIleGlnAspLysLeuAglAlaAlaAlaLysAlaArgHisLeu¶yrAspWet	505
qq	3439 (	CAAGCAATTGCTACGAAAGCGAATGAACGTAAAACAGCAATCGCTCAAACGCAAGACATT	3498
Qy	206	ProAspAspArgValLeuAlaIleAsnHisAspAspGlyValAsnArgSerIleLeuGly	525
qq	3499	ACTGCTGAAGAAATTGCAGCGGCAAAT	3528
Qy	526	ArgIleSerAspAlaValSerAlaValAlaArgAlaIleLeuProAspGluSerGluAsn	545
qq	3529 /	AATGTAGATAATGCTGTGACACAAGCAAATAACAACATTGAAGCTGCTAATAGTCAAAAT	3588
Qy	546 (	GluValgleAspLeuProGluArgThrAlaLeuAla	557
qq	3589 (	:::     GATGTAGACCAAGCGAAACAACTGGTGAAGCTAGTATGATCAAGTAACACCÃACAGTT	3648
δλ	558	AsnArgLysThrProAlaAspValTyrGlnSerLysLysValProLeuTyrValPheVal	577
qq	3649	  AATAAAAAGCAACAGCAGTTACAGACGCGAAAAATAATATTACAGCTGCA	3699
Qy	578	AlaSerAspLysProArgAspGlyGlnIleGlyLeuGlyTrpGlySerAspThrGlyThr	597
qq	3700	gaaagatgcaggta	3759
Oy	298	ArgLeuValThrLysPheGluHisAsnLeuIleAsnArgAspGlyTyrGlnAla :::	615

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3760 CAACCAGCAACAGCGGTTAAATCAAATGCTAAAAT---GATGTTGATCAAGCTGTGACA 3816
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                                                          3817 ACTCAAAATCAAGCAATTGATAATACAACTGGTGCT-----ACAACTGAAGAAAA 3867
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                                   616 -----GlyAlaGluLeuArgLeuSerGluAspLys 625
                                                                                                           LysGlyValLysLeuTyrAlaThrLysProLeuSerHisProLeuAsnAspGlnLeuArg 645
                                                                                                                                                                                                                                                     666 ThrargThrLeuGluHisGluIleSerArgSerIleIleGlnAsnGlyGlyTrpAsnArg 685
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      837 ThrGlyGlyGlnValLeuAlaValGlyThrAlaGluTyrAsnTyrGluPheMetLysAsp 856
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                                                                                                                                                                                 646 AlaThrLeuGlyTyrGlnGlnGluValPheClyHisSerThrAsnGlyPheAspLeuSer
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Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
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1411 ACTABAGAAGTTTTATTCCCAGATAAATCT------1443
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|1615 TTGCAACAAGTAAACTCACAAGTTGATAATAGTCATTACACAACAGCATCAATTGCA 1674
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1735 GAAACTGCAAATCGTGCATCTCAAGCGGCTATTGATGGTTTAGTAACTAAATTACAAGCT 1794
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                                                                                                APPLICANT: Iduinmucoc, Accet.

APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA, 011A
CURRENT FILING DATE: 2001-03-21
CURRENT FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 66/210,078
PRIOR PRIOR PELING DATE: 2000-03-21
PRIOR PELING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 66/206,848
PRIOR PILING DATE: 2000-05-29
PRIOR PAPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,737
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-10-23
PRIOR PELING DATE: 2000-11-27
PRIOR PAPLICATION NUMBER: 60/253,625
PRIOR PELING DATE: 2000-11-27
PRIOR PAPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
PRIOR PELING DATE: 2001-02-17
PRIOR PELING DATE: 2001-02-17
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Mismatches:
Indels:
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Matches:
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Wall, Daniel
Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
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29.88%
17.62%
2.91%
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Best Local Similarity:
Query Match:
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US-09-815-242-8291
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                                                             APPLICANT:
                                APPLICANT
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SerargileGlyGluGlnSerProProLeuGlyLeuAspMetSerValileGluGluThr :::	ThrProLeuSerLeuGluGluLeuPheAlaGlnGluSer	MetGlylleAsnProAsnAspTyrlleProGluTyrGlnGly ::	GTTACAACTGAAAAAGGTATCGCAGTGTTAGATCAAGATGTAACACCAACA	LeuGluProGluLysProGlyLeuIleLysArgLeuTyrAlaArg			GluThrSerAlaIleGlySerSerHisGlnLysThrGluProTyrAlaAsnIleLys :::	AlaAlaLeuGlu	AsplieThrGlnGluSerAlaMetAspLeuAsnGlySerIleProArgLeuArg	GlnThrAlaLeuValAlaAlaArgAlaValGlyTyrTyrAspIleAspLeuSer::::       :::	Ilelleargasn		: ATGGATGCCTATAATGAAGTTAAACAAGCAGCAACAGCTAGAAAAACTCAAAATGCTACA		GluprovaltyrileaspTyrargalavalGluvalargGlyGluGlyalaAspaspLys:::			SeralaGlu
96 .	116 1855	131	145	157	172 2095	180	195 2215	214	218	236	254	257	2503	258	271	291 2683	303	323
Oy Dp	Oy Dp	Oy Dp	δγ	Qy Dp	oy Op	Oy Dp	Qy Dp	oy Op	65 65	oy Op	Qy	Qy	QQ	Qy Db	S S	Qy Db	oy Op	Oy Dp

2857 GAAGCAAGAACAAATCTTGATGCTGCAAATACAAACAGTGATGTAACAACAGCTAAAGAC 2916 3139 GCAAAAACTACTAATGAAGCTACAATCGCAGCCATTACACCTGATGCAAATGTTAAACCA 3198 :::||| 3589 GATGTAGACCAAGCGAAAACAACTGGTGAAGCTAGTATTGATCAAGTAACACCAACAGTT:3648 3760 CAACCAGCAACAGGGGTTAAATCAAATGCTAAAAT---GATGTTGATCAAGGTGTGACA 3816 2917 AATGGTATTGCTGCAATTAATCAAGTACAAGCGGCAACAACTAAGAAATCGGATGCTAAA 2976 3091 GCAAACGCTGATATAGATAAT-------GCTGCAGCAAATACTGATGTAGATAAT 3138 3319 ACAGCTGATACAGCAATTGATGGTGCACATACAAATGCAGAAGTTGAAGCGGCTAAAAAT 3378 3379 GCAGAAATTGCTAAAATTGAAGCAATTCAGCCAGCAACAACAACTAAAGATAATGCGAAA 3438 3439 CAAGCAATTGCTACGAAAGCGAATGAACGTAAAACAGCAATCGCTCAAACGCAAGACATT 3498 3529 AATGTAGATAATGCTGTGACAACAATAACAACATTGAAGCTGCTAATAGTCAAAAT 3588 3199 ACAGCGAAACAAGCAATTGCTGATAAAGTACAAGGGGAAGAACAGCAATTGATGCTAAT 3258 3700 ACTGATGATAATGGTGTAGATACAGCGAAAGATGCAGGTAAAAATTCGATTCAAAGTACA 3759 3817 ACTCAAAATCAAGCAATTGATAATACAACTGGTGCT------ACAACTGAAGAAAAA 3867 -----AsnGlnLeu 376 ThrThrAspProAspLysLeuProValLysArgGluLeuLeuGluGlnLeuLeuThrVal 396 486 AsnLeuIleGlnAspLysLeuAsnLeuValAlaAlaLysAlaArgHisLeuTyrAspMet 505 459 ThrLeuGluProValIleGlu------ThrValGluLeuThrAspGlyIleLeu 474 558 AsnArgLysThrProAlaAspValTyrGlnSerLysLysValProLeuTyrValPheVal 577 578 AlaSerAspLysProArgAspGlyGlnIleGlyLeuGlyTrpGlySerAspThrGlyThr 597 LysGlyValLysLeuTyrAlaThrLysProLeuSerHisProLeuAsnAspGlnLeuArg 645 335 AspArgSerValAspValIleLeuProAspAsnThrAlaAspValSerLeuIleTyrAsp 354 2977 GCGGAAATCGCTCAAAAAGCAAGTGAAACTGCAATTGAAGCAATGATTCG 506 ProAspAspArgValLeuAlaIleAsnHisAspAspGlyValAsnArgSerIleLeuGly 526 ArgileSerAspAlaValSerAlaValAlaArgAlaIleLeuProAspGluSerGluAsn |||:::||| 3649 AATAAAAAAGCAACAGCAGTTACAGACGGGAAAAATAATT-----ACAGCTGCA -----GlyAlaGluLeuArgLeuSerGluAspLys 397 AsnMetGlyGluAlaTyrAsnLeuGlnAlaValArgAlaLeuSerAsnAspLeuIleAla ArgLeuValThrLysPheGluHisAsnLeuIleAsnArgAspGlyTyrGlnAla-----ThrangTyrPheasnMetValasnThrGluIleValPheProGlu------363 ---GluValValPhePheThrIleAspProLysThr-----475 MetAspIleSerProIleGluPhe-----432 626 oy . Db Ωy QQ οy οp Q G δŻ ΔD δ QQ ò g Pp QQ g QQ ò g g ò ογ δ ò ò ò g ò g Qγ ŏ ò 10

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22727 AGAGCAGCCACCCCCAGAATCTTTCTTCTTGTGAGTTGCTTCGTGCTAAGGCTGCCCA 22786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nSerProlleSerArglleGlyGluGlnSerProProLeuGlyLeuAspMetSerValI1 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            135 oAsnAspTyrIleProGluTyrGlnGlyGluGlnProAsnSerGluValValValProPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22787 GCTGGGGGTA------AGCAGTGCTGCAGAGTGTAT-----AT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22820 CCGCAAAATGGAGCAGGCAGGAAAAGCCACGCATTCGCTGGGTCTGAAAAGTGCAGCAGC
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                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Word Perfect 8.0 CURRENT APPLICATION DATA:
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183
126
360
286
42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-914-168-2 (1-919) x US-10-114-170-50 (1-38584)
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Indels:
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Matches:
                                                                                                                                                                                                                       APPLICATION NUMBER: US/10/114,170
FILING DATE: 01-Apr-2002
CLASSIFICATION: <Unknown>
STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-10-114-170-50
                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09.453,702
FILING DATE: 03-DEC-1999
APPLICATION NUMBER: 60,7110,955
FILING DATE: 04-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEFAX: (608) 251-9166
                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
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136.50
32.368
19.168
2.898
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                                                           COUNTRY: US
ZIP: 53701-2113
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Best Local Similarity:
Query Match:
DB:
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24175 GAGTGTGCTGGCCCCTAAAGATGAACTGATTCAGGCACTGACG------CTGCTGGA 24226 -------AAAAAAAAATTCAGCTGACCAGTCAACTGGCTGAAGAAGA 24316 :||||||| 24605 TCAGGATTTTACCGTGGATGCAGAAATACGGCAGAAACAGCAGAA----- 24650 :::||||:::||| 24767 CCTGGCGCAGGCAACCATGATGAAATCGATAAAAGGGATTGGCAGTGTACTGGGATTTGA 24826 ::: ::: ::: ||||
----GCCACGGAAAGGATGACAGCGTTGGCTTTGGCTCTGCAGCGCC- 24134 24473 CACGGATGACTACAGAAAGGCCGAGCAGGCGCTGACGAGGCCTGAACCGAACTGAA 24532 24827 TCTCAGCAGCCTTTCCCTGAAT-----GCCAATGGGGGGATTTATCAGTGG 24874 ----GGTAACTGG---AA 24583 yValAlaValHisLysThrValAlaAspAsnLeuValAsnProMetArgGlyTyrArgGl 745 pGlnAspLeuProValAspPheValAsnGlyLysProSerGlnGluAlaLeuLeuAlaGl 725 nArgTyrSerLeuGluValGlySer----SerGlyLeuValSerAspAlaAsnMetAl 763 sLeuTyrAspMetProAspAspArgValLeuAlaIleAsnHisAspAspGlyValAsnAr 521 gSerIleLeuGlyArgIleSerAspAlaValSerAlaValAlaArgAlaIleLeuProAs 541 pGluSerGluAsnGluValIleAspLeuProGluArgThrAlaLeuAlaAsnArgLysTh 561 613 rGlnAlaGlyAlaGlu---LeuArgLeuSerGluAspLysLysGlyValLysLeuTyr-- 631 ....-AlaThrLysProLeuSerHisProLeuAsnAspGlnLeuAr 645 gAlaThrLeuGlyTyrGlnGlnGluValPheGlyHisSerThrAsnGlyPheAspLeuSe 665 rThrArgThrLeuGluHisGluIleSerArgSerIleIleGlnAsnGlyGlyTrpAsnAr 685 gThrTyrSerLeuArgTyrArgLeuAspLysLeuLysThrGlnAlaProProGluThrTr 705 ----GlylleSerGlyValTyrSerPheGl 776 776 yAspAsnAlaTyrGlySerAsnArgAlaHisGlnMetThrGlyGlyIleGlnAlaGlyTy 796 uPheSerAlaSerAsnLeuIleGlnAspLysLeuAsnLeuValAlaAlaLysAlaArgHi 501 uProValileGluThrValGluLeuThrAspGlyIleLeuMetAspIleSerProileGl 481 24135 -AFCAGCGACCTGGACGGGAAAAACTGACGGCA------GAFGAA------AA rAspThrGlyThrArgLeuValThrLysPheGluHisAsnLeuIleAsnArgAspGlyTy -----GGTGATCAGCGACAGCGATATCAGGTACAACTGAGTCTTCGCCAGAAATA 24317 GCGCGCTCAGCGTCAGCAACATGACCTGGATATCGCCACGGTGGGTATG----rIleTrpSerAspAsnPheAsnHisValProTyrArgLeuArgPhePheAla---rProAlaAspValTyrGlnSerLysLysValProLeuTyrValPheValAlaSerAspLy 24533 TGAGAATCGCCGTTACTGGCAACAGCTT-------24044 AGGACAGATTGCTGCTGCCAGACAGTCAGCAGGCATT AAACGGAGTCCTGCGT----aIleAlaArgAla-501 561 593 613 685 725 745 763 461 481 645 665 705 24651 qq οy QQ οy QQ Qγ qq οy qq οy Db οy ρp οχ Dβ δλ Ωp Q Dp Ω qq ò qq ò Οp Ω q δλ QQ  $^{\circ}$ Pp οy g δ q ò

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111 | 111 | 111 | 24875 TGATTACAGTGGCACGGTGATTAACCGTCCGACGTTTTTTGCAAA 24934
                                                                                             24935 AGGCGCGGGTGTGATGGGGGAAGCGGGACCTGAAGCCATTCTGCCATTGCGTGGTGGTGC 24994
                                                                                                                                                                                       25042
                                                                                                                                                                                                                                                     25043 GATGITITCCCCGCAGIACAACAICGAGAICAAIAACGAI------GGCACGAACGG 25093
                                                                                                                                       aHisAspSerLeuSerProIleSerAspLysGlyTyrLeuThrGlyGlyGlnValLeuAl 843
                                                      -------ArgGlyAspGlnSerIle-----ArgGlyTyrAl
                                                                                                                                                                          24995 TGACGGTAAGCTGGGGGTTGTGCCGGAT-----ATTGGGGGGTTCAGGTATGGC
                                                                                                                                                                                                                  aValGlyThrAlaGluTyrAsnTyrGluPheMetLysAspLeuArgLeuAlaValPheGl
                                                                                                                                                                                                                                                                                                                          25094 GCAGATAGGTCCGCTGCCTGAAGGCGGTTTATGACCTCGGG 25136
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198
145
361
318
                                                                                                                                                                                                                                                                                                       ---TyrAspLysGly 872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Identification of Essential Genes TITLE OF INVENTION: Prokaryotes CURREWT APPLICATION NUMBER: US/09/815,242 CURREWT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
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Gaps:
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PELLING DATE: 2000-03-21
PRIOR PELLING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PAPLICATION NUMBER: 60/205
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,931
PRIOR FILING DATE: 2000-12-27
PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7474, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                               863 yAspIleGlyAsnAla-----
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136.00
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US-09-815-242-7474
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SEQ ID NO 7474
LENGTH: 8673
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5335 TATGCCACCACGCTCAAACAGGCTAAACGCATGATTGAGCAAAAGAGCAATGAAGTGTGG 5394
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395 GAGTGCTTGCAAGAATCACAGAGGGTATCCGGTGCTACTCAACCGCGCC---CCTACC 5451
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                                                                                                                                   95 IleSerArgIleGlyGluGlnSerProProLeuGlyLeuAspMetSerValIleGluGlu 114
                                                                                                                                                                                                                115 ThrThrProLeuSerLeuGluGluLeuPheAlaGlnGluSerThrGluMetGlyIleAsn 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              195 GluThrSerAlaIleGlySerSerHisGlnLysThrGluProTyrAlaAsn---IleLys 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5752 AGCGTGAATGAAATCATCACGGTATTGACACGAAAGAATTAGACATCCACGCAAAGATT 5811
                                                                                                                                                                                                                                                                                          135 ProAsnAspTyrIleProGLuTyrGlnGlyGluGLnProAsnSerGluValValValPro 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                    175 AspGlyValAsnLysValProArgLeuLysAlaLysPheTyrGlnSerGlnSerGly 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           214 AlaAlaLeuGluAspIleThrGlnGluSerAlaMetAspLeuAsnGlySerlleProArg 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5512 TIGCACCCGTIAGIGIGCICAGCGITIAACGCIGATITIGACGGGGAICAAAI&GCCGGIG 5571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   277 -----TyrArgAlaValGluValArgGlyGluGlyAlaAspAspLysAlaPheThr 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                294 ThrValAlaAspGluValProLeuLeu---IleGlyAspValPheHisHisGlyLysTyr 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              313 GluThr....-LysLysAsnLeuIleGluAsnAlaSerAlaGluH1sGlyTyrPheAsp 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuAsnAlaLysProGlnSerGlnAlaLeuAspValValAsnPheAspAspGlnSerPro
                                                                                              -----AGGATGTTGCAAGAAGCCGTGGATGTGCTTTTTGATAACGGCCGTAGCACC
                                                                                                                                                                                                                                                5140 ------AAATCGCTCAGCGAGATCATTAAAGGCAAGCAAGGGCGTTTCAGCCAAAAC
                                                                                                                                                                                                                                                                                                                                                                      ProThrLeuGluProGluLysProGlyLeuIleLysArgLeuTyrAlaArgLeuPheAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5302 ------GAAGAGCATCTGTTATCCAAGCTT-----GAAGAGAGAGGC
                                                                                                                                                                      AspValIleIleHisAspLeuGlyGluProValTyrIleAsp----------
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GGCGGTATCGCCATTACCGCAACCTTTTTGGATCATTTGAAAACGCTTGGCTTTAGGTAT		GCGACTAAGGCTGGTATTCTATCTATGGAAGATATTATCACGCCA	LysThrAsnGlnLeuThrThrAspProAspLysLeuProValLysArgGluLeu		:::    TACGATCAAGGGTTGCTCACTGACCAAGAGCGTTAC	LeuSerAsnAspLeulleAlaThrArgTyrPheAsnMetValAsnThrGlulleValPhe		ProGludrgGluGlnIleGlnAsnAspGlnValSerPheGluGln				ATGACAAAGCCGGATGGCAGTATCATTGAAACGCCCCATTATTTAT	AspGly1leLeuMetAspIleSerProIleGluPheSerAlaSerAsnLeuIleGlnAsp	TTGAATGTCTTAGAATACTTTAACTCCACGCATGGCGCTAGAAAGGGCTTAGCGGATACA		GCGCTAAAAACAGCCAATGCAGGGTATTTGACAAGAAAACTCATTGACGTTTCGCAA	ArgValLeuAlaIleAsnHisAspAspGlyValAsnArgSerIleLeuGlyArgIleSer		::::::		GTTTTATT		TTGATTGACGAAGAGGGTGCTAAAAAGGTGGTTGAAGCTGGGATTAAATCCATTACGATC		CGCACCCCAGTAACTTGTAAAGCGCCAAAGGGCGTGTGCCGAAATGCTATGGCTTGAAT		TTAGGCGAAGCCAAGATGAGCTATCCGGGTGAAGCGGTGGGGGGTGGTAGCCGCGCAATCT	SerAspThrGlyThrArgLeuValThrLysPheGluHis		AsnLeulleAsnArgAspGlyTyrGlnAlaGlyAlaGlu		LeuargLeuSerGluaspLysLysGlyValLysLeuTyrAlaThrLys
5962	355	6022	372	390	6130	410	6166	430	7 4 5	6274	456	6334	471	6394	491	6454	509	529	6565	545	6622	562	6682	574	6742	583	6802	593	6862	909	6922	619
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δλ	635		648
ОQ	7042 AT	CATTGAAACG	7101
δλ		sSerThrAsnGlyPheAspLeuSerThrArgThr	668
0 A	7±02 GT 669 Le		7175
q <sub>C</sub>	7126	:::::!!!!   :::::::::::::::::::::::::::	7158
δŏ	689 Le	LeuArgTyrArgLeuAspLysLeuLysThrGlnAlaProProGluThrTrpGlnAspLeu	708
QQ	7159 TT		7191
Oy o		ProValAspPheValAsnGlyLysProSerGlnGluAlaLeuLeuAlaGly	725
a :			7248
Š G	7249 CA	ValAlavaHilisLysThrValalabaspasanLeuValAssnProMetArgGLQTyryr 	743 7299
οy	744 Ar	uGluValGlySerSerGlyLeuValSerAspAlaAsnMetAla	763
qq	7300 AA	AATGTGCCTAATCGCATCCCTTATGCGAGTTGCTGGTTAAAGATAATGACCCT	7356
Qy Dp	764 I.1 	Llealaargalagly1leSerGlyValTyrSerPheGlyAspAsnalaTyr        ::         ::   ATCGCGCAAGATGTGTATGCCAAAGAAAAGGTGTGATGAATACTAT	780
Qy	781 G1	GlnMetThrGlyGlylleGlnAlaGlyTyr1leTrpSer	662
QQ	7405 GT	GTTTTAGAGGCCCAATCATTAGAGCGCACCCATGGAGTCAAAAAGGGCGATATTGTGGT	7464
ΟŸ	800 As	AspasnPheAsnHisValProTyrArgLeuArgPhePheAlaGly	814
QQ	7465 GA	AGTGGTAGCTGATAAT	7500
QY	815 G1 	GlyaspGlnSerIleargGlyTyralaHisaspSerLeuSerProIleSerAspLys     :::::                 GTAGGGAAGCCGCTCGCCATTATATATCGCTAGGGGTTCTGAGATCTTGATGATGATATAT	833 7560
ΟŊ	834 G1	euAlaValGlyThrAlaGlu	848
qq	7561 AG		7620
Qy	849	TyrAsnTyrGluPheMetLysAspLeuArgLeuAlaValPheGly	863
qq	7621 GC	GCCACATGGGATCCTTACAACACCCCTATCATTGCGGACTTT	7662
Qy		pIleGlyAsnAlaTyrAspLySGlyPheThrAsnAspThrLysIleGlyAlaGlyVal	883
QQ	699/	AAAGGTAAGGTGAATTTTGTGATGTTATCGCAGGGTT	7701
Qy	884 GI	GlyVal 885 	
QQ	7702 AC	ACGGTC 7707	
RES O C S O C S	RESULT 8 US-10-100-605-236, A Sequence 236, A Patent No. US20 GENERAL INFORMAY APPLICANT: Bro APPLICANT: St APPLICANT: St APPLICANT: St TITLE OF INVENT TITLE OF INVENT FILE REFERENCE	SSULT 8 5-10-108-605-236 Sequence 236, Application US/10108605 Patent No. US20020160934A1 GENERAL INFORMATION: APPLICANT: Broadus, Julie APPLICANT: Stam, Lynn APPLICANT: Bachmann, Jane APPLICANT: Kamdar, Kim TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF FILE REFERENCE: 311338	TER THAT ENCOD

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1966 CCGACTATAAATGTGATCTTCCTGAGTGACGATGCCTCTCCAAAAATATCGGAGTCGGCC 2025
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2209 CTGAGTGTTGTAGCCACCACATAAGGGAACTCCCCCTGCACGCCTCCAAATCGATCTTC 2268
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2176 CCGCTGGACAGGGAGATAGTTTCA------------AATTATACA 2208
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------GGAGGTGTTCCGCCCTTTCC 2571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 GlnGluSerThrGluMetGlyIleAsnProAsnAspTyrIleProGluTyrGlnGlyGlu 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    146 GlnProAsnSerGluValValValProProThrLeuGluProGluLysProGlyLeu--- 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179 -----LysValProArgLeuLysAlaLysPheTyrGln---SerSerGlnSerGlyGlu 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       196 ThrSerAlaIleGlySerSerHisGlnLysThrGluProTyrAlaAsnIleLysAlaAla 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             216 LeuGluAspIleThrGlnGluSerAlaMetAspLeuAsnGlySerIleProArgLeuArg 235
                                                                                                                                                                                                                                                                                                                                                                                                                                         14 ProvalAlaLeuAlaAlaTyrLeuProLeuMetThrSerGlnAlaLeuAlaGlnGlnAsn 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    236 GlnThrAlaLeuValAlaAlaArgAlaValGlyTyrTyrAspIleAspLeuSerIleIle 255
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                                                                                                                                                                                                                                                                             12404
132
103
253
257
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                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
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CURRENT APPLICATION NUMBER: US/10/108,605
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US 09/761,142
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 361
SEQ ID NO 236
LENTH: 12404
                                                                                                                                                                                   TYPE: DNA ORGANISM: Drosophila melanogaster
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QQ	72 TCCACAGCCACGGTC		2589
Qy	6 ArgAsnSerIleGl	luValAspValIleIleHisAspLeuGlyGluProVal	273
QQ	0		
Οy	TyrAr	laValGluValArgGlyGluGlyAlaAspAspLysAlaPhe	292
qq		GACCAGAGCTTCTAC	2643
Qy	293ThrThrValAlaA	alproLeu	301
QQ	ACGTAT	AACCCGTGGGCAGGTGCATACTCAAGGTCTCTGCAAGT	2703
ΟŊ	02		309
qq	ATCCAGA	GCCATGGTGAACTACACCATCGGCGAGGGCTTCAAGCAC	2763
Qy	310GlyLysTyrGluT	LysAsnLeuIleGluAsnAlaSerAlaGlu	325
qq	2764 CTCACCGAATTCGAG	GTGCGCTCCGCTTCTGGCGAGATTTGCATA	2808
Qγ	326 HisGlyTyrPheAspG	ArgTrpLeuAspArgSerValAspValIleLeuProAspAsn	345
qq	2809 GCTGGCGAACTTGAC		2823
Ολ	346 ThrAlaAspValSerL	IleTyrAspThrGlyThrGlnTyrArgPheAspGluValVal	365
Q C		TTCGAGCGGAGGAGTAGCTATGAATTTCCC	2853
δλ	hePheThrileAspP	roLysThrAsnGlnLeuThrThrAspProAspLysLeuProVal	385
QQ		GTACTGGCAACCGATCGTGGGGGTCTGAGCACT	2886
δλ	LysArgGluLeuLeu	JGInLeuLeuThrValAsnMetGlyGluAlaTyrAsnLeuGln	405
qq	7 ACTGCCATGAT	scantigacgacgtgaac	2922
δλ	alArgAlaLeuS	spLeuIleAlaThrArgTyrPheAsnMetValAsnThr	425
QQ		TOUR TOUR TOUR TOUR TOUR TOUR TOUR TOUR	6
δλ	426 GluIleValPheProGlu	ArgGluGlnIleGlnAsnAspGlnValSerPheGluGlnSer	445
QQ .	GGTTT	GAATAAA	2958
δλ	446 SerSerSerArgThrGluProAlaG	lnValAspGluSerThrLeuGluProValIleGlu	465
qq	9 GTATCG	CCTCCTCACAAGCTTCGAGTACTCCGATTGTCGCT	3018
δy	466 ThrVal	GluLeuThrAsp	471
qa	19 GTGGTGGCCACAGAT	GATTACGGAAACTTTGGCCAGGTCTCATATAGGATTGTGGCC 3	3078
Qy	2 GlyIleLeuMetAspI	SerProlleGluPhe	491
qq	AACGAGGGGGGCA	TTCCGGATTGATCGATCCACTGGTGAAATATTCGTGGTCCGT 3	3138
δλ	492 LeuAsnLeuValAlaA	laArgHisLeuTyrAspMetProAspAspArgValLeu 5	511
QQ	3139 CCGGATATCCTATCCGTTCGTA	CCCAACCCATGCACATGCTA 3	3180
δλ	512 AlaileAsnHisAspAs	alAsnArgSerIleLeuGlyArgIleSerAspAlaVal 5	531
qq	TATATCGGCGACCC	GCCGGTAATCTAAGGAGCAATGCCGACGCCGTG 3	3231
οy	AlaArgA	lleLeuProAspGluSerGluAsnGluValIleAspLeuPro 5	551
Dp	3232 GTCTTCTTGAGC		3258
Qy	552 GluArgThrAlaLeuAlarill	AsnArgLysThrProAlaAspValTyrGlnSerLysIysVal 5	57.1

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Perna, Nicole T.
Plunkett, Guy
Welch, Rod
OF INVENITON: No. US20030023075Alel Sequences of E. coli 0157
                                                                   ---TTCGAAAAGGCC 3285
                                                                                                                                                                 3346 GCTGCGAGTGGAGATGTCGCCCCATCGAAGTCCGGTTAGGTATTCGATATACTCGGGCGAT 3405
                                                                                                                                                                                                                                                                                                                                                                                                     3562 GATCICAACGATAATGCACCTGAGTTCGAGGCCAGTATGCTTAGGATTTCCGTACCGGAA 3621
                                                                                                                                                                                                                                                    ----TTCAGCATAGAAACCAACTCTGGAAAC 3444
                                                                                                                                                                                                                                                                                                                  GlyTrpGlySerAspThrGlyThrArgLeuValThrLysPheGluHisAsnLeuIleAsn 609
                                                                                                                                                                                                           ArgAspGlyTyrGlnAlaGlyAlaGluLeuArgLeuSerGluAspLysLysGlyValLys 629
                                                                                                                                                                                                                                                                                            LeuTyrAlaThrLysProLeuSerHisProLeuAsnAspGln------LeuArg 645
                                       572 ProLeuTyrValPheValAlaSerAspLysProArgAspGlyGlnIleGly-----Leu
                                                                                                                                                                                                                                                                                                                                                                             646 AlaThrLeuGlyTyrGlnGlnGluValPheGlyHisSerThrAsnGlyPheAspLeuSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                666 -ThrArgThrLeuGluHisGluIleSerArgSerIleIleGlnAsnGlyGlyTrpAsnAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPURE: US

ZIP: 53701-2113
COMPURER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-00S/MS-DOS SOFTWARE: Word Perfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/114,170
FILING DATE: 01-Apr-2002
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION OWNER: 09/453,702
FILING DATE: 01-DEC-1999
APPLICATION NUMBER: 06-1099
APPLICATION NUMBER: 06-1099
APPLICATION NUMBER: 06-1099
APPLICATION NUMBER: 06-1099
APPLICATION NUMBER: 06-1098
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REGISTRATION NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEFAX: (608) 251-9166
INFORMATION FOR EXQ ID NO: 243:
SEQUENCE CHARACTERISTICS:
LENGTH: 5629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-114-170-243/C
Sequence 243, Application US/10114170
Publication No. US20030023075A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Valerie
                                                                                                                                                                                                                                                  3406 CCCGATGCTAT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NO. NUMBER OF SEQUENCES: 26 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Burland,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3622 AGTGCAGAGCTTG 3634
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3259 CAGCGACCGCCGATC-
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100 | 11|
101 | 11|
102854 CTGGTTGCCGATTATTGCTGGCAACAGGCCAGTACTCTGACCGCC 2795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3169 CGCGTTGCCACATTATCAGCGACAAATAATGACGTTTACGCCGATAAAAAGACATTTAAT 3110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3076 AATCCCCTGACAAATCATCAGGTCACCTTTAAGAATGAAAAGGAAGCGGGAGTTTGTC 3017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3016 GAACCGCCGCAGCAAAATACGGATGCATATGGTGTTGCCACAATAAACATGGTAAGTCAG 2957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2794 ATCATCACAGACTTTCATAACAACCCGTTAAAAGATATGAAAGTGAATTTTGTGGCACCT 2735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2734 GGTGGCTCGCAACTGGACAACACGACC-----GCCACAACAGACCAGTCCGGTATTGTG 2681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2593 ATCACCGTGGTCCCAAACAGGGAACAATCGGTAATGACCTTGAATGCCGGGTCGGGCAGT 2534
                                                                                                                                                                                                                                                                                                                                                                                                                                                         94 ProlleSerArglleGlyGluGlnSerProProLeuGlyLeuAspMetSerVallleGlu 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GluThrThrProLeuSerLeuGluGluLeuPheAlaGlnGluSerThrGluMetGlyIle 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AsnPro---AsnAspTyrIleProGluTyrGlnGlyGluGlnProAsnSerGluValVal 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----ThrLeuGluProGluLysPro---GlyLeuIleLysArgLeuTyr 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AlaArgLeuPheAsnAspGlyValAsnLysValProArgLeuLysAlaLysPheTyrGln 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                232 ProArgLeuArgGlnThrAlaLeuValAlaAlaArgAlaValGlyTyrTyrAspIleAsp 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            252 LeuSerIleIleArgAsnSerIleGlyGluValAspValIleIleHisAspLeuGlyGlu 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                272 ProvalTyrIleAspTyrArgAlaValGluVal------ArgGlyGluGlyAla 287
                                                                                                                                                                                                                                                                                                            54 AlaGlyAsnProProValLeuLeuThrProGluGlnIleGlnAlaArgLeuAsnAlaAla 73
                                                                                                                                                                                                                                                                                                                                                                                    GlyLeuAsnAlaLysProGlnSerGlnAlaLeuAspValValAsnPheAspAspGlnSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3229 AACTGGAATGCTCCACTGCAATCGCATATTATAACATTGAGGCAAACCAGAATAAGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----AlaAlaLeuGluAspIleThrGlnGluSerAlaMetAspLeuAsnGlySerIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SerSerGlnSerGlyGluThrSerAlaIleGlySerSerHisGlnLysThr----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------GluProTyrAlaAsnIleLys------
                                                                                                                                                 5629
205
157
365
365
51
                                                                                                                                                                                   Conservative:
Mismatches:
                                                                                                                                                                                                                                                                        US-09-914-168-2 (1-919) x US-10-114-170-243 (1-5629)
                                                                                                                                               Length:
Matches:
                                                                                                                                                                                                                       Indels:
                                                                           NO: 243:
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID IUS-10-114-170-243
                                                                                                                                         0.00373
135.00
31.34%
17:75%
2.86%
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                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                3289
                                                                                                                                                                                                                                                                                                                                                                                    74
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ογ	287	287
QQ	2533	GCGATCGCTAACAATACAAATATCGTTACCCTGACTGCCAGTGTGAAAGATGTTTATGGA 2474
Οy	288	AspAspLysAlaPheThrThrValAla 296
qq	2473	CACCCGTIGCCGGATGAGGATGTGAAATTTACCTTGCCAGCCTCCATGACCGGGAACTTC 2414
δλ	297	
Op	2413	ACGCTAAGTAGTGAAACCGCCCGCACCGATGCAAACGGTGATGCCGTGGTCACATTGCGA 2354
Oy Dp	304	GlyaspValPheHisGlyLysTyrGluThrLysLysAsnLeulleGluAsnAlaSer 323 
δ	324	AlaGluHisGlyTyrPheAspGlyArgTrpLeu
QQ	2299	GTIGCTTATCAGCAAGTCACTTTTATTGGGGATACAAACAGTGCGCAGCTCCAGCCGCTG
δō	335	AspArgSerValAspValIleLeuProAspAsnThrAlaAspValSerLeu 351
q	2239	
ò à	352	IleTyrAspThrGlpThrGlnTyrArgPheAspGluValValPhePhe
3 8	367	ALCCIGGROSCITACCARARATCCGCTTARAGACCAGTTGGTCACTTTCCAGAGTAACGAT
7	)	
qq	2119	GTCACTCTAAGGGAAACAGAAGTCACCACCAATACGCTGGGTCAGGCGACGGTAACAATG 2060
ογ	368	
QQ	2059	ACCAGCAATATTGCCGGACAACATAACGTCGTGGTGAGCCGGAAAGCGCA
οy	371	
QQ	1999	
δλ	390	
QQ	1939	ACCGGAGCCGAAAAAAGGATGGGGGGGGGAAAACATCACGCTACGGATACTCGTCCAG 1880
οy	409	
qq	1879	GACGCGTTTAACAATGTAATCGCCGGGTCAACGCGTCAGATTAAGTGCGCAGCCAACAACT 1820
Qy	419	
οg	1819	
οy	423	levalPheProGluArgGlu
QQ	1759	CTCAGCACCCAACCTGGGGTTTATCAGGTGACGGCAACGCTG 1718
δy	443	GluGinserserserseragThrGlu
QQ	. 1717	GACAATAACAGTAGTAAGGGTTGAAGTGTGGAATGTGGCAAATGGCAAACTCGAGTTAACA 1658
οy	451	451
Dp	1657	TCATCGAAACCAGAAACTACGGTCCATAATAGTGAGGGTATTACGCTGACCGCAACGGCG 1598
οy	452	
qq	1597	
οy	464	IleGluThrValGluLeuThrAspGlylleLeuMetAspIleSerProlleGluPheSer 483
Q	1537	GGTGCAACGTAAGCAATACAGGGGAAGTCCTTACTGACCAGTCAGGTCAGGCC 1484
Οy	484	AlaSerAsnLeuIleGlnAspLysLeuAsnLeuValAlaAlaLysAlaArgHisLeuTyr 503

qq	1483	AAAGTGACGCTG
ογ	504	AspмetProSspAspArgValLeuAlaIleAsnHisAsp516
Op	1423	GATGTTCCCGTTCAGAGCCAGGT
δy	517	
qq	1363	8
Οy	523	IleLeuGlyArg1leSerAspAlaValSerAlaValAlaArgAlaIle 538
QQ	1303	ATCACTICACGAGIAGAAGAIGAITACGGAITCCCGGITGAAGGIGTCGAIAITAGICAI 1244
ΟŊ	539	LeuProAspGluSerGluAsnGluVallleAspLeuPro551
QQ	1243	GGCTTAGACACCAAAGGCAGCCCGGTAGTTAATATTCCAACTACGCGTACCGATCAGTCC 1184
δy	552	Ā
QQ	1183	
οy	561	ThrProAlaAspValTyrGlnSerLysLysValProLeuTyrValPheValAlaSerAsp 580
ДD	1123	GTTCCTGGCACAGCCAACCATTCGCTTGGTTGCCGGCACGCCGATGAA 1064
δλ	581	${f sProArgAspGlyGlnIleGlyLeuGlyTrpGlySerAspThrGly}$
Dp	1063	1052
δý	601	lyTyrGlnAl
Dp	1051	TTGAAATCCGATGTTGACACTCTGAAGGCTGACTACCAGCAGAGGCGCAAAACTTACG 995
δŏ	7	
ДQ	994	CTAACATTGCAAGACAAGTACGGTAACCCGATAGTGACGTCTGATCATCTGGAATTTGTC 935
οy	637	SerHisProLeuAsnAspGlnLeuArgAlaThrLeuGlyTyrGlnGlnGluVal 654
Dp	934	CTTTCTCAAGTTGAGCGATATTGATTACAGC
οy	655	SlyHisSerTh
QQ	874	TATGGGGAGTACACCGTGACTGTCACTGGCGGAAAAGGGGAACAGCGACACTCATTCCC 815
Qγ	099	AsnGlyPheAspLeuSerThrArgThrLeuGluHisGluIleSerArgSerIle 677
Dp	814	ACG.
οy	678	lleGlnAsnGlyGlyTrpAsnArgThrTyrSerLeuArgTyrArgLeu 693
Db	754	AAAGAAATGTCCGGTCATGTCACTGCAAACAACCATACCTTCTCCACGGCT 704
Οÿ	694	ThrGlnAlaProProGluThrTrpC
qq	703	
ΟŸ	714	alAlaVal
QQ	661	
Οy	734	TyrSerLeuGluvalGlySe
Dp	625	GATTATATGTTTTCAAGTTCACAGGTTGGGTGTCTGTCGTTGGT 581
οy	754	AlaArgAlaGly
qq	580	TCGCCTAAAGTTTCTTTCCCAAATATC554
٥y	774	SerPheGlyAspAsnAlaTyrGlySerAsnArgAlaHisGlnMetThrGlyGly 791

553	GGCGA	TCAAACGTCAGTC!	-GGCGATCAAACGTCAGTCACAATAAGCGCTGTTCCCCGACAAGGAGGTACAACC	CCCGACAA	GGAGGTACAACC 500	Perc	Percent Similarity: Best Local Similarity
792	CCAGACCTT	-IleGlnAlaGly:    :::  ATTAAGCTGAAA	IleGinAlaGlyTyrIleTrpSerAspAsnPheAsnHisValProTyr	AsnPheAsn 	IleGinalaGlyTyrIleTrpSeraspasnPheasnHisValProTyr 807 	Quer DB:	Query Match: DB:
	or one to	an De Lande	100 [00   10	e [ 6 miles   10		0-SD	US-09-914-168-2 (1-919
	TGGCTA	74074004700470		1135GCT		QY	24 MetThrSerGln
828 Se	rProlleSe	SerProlleSerAspLysGlyTyr:::		Leu		oy vo	4144 GTTGCTTCACAAO 44 AlaHisAspThr
418 TG	TCATGCTAA	AAATGATGGATAT	IGTCATGCTAAAAATGATGGATATAATCTTCCTGGCATCACACATTTGACGTCTGGCGAA	ACACATTTG		qa	4186GCAC
841 Va.	LeuAlava	lGlyThrAlaGlu	ValLeuAlaValGlyThrAlaGluTyrAsnTyrGluPheMetLySAspLeuArgLeuAla ::: :::	WetLysAsp		QY	64 GluGlnIleGln/
				אראארפר	ACCCAGGGAICA 336	qa	4204CAAACGAAT
861 Va. 337 CT	alPheGlyAsp ::::   ::: TGTATGGTGAA	ValPheGlyAspileGlyAsnAlaTyrA ::::::   :::             CTGTATGGTGAATGGGGGAACGTT		'nrasnasp :::::::: rccagraar	SPLYSCIYPNeThTASDASPTHTLYSIIEGIY 880 GGAGCGTTTTCCAGTAATTCGCAATTTACA 284	δŏ	77
	aGlyvalGly	yValArgTrpAla		/alArgVal		qa	
283 CC		CCGGGAGCTTACTGGACAAGT	 AGT			oy.	SerProile
01 G1	yValLysGlı	uGluGlyAsnPro	901 GlyValLysGluGluGlyAsnProlleLysLeuHisPhePheIle	Pheile 915	51	g ò	4309CAAV
262	1 1 1	-GAATCTGATGAT	-GAATCTGATGATTACAGTCGGCACTACTATGTG 230	ratgig 23	08	qa	   4360 GCAGAAGAAGA(
10 15-24	RESULT 10 US-09-815-242-4760					QY	130 GluMetGlyIle
nce 4 t No.	760, Appl US200200	Sequence 4/60, Application US/09815242 Patent No. US20020061569A1	815242			qa	4420 GATATTACGAAT
APPLICANT: APPLICANT: APPLICANT: APPLICANT:	APPLICANT: Haselber APPLICANT: Haselber APPLICANT: Ohlsen,	ENEKAL INFORMATION: APPLICANT: Haselbeck, Robert APPLICANT: Oblisen, Kari L.				vo 4	.149 SerGluvalval
APPLICANT:		Wall, Daniel Trawick John D				3 8	169 Turalabralen
APPLICANT:	: Carr, (	Carr, Grant J. Yamamoto, Robert T.				qq	4519 GCTGCTAGA
ICANT E OF	: Xu, H. INVENTION	Howard : Identificat	APPLICANT: Xu, H. Howard TITLE OF INVENTION: Identification of Essential Genes		in	00	189 GlnSerSerGln
E OF REFE	INVENTION RENCE: EL	: Prokaryote: ITRA.011A	ν.			qa	:::
ENT A	PPLICATION ILING DAT	CURRENT APPLICATION NUMBER: US/09/815,242 CURRENT FILING DATE: 2001-03-21	09/815,242 1			0y	209 TyrAlaAsnIle
PRIOR APP PRIOR FIL	LICATION I	APPLICATION NUMBER: 60/19 FILING DATE: 2000-03-21	1,078			qa	
	FILING DATE:	APPLICATION NUMBER: 60/206,848 FILING DATE: 2000-05-23	6,848			QY	229 GlyserilePro
	LICATION I	APPLICATION NUMBER: 60/207,727 FILING DATE: 2000-05-26	7,727			qq	4675 AATGATGTGAAA
PRIOR APP PRIOR FIL PPIOP APP	LICATION I	APPLICATION NUMBER: 60/242,578 FILLING DATE: 2000-10-23	2,578			ζO	249 AspileAspLeu
	FILING DATE: 2000-11	2000-11-27	3, 623			qq	4726
	APPLICATION : FILING DATE:		7,931			Qy	269 LeuGlyGluPro
PRIOR APPL PRIOR FILI	PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 2001-0	NUMBER: 60/269,308 2001-02-16	y, 308			qa	4750GAAGCA
SOFTWARE:	FastSEQ	FastSEQ for Windows Version	ersion 4.0			Qy	289 AspLysAlaPhe
LENGTH: 6228	6228					qa	4804 GATACACCACAT
ORGANISM: St -09-815-242-47	Staphylo 2-4760	Staphylococcus aureus	Ø			QY	307 PheHisHisGly
1 1 1	Alignment Scores:					qq	4864 CTCAAACAAGCG
. No. :		0.00432	Length: Matches:	6228 154	m	Oy	327 GlyTyrPheAsp

ŭ ŭ Ø Ö	Percent S. Best Loca Query Mata	Similarity: al Similarity: tch:	32.63% 19.04% 2.86% 10	Conservative: Mismatches: Indels: Gaps:	110 301 244 35	
Þ	US-09-914	-168-2 (1-919)	x US-09-815-24;	2-4760 (1-6228)		•
0 0	Oy 24 Db 4144	MetThrSerGlnAla ::: GTTGCTTCACAAGCA	LeuAlaGlnG        ::::  TTAGCTAAAG	lnAsnAsnProAlaAsnIl :: AAAAAGAAAAAGCACTT	elleAsnHisValPro	43
Ø	4	laHisAspTh	IleAsnGlnA	ysAlaGlyAsnProPr	oValLeuLeuThrPro	63
Ω	41	GCA	CAAGCT			
0 0	Oy 64	GluGlnIleGln/       CAAACGAATA	AlaArgLeuAsnAlaA   :::::::     AGTCAGGTGAATCAAGC	aGlyLeuAsn   	GTATCAGCGATTAAAATT	76
Ċ			Glusera	nAlate.	heaen	
ם כ	426	TTCAACCT	ALYSELOGIUSE       AAAAGTTAAACC	AGCTGCACGTGAAAAAATCAAT-		
o	Qy 93	SerProlleSer/	IleGlyGluGlnS	erProProLe	uAspMetSerValIle	112
Δ	Db 4309	CAA	: AGCGAATGAATTAC	::: STGCTAAGATTAAT	CAGGATAAAGAAGCAACA	4359
ø	oy 113	Ö	luGluThrThrProLeuSerLeuGlu	GluLeuPhe	eAlaGlnGlu	129
Ω	Db 4360	G	CAAGTAGCACTAGATA	CAATG	AAATCAAGCCATGA	4419
α	oy 130	GluMetGlyIle	snProAsnAspT	yrIleProGlu	nProAs	148
Ω	Db 4420	GATATTACGAAT	   AATAGAACAAATCAACA	AAGTTGATGAT	ACAACAAGTCAAGCGCTTGAT	4479
a	.14	თ <b>—</b>	roProThrLeuG	luProGluLysPro	eLysArgL	. 68
Ω	Db 4480	AGCATI	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	ACGCC1	TGTTAG	4518
a	0y 169	TyrAlaArgLeu	AsnAspGlyValA	snLysValPro	ArgLeuLysAlaLysPheTyr	188
Ω	Db 4519	GCTGCTAGA	- E-1	)	TGAAGCTAAAAAGCGC	4563
Ø	Qy 189	 G	SerGlyGluThrSerAla	lalleGlySerSerHi	isGlnLysThrGluPro	208
Ω	Db 4564	GAAATTGAGCAA	AAATTGAGCAAGCGGAACATGCGACTG	CTGATGAAGAAAACAAGTTGCTTTAAATCAATT	TGCTTTAAATCAATTA	4623
O	Qy 209	TyrAla	AsnIleLysAlaAlaLeuGluAspIleThrGlnGluSerAlaM	spileThrGlnGluSe	rAlaMetAspLeuAsn	228
Д	Db 4624	GCGAATAATGAA	AAACGTGCATTACAAA	ACATCGATCAAGCAAT	į	4674
O	QY 229	Glyser	rgLeuArgGlnThr	>	gAlaValGlyTyrTyr	248
Ω	Db 4675	AATGATGI	STGTTGAAACAAAT	GGCATTGCTACACTAAAAGGTGT	AGGTGTA	4725
0	QY 249	AspileAspLeu	SerIleIleArgAsnS	erlleG	spValllelleHisAsp	268
Ω	Db 4726			CA	TATTGTAATTAAGCCT	4749
0	Qy 269	LeuGlyGluProVa	alTyrIleAspTyı	rgAlaValGluValAr	gGlyGluGlyAlaAsp	288
Ω	Db 4750	9	I I AAGCACAACAAGCAATAAAAG(	CAG	:::	4803
α	Qy 289	Asp	FhrThrvalA	laAspGluValProLe	eG1yA	306
Ω	Db 4804	GATACACCACATGCAA			AATTAATTAGCGACACA	4863
α	Qy 307	PheHisHisGl	yLysTyrGluThrLysL	LysAsnLeuIleGluAsnAl	aSerAlaG	326
Ω	Db 4864	CTCAAACAAGCGCA	CAACAAGAA		ATACAAATCAAGATGCT	4908
O	Qy 327	GlyTyrPheAs	pGlyArgTrpLeuA	spArgSerValAspVal	alileLeuProAsp	344
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AAATAAAACTAAAGTA 4968	yrArgPheAsp 362	AAAAT 5016	hrThrAspProAspLys 382			hrArgTyrPheAsnMet 422					TValstureuThrAsp 4/1			MetProAspAspArgValLeu 511    :::  GATAGASPAGG				AAATAAAATTAA 5490	IlleAspLeuProGlu 552	AATAGCACAAGTTGAA 5550	rProAlaAspValTyr 566              TAATGCAGANGNG 5607			rLysPheGluHisAsn 606			ATTCAACGATAAAAA 5715	IASpGInLeuArgala 646 	PheAspLeuSerThr 666        THIRD
909 GCTGTTACTGATGTTAGAAATCAAACAATCAAGGCAATAGAGCAAATAAAACCTAAAGTA		4969 AGACGTAAACGAGCTGCGCTTGATAGCATTGAAGAAATAATAAAAT	363 GluValValPhePheThrIleAspProLysThrAsnGlnLeuThrThrAspProAspLys	383 LeuProValLysArgGluLeuLeuGluGluGlnLeuLeuThrValAsnMetGlyGluAlaTyr		403 AsnLeuGlnAlaValArgAlaLeuSerAsnAspLeuIleAlaThrArgTyrPheAsnMet.	ValAsnThrG				:::	0		LeuAsnLeuValAlaAlaLysAlaArgHisLeuTyrAsp           CTTAATCAGGTATTGATCAACAATCATGGA	AlalleAsnHisAspAspGlyValAsnArqSerIleLem	CAAGTTAATCAAGATAGTATAAATGCTCAAAATATTATTTCAAAAATTAAACCAGCGACA					3			IleGlyLeuGlyTrpGlySerA		'LeulleAsnArgAspGlyTyrGlnAlaGlyAlaGluLeuArgLeuSerGluAspLysLys :::		oryvarnysheuryralarnrhysproLeuSerHisproLeuAsnAspGlnLeuArgAla;::::::::::::::::::::::::::::::::::::	
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5803 GGACAAATTGATCAAGATCGTAGC------AATGCACAAGTTGATAAAACA 5847
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                                                                                                                                                                  667 ArgThrLeuGluHisGluIleSerArgSerIleIleGlnAsnGlyGLyTrpAsnArgThr 686
                                                                                                                                                                                                                                                                                                                               727 AlaValHisLySThrValAlaAspASnLeuValAsnPro------MetArgGlyTyr 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            687 TyrSerLeuArgTyrArgLeuAspLysLeuLysThrGlnAlaProProGluThrTrpGln 706
                                                                                                                                                                                                                      707 AspLeuProValAspPheValAsnGlyLysProSerGlnGluAlaLeuLeuAlaGlyVal 726
                                                                                                                                                                                                                                                                                                                                                                                                                                          744 ArgGlnArgTyrSerLeuGluValGlySerSerGlyLeuValSerAspAlaAsnMetAla 763
                                                                                                                                                                                                                                                                     5875 GATTTAGATCTACCTATTAAA---AAGCCAGATGCTGAA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
US-09-815-242-8815
Sequence 8815, Application US/09815242
Patent No. US20202061569A1
Patent No. US20202061569A1
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Wall, Daniel
APPLICANT: Au, H. Howard
APPLICANT: Trawick, John D.
APPLICANT: Vamamoto, Robert T.
APPLICANT: Vamamoto, Robert T.
APPLICANT: Van H. Howard
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REPERENCE: ELITRA, 0.1A
CURRENT APPLICATION NUMBER: 06/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PRIOR OATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-24
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Matches:
Conservative:
Mismatches:
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ORGANISM: Staphylococcus aureus
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NAME/KEY: CDS

LOCATION: (1)...(6561)

US-09-815-242-8815
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Percent Similarity:
Best Local Similarity:
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Qγ	345	AsnThrAlaAspValSerLeuIleTyrAspThrGlyThrGlnTyrArgPheAsp	362
qq	4969	AGACGTAAACGAGCTGCGCTTGATAGCATTGAAGAAAATAATAAAAAT.	5016
Qy	363	GluValValPhePheThrIleAspEroLysThrAsnGlnLeuThrThrAspEroAspEys :::	382 5061
ος G	383	LeuProValLysArgGluLeuLeuGluGlnLeuLeuThrValAsnMetGlyGlyAlaTyr	402
3 8			3034
S S	0 0	SILLEGUSTIRATATATATATATATATATASIRASPEGITT	422 5130
οy	423	ValAsnThrGlulleValPheProGluArgGluGlnIleGlnAsnAspGlnVal	440
Db	5131		5190
Οy	441	SerPheGluGlnSerSerSerArgThrGluPro	452
Dp	5191	CCTAAAGTTCAAGTTAAACCAGCAGCGCGTCAATCTGTTGGTGTAAAAGCCGAAGCTCAA	5250
QY	453	AlaGlnValAspGluSerThrLeuGluProValIleGluThrValGluLeuThrAsp	471
QQ	5251	AATGCACTAATCGATCAAAGCGATTTATCAACTGAAGAA	5292
δλ	472	GlyIleLeuMetAspIleSerProIleGluPheSerAlaSerAsnLeuIleGlnAspLys	491
QQ	5293	.::    ::::::::::::::::::::::::::::::::	5325
δ	492	LeuAsnLeuValAlaAlaLysAlaArgHisLeuTyrAspMetProAspAspArgValLeu	511
QQ	5326	CTTAATCAGGCTATTGATCAGATCATGCAGATAAGACTGCC	5370
ò i	51	AlaIleAsnHisAspAspGlyValAsnArgSerIleLeuGlyArgIleSerAspAlaVal	31
9	_	CAAGTTAATCAAGATAGTATAAATGCTCAAAATATTATTTCAAAAATTAAACCAGGGACA	5430
oy.	532	laArgAlaIl	00
Op	5431	FAAAGCA	5490
δÿ	539		552
QQ	5491	ATTAAAGCAAATAACGAAGGACAAGATGAAGAACAAAATATTGCAATAGCACAAGTTGAA	5550
οy	553		266
QQ	5551	AAAGAGTTAATTAAAGCTAAACAACAACAATTGCTAGTGCAGTGAGTG	2607
οy	567	GlnSerLysLysValProLeuTyrValPheValAlaSerAspLysProArgAspGlyGln	586
qq	2608	GCATATTTGCATGATGGAAAAACGAA	5637
δÿ	587	lleGlyLeuGlyTrpGlySerAspThrGlyThrArgLeuValThrLysPheGluHisAsn	909
qq	5638		2655
Oy Db	5656	LeulleAsnArgAspGlyTyrGlnAlaGlyAlaGluLeuArgLeuSerGluAspLysLys :::	626 5715
οχ	627	GlyValLysLeuTyrAlaThrLysProLeuSerHisProLeuAsnAspGlnLeuArgAla	646
QQ	5716		5742
δy	647	ThrLeuGlyTyrGlnGlnGluValPheGlyHisSerThrAsnGlyPheAspLeuSerThr	999
QΩ	5743		5802
Qλ	199	${\tt ArgThrLeuGluHisGluIleSerArgSerIleIleGlnAsnGlyGlyTrpAsnArgThr}$	989

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5874
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                   ---AATGCACAGTTGATAAAACA 5847
                                                                                                                                                                                                                                  5914 -----AAAACGATTAATGATCATCTTGCACGCGTCACTTTAGTGCAAAATAT 5964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                  -----GTAAGTAATCGTAATAAGGCT 5991
                                              687 TyrSerLeuArgTyrArgLeuAspLysLeuLysThrGlnAlaProProGluThrTrpGln 706
                                                                                                                        AspLeuProValAspPheValAsnGlyLysProSerGlnGluAlaLeuLeuAlaGlyVal 726
                                                                                                                                                                                               AlavalHisLysThrValAlaAspAsnLeuValAsnPro------MetArgGlyTyr 743
                                                                                                                                                                                                                                                                       744 ArgGlnArgTyrSerLeuGluValGlySerSerGlyLeuValSerAspAlaAsnMetAla 763
                                                                                           -----CAAACAATACAT
                                                                                                                                                        5875 GATTTAGATGTACATCCTATTAAA---AAGCCAGATGCTGAA-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20850
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486,33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCIT Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,272
FILING DATE: 22-Jan-2001
CLASSIFICATION: <URKNOWN>
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Conservative:
Mismatches:
Indels:
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STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
TELECOMMUNICATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NO: 117:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/961,083
FILING DATE: <UNKnown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                            5965 CGAAAA-------
                                                                                                                                                                                                                                                                                                                                                                                  5992 GATGCATTAAAAGCTATAACTGCTTTA 6018
                                                                                                                                                                                                                                                                                                                                               764 IlealaArgAlaGlyIleSerGlyVal 772
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 117, Application US/09765272 Patent No. US20020061545Al GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID
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INFORMATION FOR SEQ ID NO: 117:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 3121 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                   5848 GCATCATTAAATCTA-----
5803 GGACAAATTGATCAAGATCGTAGC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.00198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity:
Query Match:
DB:
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TTGACCAGCTGTTTATCTGCCTATAATAGTCAGCTTTCTATCGGAGTCGGGGAACAT 214
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215 TTACCAGAGCCTCTGAAAATCGAAGGTTATCAATATTTGGTTATATCAAAACTAAGAAA 274
                                                                                                                                                                                                                                                                                                                                                                                                                                         386 TGGAACCAAGGACAGGGGAAGGTTAGTTTACAAGGTGAAGCATCAGGGGATGATGGACTT 445
                                                                                                                                                                                                                                                                                                                                                     ------GlnSerProIleSerArgIleGlyGluGlnSerProProLeuGlyLeu 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 AspMetSerValIleGluGluThrThrProLeuSerLeuGluGluLeuPheAlaGlnGlu 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SerThrGluMetGlyIleAsnProAsnAspTyrIleProGluTyrGlnGlyGluGlnPro 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148 AsnSerGluValValValProProThrLeuGluProGluLysProGlyLeulleLysArg 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  168 LeuTyrAlaArgLeuPheAsnAspGlyValAsnLysValProArgLeuLysAlaLysPhe 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  227 LeuAsnGlySerIleProArgLeuArgGlnThrAlaLeuValAlaAlaArgAlaValGly 246
                                                                                                                                                                                                                        54 AlaGlyAsnProProValLeuLeuThrProGluGLnIleGlnAlaArgLeuAsnAlaAla 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           188 TyrGlnSerGlnSerGlyGluThrSerAlaIleGlySerSerHisGlnLy&ThrGlu 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        247 TyrTyrAspileAspLeuSerileIleArgAsnSerileGlyGluValAspValileIle 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                267 HisAspLeuGlyGluProValTyrIleAspTyrArgAlaValGluValArgGly---Glu 285
                                                     4.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              755 GGACCCGGACATGAAGGTGAAGCTGCAGTTCGCGAAGAAGCAGCTTACACAGAACCG 814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----HisHisGlyLysTyrGluThrLysLysAsn 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      815 TTAGCAACGAAAGGCACGCAAGACCAGGTCATGAGGGCAAAGCTACAGTCCGCGAAGAG 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----AsnAlaSerAlaGluHisGlyTyr 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          875 ACTCTAGAGTACACGGAACCGGTAGCGACAAAAGGCACACAAGAACCCGAACAT---- 928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      329 PheaspGlyargTrpLeuaspargSerValAspValIleLeuProaspasnThrAlaAsp 348
                                            MetThrSerGlnAlaLeuAlaGlnGlnAsnAsnProAlaAsnIle...-.IleAsnHis
                                                                                                                                                                                                                                                               275 CAGGATAATACAGAGCTTTCAAGGACA-----GTTGATGGGAAATACTCTGCTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   491 TCATTCGCAAGTCAAGTTGAGCAGAAT-----CCGGATCACAAAGGAGAATCT---
                                                                                                                                      ...----AlaHisAspThrAlaIleAsnGlnAlaLys
                                                                                                                                                                                                                                                                                                         74 GlyLeuAsnAlaLysProGlnSerGlnAlaLeuAspValValAsnPheAspAsp----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProTyralaAsnIleLysAlaAlaLeuGluAspIle...ThrGlnGluSerAlaMetAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               446 ------TCAGAAAATCTTCTATAGCAGCAGACAATCTTCTAATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           584 ---ACAACGGTGCAGAGTGCGGAAGAGGAAGTATTGGCGACGACAAATGATCGACCAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----TATAAACTTCCATTGGAAACCAAAGGCACGCAAGAACCCGGTCATGAG
US-09-914-168-2 (1-919) x US-09-765-272-117 (1-3121)
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g G	929	GAGGGCGAACGGSCAGTAGAAGAAGTTCCG	961	
οy	349	Va	368	
QQ	962	:::    GCTTTAGAGGTCACTACACGAAATAGAACGGAAATCCAGAATATT	1006	
γo	369	I	388	
g	1001	CCTTATACAACAGAAGAAATTCAGGATCCAACACTTCTGAAAAATCGTCGTAA	1060	
ογ	389	LeuLeuGluGlnLeuLeuThrValAsnMetGlyGluAlaTyrAsnLeuGlnAlaValArg	408	
qq	1061		1081	
ογ	409	AlaLeuSerAsnAspLeuI	424	
qq	1082		1120	
οχ	425	ThrGluIleValPheProGluArgGluGlnIleGlnAsnAspGlnValSerPheGluGln	444	
QΩ	1121		1138	
ογ	445	SerSerSerArgThrGluProAlaGlnValAspGluSerThrLeu	460	
QQ	1139		1198	
δ	461	GluProValIleGluThrValGluLeuThrAspGlyIleLeuMetAspIleSerProIle	480	
qq	1199		1243	
οy	481		495	
QQ	1244		1303	
٥y	496	AlaAlaLysAlaArgHisLeuTyrAspMetProAspAspArgValLeuAl	515	
QO	1304	TCTGCAAAAACGCAAGTTTCCAT	1327	
٥٧	516	AspAspGlyValAsnArgSerIleLeuGlyArgIleSerAspAlaValSerAlaValAla	535	
qo	1328	GGAGACAAGCTAGTTAAA	1345	
ογ	536		555	
QQ	1346		1384	
ογ	556	LeuAlaAsnAr	575	
qq	1385	:::	1429	
οy	576		595	
qq	1430		1459	
٥٧	296	GlyThrArgLeuValThrLy	612	
Ωp	1460		1510	
δy	613	TyrGlnAlaGlyAlaGluLeuArgLeuSerGluAspLysLysGlyValL	632	
qq	1511	:::         ATTAAAGATATTGATTCAGTAGTATACGGT	1543	
0y	633	ThrLysProLeuSerHisPro	652	
QQ	1544	AAAGAAAATGATCGTATCGTAGATATTTAAGTCTAAGT	1582	
οy	653	GluValPheGlyHisSerThrAsnGlyPheAspLeuSerThrArgThrLeuGluHisGlu	672	
Dp	1583	GAAGCGCCGACTGATACGGCTAAA	1606 .	
δý	673	IleSerArgSerIleIleGlnAsnGlyGlyTrp	692	
QQ	1607	THE STATE OF THE S	1624	

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APPLICANT: EXELIXIS, INC.
TITLE OF INVENTION: CADS AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
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PRIOR PLICATION NUMBER: US 60/357,253
PRIOR FILING DATE: 2001-10-10
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PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.1
LENGTH: 14536
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                                                                                                                 1769 AAATCTAAAGCAGAGCAACCAGGAGTTTACACATCCTTTAAACAGCTGGTAACAGCCATG 1828
                                                                                                                                                                                                                                                                                                                                                                                    2069 GCAGCGCTGGCGAAGGCAGCGAATAGCGCGAATATTAATAATGTTGCAGTAGAAGAAAA 2128
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                                                                                                                                                                                                                       1721 GAAGAAGGT-----ACAGACGGTTACAAAGATGATTACACATTTACTGTAGCT 1768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2189 AACAGCTCGTTTACAGGGAAACTT---------ATCGCAAATCACCAG 2227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2228 GACAGTAAT---AAAAATGATACT-----GGAGGAATAGTAGGTAATATAACAGGAAAT 2278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            800 AspAsnPhe---AsnHisValProTyrArgLeuArg-------PhePheAla 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AsnTyrGluPheMetLysAspLeuArgLeuAlaValPheGlyAspIleGlyAsnAlaTyr 869
                                                                                                                                                                               733 AlaaspasnLeuValasnProMetArgGlyTyrArgGlnArgTyrSerLeuGluValGly 752
                                                                                                                                                                                                                                                                    SerSer------GlyLeuValSerAspAlaAsnMetAlaIleAla----- 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                      780 TyrGlySerAsnArgAlaHisGlnMetThrGlyGlyIleGlnAlaGlyTyrIleTrpSer 799
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 888 AlaSerProValGlyGlnValArgValAspValAlaThrGlyValLysGluGluGlyAsn 907
693 LeuAspLysLeuLysThrGlnAlaProProGluThrTrpGlnAspLeuProValAspPhe 712
                                                                                                                                                                                                                                                                                                                                                              ArgAlaGlyIleSerGlyValTyrSerPheGlyAspAsn-------Ala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LeuThrGlyGlyGlnValLeu-------AlaValGlyThrAlaGluTyr
                                                                                     ValAsnGlyLysProSerGlnGluAlaLeuLeuAlaGlyValAlaValHisLysThrVal
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; Sequence 6, Application US/10160758
; Publication No. US20030036076a1
; GENERAL INFORMATION:
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; ; us-1	TYPE: DNA ORGANISM: 10-160-758-	Homo s	apiens				
Alig Pred Scor Perc Best Quer DB:	Alignment Pred. No. Score: Percent S Best Loca Query Mata	Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match:	0.0211 313.50 31.69\$ 17.47\$ 2.82\$	Length: Matches: Conservative: Mismatches: Indels: Gaps:	14536 1199 162 393 385		
ns-0	9-914	-168-2 (1-919)	x US-10-160-758	3-6 (1-14536)			
Oy Dp	52		AlaLysAlaGlyAsnProProValLeuLeuThrProGluGln     ::                  GCTCGGGATGAGAAGAG	<pre>euThrProGluGln :::    ::: AGAGGGAAGAGGT</pre>	AlabysalaGlyasnProProValLeuLeuThrProGluGlnIleGlnAlaArg	69 6505	
οy	70		lyLeuAsnAlaLysP	roGlnSerGlnAlaLe	LeuAsnAlaAlaGlyLeuAsnAlaLysProGlnSerGlnAlaLeuAspValValAsnPhe	68	
q	6506		CACTGTTTCAGAGTCC	::: CTTATTACAAAGTCAG		6565	
οχ	06		AspAspGlnSerProlleSerArg1leGlyGluGlnSerProProLeuGlyLeuAs:	LyGluGlnSerProPr	oLeuGlyLeuAsp	108	
QQ	6566		CAATTCTCCACACCC	AGGCCCGGAGTCCAGA	ACCCTCTATACCCCAATTCTCCAACCCCAGGCCCGGAGTCCAGAGGGACTCCGGCTCATC	6625	
٥y	109		11uG1u	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		114	
QΩ	9299		AGGAAGAACCCTTGAI	IGCTGTTCACCACTGA	TACAACATTGTGGAGGAAGAACCCTTGATGCTGTTCACCACTGACTTCAAGACTGGTGTC	6685	
δ	115		-ThrThrProLeuSerLeuGlu	[uG]	-GluLeuPheAlaGlnGlu	127	
ДQ	9899		GGCCTTTGGACTATG	AGTCCAAGACCAAACA	CTAACAGTAACAGGGCCTTTGGACTATGAGTCCAAGACCAAACATGTGTTCACAGTCAGA	6745	
οy	128		SerThrGluMetGlyIleAsnProAsnAspTyrIleProGluTyrGlnGlyGluGl :::   ::: 	snAspTyrlleProGl	uTyrGlnGlyGluGln	146	
g	6746		CTCTGGGGTCATTTT	TGAAGCCACAGTGGA	GCCACGGATACAGCTCTGGGGTCATTTTCTGAAGCCACAGTGGAAGTCCTAGTGGAGGAT	6805	
ολ	147	ProAsnSerGluV	ProAsnSerGluValValValProProThrLeuGlu-	rrLeuGlu		158	
Ωp	9089	GTCAATGATAAC	:	TTTTCCCAATTGGT	cciccacititiccaatiggictataccacitccatc	. 9589	
ογ	159	d	-ProGluLysProGlyLeuIleLysArgLeuTyrAla-	ulleLysArgLeuTy	rAla	170	
QQ	6857	TCAGAAGGCTTGC	CTGCTCAGACCCCTGT	GATCCAACTGTTGGC	TCAGAAGGCTTGCCTCAGACCCCTGTGTTCCAACTGTTGGCTTCTGACCAGGACTCA	6916	
οy	171		Argle	-ArgLeuPheAsnAspGlyValAsnLysValProAr	lAsnLysValProArg	182	
qq	6917	GGGGGAACCGTG	GGGCGGAACCGTGACGTCTTTATCAGATTGTGGGGGATGGCTCAGAT	: TGTGGAGGATGGCTC	::: AGAT	6964	
٥y	183	LeuLysAlaLysP	heTyrGlnSerSe	rGlnSerGlyGluTh	LeuLysAlaLysPheTyrGlnSerSerGlnSerGlyGluThrSerAlaIleGlySer	201	
qq	6965	GTTTCCAAGT	TCTTCCAGATCAATG	GAGCACAGGGGAGAT	-GTTTCCAAGTTCTTCCAGATCAATGGGAGCACAGGGGGAGATGTCCACAGTTCAAGAA	7021	
٥y	202	SerHisGlnLysT	SerHisGlnLysThrGluProTyrAlaAsnIleLysAlaAlaLeuGluAsp	nIleLysAlaAlaLe	uGluAsp	218	
ДQ	7022	CTGGATTATGAAG	CCCAACACACTITCA	TGTGAAAGTCAGGGC	CTGGATTATGAAGCCCAACAACACTTTCATGTGAAAGTCAGGGCCATGGATAAAGGAGAT	7081	
ΟY	219	IleThrG	IleThrGlnGluSerAlaMet	AS	-AspLeuAsnGlySerIle	231	
QQ	7082	CCCCCACTCACTG	GTGAAACCCTTGTGGT	TGTCAATGTGTCTGA	CCCCCACTCACTGGTGAAACCCTTGTGGTTGTCAATGTGTCTGATATCAATGACAACCCC	7141	
οy	232	ProArgLeuArgG	InThrAlaLeuValAl	aAlaArgAlaValGl	Ωı	251	
QQ	7142	CCAGAGITCAGAC		CAATGTCAGT		7183	
δ d	252	LeuSerllelleA	rgAsnSerIleGlyGl	GluvalAspValIleIl		271	
3	* 01	C188CAACC1818	GACACCIGGIICIIAA	AGTCCAGGCTATTGA	CIGGCAACCIGIGGACACCIGGIICIIAAAGICCAGGCIAIIGACCIGGACAGAGAGAC	7243	
οy	272	ProvalTyrileA:	ProValTyrIleAspTyrArgAlaValGluValArgGlyGlu::::::::::::::::::::::::::::::::::	uValArgGlyGlu		285	
qq	7244	ACCTCCCGCCTGG	AGTACCTGATTCTTTC	TGGCAATCAGGACAG	ACCTCCCGCCTGGAGTACCTGATTCTTTCTGGCAATCAGGACAGGCACTTCTTCATTAAC	7303	

Qy	285		285
qq	7304	AGCTCATCGGGAATAATTTCTATGTTCAACCTTTGCAAAAAGCACCTGGACTCTTTAC	7363
Oy	2	GlyalaAspAspLysAlaPheThrThrValAlaAs	301
q	9	STAGGTGCTTCTGATGGAGTCTTCCGAGCAACTGTCCCTGT	7414
0y	0		
Dp	7415	ATCAACACTACAAATGCCAACAAGTACAGCCCAGAGTTCCAGCAGCACCTTTATGA	7474
δ <sub>λ</sub>	- 1	hrLysLysAsnLeulleGluAsnAlaSerAlaGluHisGlyTyrPheAspGlyArgTr	33
a d		HGAA IIAGCAGAGAAIGCAA	Ω
d d	7529	LeuaspargservalaspvallieLeuroaspasnThrAlaaspvalserLeulletyr :::   :::::::	353
Qy	354	GlnTyrArgPheAspG	73
qq	7580	: 3AAGTTCTCCATAAACCC	7615
οy	374	pProAspLysLeuProValLysArgGluLeuGluGlnLe	393
QQ	. 7616	GGCCAGATTGCCACTCTGCAGAACTG	7642
Qy	394	GluAlaTyrAsnLeuGlnAlaValArgAlaLeuSerAsn	413
qq	7643	GATCGGGAAAATTCAACAGGAGAGTCATTACTTATAAGGTCATGGGTCGGGAT	9692
δλ	413	:	413
qq	7697	GGAGGAGGAAGAGTAGCCTTCTGCACGGTGAAGATCATCCTCACAGATGAAAATGACAAC	7756
Qy	414	LeuIleAlaThrArgTyrPheAsnMetValAsnThr	425
QQ	7757	CCCCCACAGTTCAAAGCATCTGAGTACACAGTATCCATTCAATGCAATGTCAGTAAAGAC	7816
οy	426	GlulleValPheProGluArgGluGlnIleGlnAsnAspGlnValSer	441
QQ	7817	TCTCCGGTTATCCAGGTGTTGGCCTATGATGCAGATGAAGGTCAGAACGCAGATGTCACC	7876
οy	442	SerS	461
qq	7877	ACT	7924
Qy	462	ProvallleGluThrValGluLeuThrAspGlyIleLeuMetAsp1leSerProlle	480
QQ	7925	CAGTCACTGGTGTGTGAAAGACAGCTGGTGGTTGGAAATCAGACCTT	7984
Οy	481		490
QQ	7985	GACTTCTTCATCAAGGCCCAAGATGGAGGCCCTCCTCACTGGAACTCTCTGGTGCCAGTA	8044
δy	491	#	502
qq	8045	::: ACTTCAGGTGGTTCCTAAAAAGTATCCTTACCGAAATTTTCTGAACCTTTGTATACT	8104
Qy	503	gValLeuAlaIleAsnHisAspAspGlyValAsnArgSer	522
qq	8105		8158
οy	523	eSerAspAlaValSerAlaValAlaArgAlaIleLeuProAspGlu	542
qq	8159	GTGGCAGCTCAAGATCCAGTCATCTACAGTCTAGTGCGGGCACTACACACTGGGGGC	8215
οy	543	SerGluAsnGluValIleAspLeuProGluArgThrAlaLeuAlaAsnArgLysThrPro	562
QQ	8216	CAAGGATGGTGTCTCCCTAGACCCAGACACAGGGGTCATAAAGGTGAGGAAGCCC	8275

Oy	563		267		
q	8276	   ATGGACCACGAATCCACCAAATTGTACCAGATTGATGTGATGGCACATTGCCTTCAGAAC	8335	QΩ	9242
ò	567		567	δλ	818
· qd	8336	ACTGATGTGGTGTCCTTGGTCTCTGTCAACATCCAAGTGGGAGACGTCAATGACAATAGG	8395	qq	9293
à	9 4			οy	838
S 8	8396	CCTGTATTTGAGGCTGATCCATATAAGGCTGATCCTGAGAATATGAGGCTGATCGAAATAAGGCTGATCGAAATAAGGCTGATCGAGGAAATAAGGCTGAGGAAAAAGGCTGAGAAAAAGGCTGAAAAAGGCTGAAAAAGGCTGAAAAAGGCTGAAAAAAGGCTGAAAAAAGGCTGAAAAAAAA	8455	QQ	9344
; ;	624		0 0	Qy	828
S 6	**************************************		585	QQ	9368
3 3	9 0		8515	QY	876
Š i	080	ValThrLysPheGluHisAsnLeulleAsn 	609	QQ	9428
αΩ	8516 AGGCTGTCTGCAGACCCTGGTAGCAATGTC	CATGAGCTCTTTGCC	8560	λO	893
Ολ	610 ArgAsp		611	: E	9489
QQ	8561	ATTGACAGTGAGAGTGGTTGGATCACCACACTCCAGGAACTTGACTGTGAGACCTGCCAG	8620		
Οy	612	GlyTyrGlnAlaGlyAlaGluLeuArgLeuSer	622	NESU US-1	NESULT 14 US-10-160-
qq	8621		8680		Publicat
ογ	. 622		622	_	APPLICA
qq	8681	GCCCTGGTTCAGGTCTCCATTACAGATGAGAATGACAATGCTCCCCGGATTTGCTTCTGAA	8740		FILE RE
ολ	623		634		CURRENT
qq	8741	GAGTACAGAGGATCTGTGGTTGAGAACAGTGAGCCTGGCGAACTGGTGGCGACTCTAAAG	8800		PRIOR F
ΟŊ	635	LeuArgAlaThrLeuGlyTyrGlnGlnGlu	653		PRIOR F
qa	8801	AACAGGCAGGTCACCTGCTACATCACAGAGGA	8860		PRIOR F
Qγ	654		999		SOFTWAR
qq	8861	GACCCCCTGGGCCAGTTTGGCATCAGCCAAGTTGGAGATGAGTGGAGGATTTCCTCAAGG	8920		SEQ ID N LENGTH
Οy	299	IleGlnAsnGlyGlyTrpAsnArgThr	989		ORGANI ORGANI
qq	8921 AAGACCCTGGACCGCGAGCATACAGCCAAG		8950	2	001-0
Οy	687	ProProGluThrTrpGln	706	Aligr Pred	Alignment Pred. No.:
q	8951		2006	Score: Percen	Score: Percent Si
οy	707		726	Best Quer	Best Local Query Matc
qa	8006		29067	DB:	
ολ	727	AlaValHisLysThrValAlaAspAsnLeuValAsnProMetArgGlyTyrArgGlnArg	746	0-sn	US-09-914-
QQ	8906		2606	Οy	52
ò	747	TyrSerLeuGluValGlvSerSerGlvLeuValSerAspAlaAspMetAlaTleAlaArd	766	qa	6446
q <sub>Q</sub>	8606		9151	Qy	70
Qy	797		786	QQ	9059
qa	9152		9181	Οy	90
Qy	. 787 GlnMetThrGlyGlyIleGlnAlaGlyTyrIleTrpSer		199	QQ	6566
qa	9182	CTCACTGCCCTAGACCGAGAA	9241	Οy	109
Qy	800		817	QQ	6626

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THE OF INVENTION: CADS AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE INE OF INVENTION: CADS AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE TREP INVENTION: CADS AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE REFERENCE: EX20-089C

REBY APPLICATION NUMBER: US 60/296,076

TOR FILING DATE: 2001-06-05

TOR FILING DATE: 2001-06-05

TOR FILING DATE: 2002-02-15

TOR FILING DATE: 2002-02-15

TOR FILING DATE: 2002-02-15

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TOR FILING DATE: 2002-03-15

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TACAACATTGTGGAGGAAGAACCCTTGATGCTGTTCACCACTGACTTCAAGACTGGTGC 6685
|||| :::
TCGTGCCAGGCAGACATCACCCTCCATGTGGGGGTGATGACAATGCC----- 9343
                                                                                                                                                                                                                                                                                                                                                                                                                                 GCTCGGGATGGAGGAACGCCATCCCTCCAGAGTGAGGAAGAGGTACTTGTCACTGTGAG 6505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AATAAATCCAACCCACTGTTTCAGAGTCCTTATTACAAAGTCAGAGTACCTGAAAATATC 6565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCTCTATACCCCAATTCTCCACACCCAGGCCCGAATCCAGAGGGACTCCGGCTCATC 6625
                                                                                                                                                                                                                                        -----CCGCGGTTCTTCCCCAGCTGT 9367
                                                                                                                                                                                                                                                                                                                               ArgLeuAlaValPheGlyAsp-----IleGlyAsnAlaTyrAspLysGlyPheThrAsn 875
                                                                                                                                                                                                                                                                                                                                                                                                     AspThrLysIleGlyAlaGlyValGlyValArgTrpAlaSerPro-----ValGly 892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AspAspGlnSerProIleSerArgIleGlyGluGlnSerProPro---LeuGlyLeuAsp 108
                                                                           SerIleArgGlyTyrAlaHisAspSerLeuSerProIleSerAspLysGlyTyrLeuThr 837
                                                                                                                                                                                      GlyGlyGlnValLeuAlaValGlyThrAlaGluTyrAsnTyrGluPheMetLysAspLeu 857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MetServalIleGluGlu------114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AlaLysAlaGlyAsnProProValLeuLeuThrProGluGln-----IleGlnAlaArg 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LeuAsnAlaAlaGlyLeuAsnAlaLysProGlnSerGlnAlaLeuAspValValAsnPhe 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CACTITICCATCGACGCCACCACCAGGGGTGATCCGCCTGGAAAAGCCGCTGCAGGTC 9544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlnValArgValAspValAlaThrGlyValLysGluGluGlyAsnProlleLysLeu 911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           168-2 (1-919) x US-10-160-758-7 (1-14536)
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-7, Application US/10160758

-ion No. US20030036076A1

INFORMATION:
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17.47%
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SM: Homo sapiens
758-7
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1 Similarity:
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ž g	115	<ul> <li>ThrThrProLeuSerLeuGluGluLeuPheAlaGlnGlu 127</li> <li></li></ul>	
λ Sp	128	SerThrGluMetGlyIleAsnProAsnAspTyrIleProGluTyrGlnGlyGluGln 146 	
ž q	147		
2 <u>7</u>	159		
2 <u>4</u>	171 6917	GGGCGGAACCGTGACGTCTTTATCAGATTGTGGAGGATGGCTCAGAT	
ž, q	183 6965	LeuLysAlaLysPheTyrGlnSerSerGlnSerGlyGluThrSerAlaIleGlySer :::                         GrrSerGlnSerGlyGluThrSerAlaIleGlySer :::	
≿ q	202	SerHisGlnLysThrGluProTyrAlaAsnIleLysAlaAlaLeuGluAsp	
ž q	219	IleThrGinGluSerAlaMetAspLeuAsnGlySerIle 231 :::        :::      :: CCCCCACTCACTGGTGAAACCCTTGTCAATGTGTCTGATATCAATGACAACCC 7141	
z q	232	ProArgLeuArgGinThrAlaLeuValAlaAlaArgAlaValGlyTyrTyrAspIleAsp 251 	
<u>≯</u>	252 7184		
ž g	272	ProvaltyrileaspTyrargAlaValGluValArgGlyGlu	
≱	285		
ą	7304	AGCTCATCGGGAATAATTTCTATGTTCAACCTTTGCAAAAGCACCTGGACTCTTCTTAC 7363	
۾ ج	286 7364	GlyAlaAspAspLySAlaPheThrThrValAlaAspGluValProLeu 301 	
<u>ب</u> ۵	302		
> Q	314	ThrLysLysAsnLeulleGluAsnAlaSerAlaGluHisGlyTyrPheAspGlyArgTrp 333 :::	
× •	334	LeuAspArgSerValAspValileLeuProAspAsnThrAlaAspValSerLeuileTyr 353 :::   ::: ATAGACAAAGATAGTGGTCCCTATGGCACTATAGATTATACTATAC	
>+	354	дБ	
Q	7580	AAACTAGCAAGTGAGAAGAAT 7615	
ъ д	374	AsnGlnLeuThrThrAspProAspLysLeuProValLysArgGluLeuLeuGluGlnGlnLeu 393     :::      GCCAGATTGCCACT	
>	394	413	

QQ	7643 GAT	CGGGAAAATTCAACAGAGAGAGTCATTGCTATTAAGGTCATGGGTCGGGAT 7696
Qγ	413	413
qq	7697 GGA	GGAGGAGGAAGAATAGCCTTCTGCACGGTGAAGATCATCCTCACAGATGAAAATGACAAC 7756
Οy	41,4	LeuilealaThrargTyrPheAsnMetValAsnThr 425
QQ	7757 CCC	CCACAGTTCAAAGCATCTGAGTACAGTATCCATTCAATGCCAATGTCAGTAAAGAC 7816
ΟŊ	426	GlulleValPheProGluArgGluGInIleGlnAsnAspGlnValSer 441
qq	7817 TCT	CCGGTTATCCAGGTGTTGGCCTATGATGCAGATGAAGGTCAGAACGCAGATGTCACC 7876
δy	7	3luGlnSerSe
qq	7877 TAC	
Qγ	462 Pro	SluLeuThrAspGlyIleLeuMetAspIleSerPro
Op	7925 CCAC	- A
Qy	481 GluE	GluPheSerAla
qq	7985 GAC	CTCCTCAC
ολ	-	
QQ	8045 CGAC	CTTCAGGTGGTTCCTAAAAAGTATCCTTACCGAAATTTTCTGAACCTTTGTATACT 8104
δλ	503 Tyr	lAsnArgSe
qq	8105 TTC1	TCTGCACCTGAAGACCTTCCAGAGGGGTCTGAAATTGGGATTGTTAAAGA 8158
δλ	523	CleLeuGlyArglleSerAspAlaValSerAlaValAlaArgAlaIleLeuProAspGlu 542
qq	8159 GTG	AGATCCAGTCAT
ΟŸ	43	SerGluAsnGluVallleAspLeuProGluArgThrAlaLeuAlaAsnArgLysThrPro 562
qq	8216 AACA	- Ö
ΟŸ	563 AlaA	ValTyrG
qq	8276 ATG	
Oy	295	295
qq	8336 ACTGAT	SATGTGGTGTCCTTGGTCTCTGTCAACATCCAAGTGGGAGACGTCAATGACAATAGG 8395
Qy	568	SerLysLysValProLeu 573
qq	8396 CCTGT	ATTTGAGGCTGATCCATATAAGGCTGTCCTC
Qγ	574	TyrValPheValAlaSerAspLysProArgAspGlyGlnIleGlyLeu 589
qq	8456 TCAG	AGTCATTCAAGTGACTGCCATTGACAAGGACACTGGGAGAGATGGCCAGGTGACTAC 8515
Qy	590 GlyT	SASE
qq	8516 AGGC	TGTCTGCAGACCCTGGTAGCATGTCCATGAGCTCTTTGCC 8560
Οy	610 ArgA	Asp
qq	1 ATT	agtgagagtggttgg
οχ	612	
οp	8621 ACTT	ATCATTTTCATGTGGTGGCCTATGACCACGGACAGACCATCCAGCTAT
Οy	622	622

us-09-914-168-2.rnpb

API			######################################		######################################	, NUN ; NUN ; SOI ; SEQ ; LI		; LC US-09-	Score: Percer Percer Best I	Query DB: US-09	QV Db	Qy	qa	Qy	Oy d	g vo	qa	ογ	qa	Qy Db
8681 GCCCTGGTTCAGGTCTCCATTACAGATGAGAATGACAATGCTCCCCGATTTGCTTCTGAA 8740 623	635 ProLeuSerHisProLeuAsnAspGlnLeuArgAlaThrLeuGlyTyrGlnGlnGlu 653 	654ValPheGlyHisSerThrAsnGlyPheAspLeuSerThr 666	667 ArgThrLeuGluHisGluIleSerArgSerIleIleGlnAsnGlyGlyTrpAsnArgThr 686 :::       ::      ::	687 TyrSerLeuArgTyrArgLeuAspLysLeuLysThrGlnAlaProProGluThrTrpGln 706 	707 AspLeuProValAspPheValAsnGlyLysProSerGlnGluAlaLeuLeuAlaGlyVal 726 :::	727 AlaValHisLysThrValAlaAspAsnLeuValAsnProMetArgGlyTyrArgGlnÀrg 746       ::     9068 AAGGTTCATGAAGATGTATTTCCAGGACAC 9097	747 TyrserLeuGluValGlySerSerGlyLeuValSerAspAlaAsnMctAlaIleAlaArg 766 :::	767 AlaGlyIleSerGlyValTyrSerPheGlyAspAsnAlaTyrGlySerAsnArgAlaHis 786	787 GlnMetThrGlyGlyIleGlnalaGlyTyrIleTrpSer 799 :::	800AspasnPheAsnHisValProTyrArgLeuArgPhePheAlaGlyGlyAspGln 817	818 SerIleArgGlyTyrAlaHisAspSerLeuSerProIleSerAspLysGlyTyrLeuThr 837 :::::::        :::	GlyGlyGlnValLeuAlaValGlyThrAlaGluTy	9344	858 ArgLeuAlaValPheGlyAspIleGlyAsnAlaTyrAspLysGlyPheThrAsn 875	876 AspThrLysIleGlyAlaGlyValGlyValArgTrpAlaSerProValGly 892 	GlnValArgValAspValAlaThrGlyValLysGluGluGlyAsnProlleLysLeu 911	9488 CACTITICCATCGACGCCACCACGGGGTGATCCGCCTGGAAAAGCCGCTGCAGGTC 9544	SULT 15 -09-815-242-8512	Sequence 8512, Application US/09815242 Patent No. US20020061569A1	GENERAL INFORMATION: APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
Oy Ob	Qy Db	Oy Dp	Oy Db	Qy Db	Qy Db	Qy Db	Oy Db	O <sub>Y</sub>	Qy Db	Qy Db	Qy Db	ογ	qa	Oy Op	Qy Db	δ	Q	RES US-		

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2434 TTACAAAAAGTACCTGTTAATATTTCTGGAATACCGTTGGATCCATCAGCATTGGTTTAT 2493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2692 TCTAATATGAGTAATGCTGTTACTATTTTGCCAGATGACATTCCACCAACA------ 2742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147 -----ProAsnSerGluValValValProProThrLeuGluProGluLysProGly 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85 AspValValAsnPheAspAspGlnSerProIleSerArgIle-----GlyGluGln 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102 SerProProLeuGlyLeuAspMetSerValIleGluGluThrThrProLeuSerLeuGlu 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 GluLeuPheAlaGlnGluSerThrGluMetGlyIleAsnProAsnAspTyr----- 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 GlnAlaLysAlaGlyAsnProProValLeuLeuThrProGluGlnIleGlnAlaArg--- 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITERA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative:
Mismatches:
Indels:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Staphylococcus aureus
Zyskind, Judith W. Wall, Daniel
Trawick, John D. Carr, Grant J. Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133.00
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16.68%
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9-815-242-8512
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Local Similarity:
/ Match:
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                                                           PPLICANT:
PPLICANT:
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δ	164	LeulleLysArgLeuTyrAlaArgLeuPheAsnAspGlyValAsnLysValProArgLeu 183
qq	2743	
Qy Dp	184	LysAlaLysPheTyrGlnSerSerGlnSerGlyGluThrSerAlaIleGlySerSerHis 203          :::    :::   AATGCCAAATACTATGGAGGGAGGAGTCAACTTTACAATGGGTGTCTCTGATAGACAT 2823
δ i	204	GlnLeuGluAspileTyrAlaAsnIleEysAlaAlaLeuGluAspileThr 220
QQ	2824	TCTGGATTAAAAAGTACAACTATTACGACATTGCCAAGTGGTTGGACATCAAATTTAACT 2883
oy Og	221	GInGluSerAlaMetAspLeuAsnGlySerIleProArgLeuArgGlnThrAlaLeuVal 240  : :
ογ	241	
qq	2938	::::::      ::::::
δ	261	GluValAspValIleIleHisAspLeuGlyGluProValTyrIleAspTyrArgAlaVal 280
qq	2983	AATGTCAATAATACGACAAATGATAGTCAATCTAAACATGTGTCAATTCATGTAGGT 3039
ογ	281	lyGluGlyAlaAspAspLysAlaPheThrThrValAlaAspGluValPro 300
g	3040	AAAATTAGTGAAGATGCTCATCCG 3063
Oy Dp	301	LeuLeuIleGlyAspValPheHisHisGlyLysTyrGluThrLysLysAsnLeuIleGlu 320 
ογ	321	AsnAlaSerAlaGlu 325
QQ	3100	
0y	326	pGlyArgTrpLeuAspArgSerValAspValIle
QQ	3160	AACCAAAATATAAGAGGATATTTAGCATCAACTGATCCAGTA 3201
Qy Dp	342	LeuProAspAsnThrAlaAspValSerLeuIleTyrAspThrGlyThrGlnTyrArgPhe 361         :::                 ACAGTCGATAAATAGTAACAACGCTT 3261
ò	362	- ;
g q	3262	TGAAATCTGAATATCAAACTGCCAAT 33
οy	380	ProAspLysLeuProValLysArgGluLeuLeuGluGlnLeuLeuThrValAsnMetGly 399
qa	3322	GCTGCTAAAACAGCAACGGTAACGTTGCTAAAGGA 3357
oy 4	400	laLeuSerAsnAspLeulleAlaThrArgTyr
3 (		CAATAT 33
δ	420	PheProGluArgGluGlnIle(
qq	3391	TTTACTTTAAGTAATGGACAAGCTATT
Οy	440	ValSerPheGluGlnSerSerSerArgThrGluProAlaGlnValAspGluSer 458
qq	3424	GGAACATTIACAAATATTACATCIGATAGAACTATTCCAACTGCACA 3471
οy	459	ThrLeuGluProValIleGluThrValGluLeuThrAspGlyIleLeuMetAspIleSer 478
qq	3471	3471
οy	479	ProlleGluPheSerAlaSerAsnLeulleGlnAspLysLeuAsnLeuValAlaAlaLys 498
qq	3472	GAAGTTAGTCAAATGAATGCAGGTACACAGCTATATCATATGGTTGCTTCAAAT 3525

δ	499	pAspArgvalLeuAlaIl
QQ	3526	
Qy	515	HisAspAspGlyValAsnArgSerileLeuGlyArglieSerAspAla 530
QΩ	3583	CAACCTGAAGGCGATCAACGTGTATGTACGTCAACATATGATTTAACTACTGATGAA 3642
δλ	531	ProAspGluSerGluAsnGluVallleAspLeu 55
QQ	3643	ACAAGCTTTTATT
δŏ	551	ProGluArgThrAlaLeuAlaAsnArgLysThrProAlaAspValTyr 566
qq	3697 (	GCCGAAGGTGATATTTCAGTTACAAATACACCTAATGGTGCTAATGTAAGTACTATTACA 3756
Οy	266	995
qq	3757 (	GTAAATTTAATAAAAGGTCGATTAACGAAATCATTCGCGTCTAACCTAGCTAATATGAAT 3816
δy	567	GlnSerLysLysValProLeuTyrValPheValAla 578
QQ	3817	TTCTTGCGTTGGGTTAATTTCCCACAAGATTATACAGTGACATGGACGAATGTAAAATT 3876
Qγ	579	SeraspLysProArgaspGlyGln1leGlyLeuGlyTrpGlySerAspThrGlyThrarg 598
qq	3877 (	GCAAACAGACCAACAGATGGTGGTTTATCATGGTCCGATGAC3918
Qy	599	LeuValThrLysPheGluHisAsnLeuIleAsnArgAspGlyTyrGlnAlaGlyAlaGlu 618
QQ	3919	
ΟŸ	619	LeuArgLeuSerGluAspLysLysGlyValLysLeuTyrAlaThrLysProLeuSerHis 638
QQ	3964	ATTACAACTAATGATATTTTAACGATGCTAAAAGCGACTACTACAGTGCCT 4014
Qy	639	ProLeuAsnAspGlnLeuArgAlaThrLeuGlyTyrGlnGlnGluValPheGly 656
qq	4015 (	TACTGGTAATGAAAAAGCAC
QY	657	HisserThrAsnGlyPheAspLeuSerThrArgThrLeuGluHisGluIleSerArg 675
QQ	4075	AACTATAGAACAGGTTATTCACAAGGAAATGCATCATCTGATGGCCAA 4125
δy	929	SerIleIleGlnAsnGlyGlyTrpAsnArgThrTyrSerLeuArgTyrArgLeuAspLys 695
QQ	4126	
Οy	696	LeuLysThrGlnAlaProProGluThrTrpGlnAspLeuProValAspPheValAsnGly 715
qq	4141	
Οy	716	LysProSerGlnGluAlaLeuLeuAlaGlyValAlaValHisLysThrValAlaAspAsn 735
QQ	4147 (	CAAGTGATTCAA4167
Qy	736 1	LeuValAsnProMetArgGlyTyrArgGlnArgTyrSerLeuGluValGlySerSerGly 755
QQ	4168 4	ATCATCAACCCTTCAAACGGTTATGGTGGGCAACCTGTTACAAATTCAAATACTCGTGCA 4227
Οy	756	LeuValSerAspAlaAsnMetAlaIleAlaArgAlaGlyIleSerGlyVal 772
qq	4228 #	AACCATAGTAAACGCAACTGTTGTTAACGTAAACGAACCGGCAGCTAATGGTGCTGCGCA 4287
οy	773 1	TyrSerPheGlyAspAsnAlaTyrGlySerAsnArgAlaHisGlnMetThrGlyGlyIle 792
qu	4288	GACCACGTTGTAAAAAGTAATTCTACACATAATGCAAGTGATGCAGT
Qy	793 (	GlnAlaGlyTyrlleTrpSerAspAsnPheAsnHisValProTyrArgLeuArg 810
qq	4345 1	TATAAAGCACAGTTATACTTAACGCCATATGGGCCAAAACAATATGTTGAACATTTAAAT 4404
٥٨	811	PhePheAlaglvGlvAspGlnSerIleAraGlvTvrAlaHisAspSerI.ou 827

:::  4405 CAAAATACGGGAAATACTGATGCTATTAACATTTATTTTGTACCAAGTGATTTAGTG 4464  828 SerProlleSerAspLysGlyTyrLeuThrGlyGlyGlnValLeuAla 843	Perce Best Query DB:	Percent Similarity: 34.47% Conservative: 79 Best Local Similarity: 21.05% Mismatches: 197 Ouery Match: 189 DB: Gaps: 33
GGTGAAACATTT 45	60-sn	-914-168-2 (1-919) x US-09-815-242-9166 (1-1488)
8	Qy	AsnSerGluValValValProProThrLeuGluProGluLysProGlyLeuIleLysArg
ACAAACACTATTACAGCGAATGATAACTTTGGTGTGCAATCGGTAACTGTACCAACTACA 4584	qa	4 TCATCTAAGGTTATTGTTACAATTTTCGGTGCGAGTGGAGCCTGGCTAAACGC 57
	Qy	168LeuTyrAlaArgLeuPheAsnAspGlyValAsnLysValProArgLeuLysAlaLys 186
	Qy Dp	187 PheTyrGlnSerSerGlnSerGlyGluThrSerAlaileGlySerSerHisGlnLys 205
869 TyraspLysGlyPheThrasnAspThr	Qy	206 ThrGluProTyrAlaAsnIleLysAlaAlaLeuGluAspIleThrGlnGluSerAlaMet 225
883 ValGlyValArgTrpAlaSerProVal 891    :::       4762 ACTTCATCAAGGCTGCTGTG 4788	da Db	25 AspLeuasnGlySerIleProArgLeuArgGlnThrAlaLeuValAlaAlaArgAlaVal 245
	δλ	246 GlyryrTyrAspileAspLeuSerileIleArgAsnSerileGlyGluValAspValile 265
Sequence 9166, Application US/09815242	qa	232 TTCTACTATCAA 243
NMATION: Haselbeck, Robert Ohlsen, Kari L.	oy da	266 IleHisAspLeuGlyGluProValTyrIleAspTyrArgAlaValGluVal 282
ryshin, Dunti m. Wall, Daniel Trawick, John D. Carr, Grant J.	QY	283ArgGlyGluGlyAlaAspAspLysAlaPheThrThrValAlaAspGluValPro 300
APPLICANT: Yamamoto, Robert T. APPLICANT: Xu, H. Howard TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes	Qy	301 LeuLeuIleGlyAspValPheHisHisGlyLySTyrCluThrLysLySAsnLeuIleGlu 320
FILE REFERENCE: ELITRA 011A CURRENT APPLICATION NUMBER: US/09/815,242	Qy	321 AsnAlaSerAlaGluHisGlyTyrPheAspGlyArgTrpLeuAspArgSerValAspVal 340
1 F LLING DATE: 201 03-21 APPLICATION NUMBER: 60/191,078 FILING DATE: 2000-03-21	qq	406
APPLICATION NUMBER: 60/206,848 FILING DATE: 2000-05-23 APPLICATION NUMBER: 60/207,727	qa .	341 IleLeuProAspAsnThrAlaAspValSerLeuIleTyrAspThrGlyThrGln 358
LILING DATE: 2000-05-26 APPLICATION NUMBER: 60/242,578 FILING DATE: 2000-10-23	Qy	359 Tyr
APPLICATION NUMBER: 60/253,625 FILING DATE: 2000-11-27	qa	457 TACGCAACTGCAAACAAGTTGAATGACGAACTCCTAGCAACATTTGACGAAGAACAAATT 516
APPLICATION NUMBER: 60/257,931	QY	367 PheThrIleAspProLysThrAsnGlnLeuThrThrAspProAspLysLeuProValLys 386
APPLICATION NUMBER: 60/269,308 FTI-NG DAME: 3001-07-16	qq	517 TTCCGTATCGACCATTATCTTGGT 540
NUMBER OF SEQ ID NOS: 14110 SOFTWARE: FastSEQ for Windows Version 4.0 EQ ID NO 9166	da Pb	387 ArgGluLeuGluGluGlnLeuLeuThrValAsnMetGlyGluAlaTyrAsnLeuGlnAla 406 :::   :::::::::::::
LENGYII. 1488 TYPE: DNA ORGANISM: Streptococcus pneumoniae	δò	ValArgAlaLeuSerAsnAspLeuIleAlaThrArgTyrPheAsnMetValAsnThrGlu :::         :::
	qa	592 GAAAACGTTTGGAACAAGGATTTTATCGACAATGTTCAA 630
(1488)	QY Db	427 IleValPheProGluArgGluGlnIleGlnAsnAspGlnValSerPheGluGlnSerSer 446
0.000949 Length: 1488 132.50 Matches: 124	Oy	447 SerSerArgThrGluProAlaGlnValAspGluSerThrLeuGluProValIleGluThr 466 :::

Page 28

, PRIC	PRIC : PR	PRIC PRIC PRIC	PRIC PRIC PRIC	NUME SOFT	TYF	; NAN ; LOC US-09-8	Alignme Pred. N	Percent Best Lo	Query M	λο	0b 3	VO 4	Dp 4	Qy	Db 4		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	s qu	0y 1	S qq	Qy 10	9 qq	Δλ 16	)	ογ 20	da
Db 691 GCCCTCCGTGACATGGTCCAAAACCACACTCTA723	<pre>Qy 467 ValGluLeuThrAspGlyIleLeuMetAspIleSerProlleGluPheSerAlaSerAsn 486 :::    :::                            </pre>	Oy 487 LeuileGinAspLysLeuAsnLeuValalaAlaLysAlaArgHisLeuTyrAspMetPro 506	SPASPGLyValAsnArgSerIleLeuGlyArg	SerGluAsnGlu 54	ProAlaAspValTyr	567 GInSerLysLysValProLeuTyrValP	Db 949 ACATCTGGTGCCTTCTTTGTAGACAGGGATCGATTCGT 987 QY 587 IleglyLeuGlyTrpGlySerASpThrGlyTrbTargLeuValThrLysPheGluHis 605	STC	Oy 606 AsnLeuIleAsnArgAspGlyTyrGlnAlaGlyAlaGluLeuArgLeuSerGluAspLys 625    ::::::   Db 1045 AACATCGTC	Qy 626 LysGlyValLysLeuTyrAlaThrLysProLeuSerHisProLeuAsnAspGlnLeuArg 645	Db 1054TTTAAACAAATGGATTCTATCTATCTATGAACCACTTGCT 1092	Qy 646 AlaThrLeuGlyTyrGlnGlnGluValPheGlyHisSerThrAsnGlyPheAspLeuSer 665  Db 1093 CCAAATATTTTGACCATCTATATTCAACAAAGGGCTTCTCTTTTAAC 1143	Db 1144 CTAAATGGGAAGCAAGTAGGAGAATTTAACTTGGCTCCTAAC1188	ThrTyrSerLeuArgTyrArgLeuAspLysLeuLysThrGlnAlaProProGluThrTrp [1111]	1189TCACTTGATTACCGTACAGATGCGACTGCAACTGGTGCTTCTCCAGAACCAT	Oy 706 GInaspLeuProValaspPheValasn 714 b :::             :::	RESULT 17 IIC-00-815-040-7039	; Sequence 7037, Application US/09815242 ; Patent No. US20020061569A1	; GENERAL INFORMATION: ; APPLICANT: Haselbeck, Robert	; APPLICANT: Ohlsen, Kari L. ; APPLICANT: Zyskind, Judith W.	; APPLICANT: Wall, Daniel ; APPLICANT: Trawick, John D.	; APPLICANT: Carr, Grant J. ; APPLICANT: Yamamoto, Robert T.	≥	OF INVENTION: Prokaryotes EFERENCE: ELITRA.011A	; CURRENT APPLICATION NUMBER: US/09/815,242 ; CURRENT FILING DATE: 2001-03-21	; PRIOR APPLICATION NUMBER: 60/191,078

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433 GGGGGACAAAAGGTGAACGATCAAAATGCAGAAGAAAGCAGAGCACCTTGAAAAATAT 492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    493 ACGATT---GATTTAACCGCTCGTGCAGAAGTGGCAAACTTGATCCTGTAATTGGGCGT 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108 AspMetSerVallleGluGluThrThrProLeuSerLeuGluGluLeuPheAlaGlnGlu 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 SerThrGluMetGlyIleAsnProAsnAspTyrIleProGluTyrGlnGlyGluGlnPro 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  148 AsnSerGluValValValProProThrLeuGluPro-----GluLysProGlyLeuIle 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 166 LysArgLeuTyrAlaArgLeuPheAsnAspGlyValAsnLysValProArg---LeuLys 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185 AlaLysPheTyrGlnSerSerGlnSerGlyGluThrSerAlalleGlySerSerHisGln 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48 AlaileAsnGlnAlaLysAlaGlyAsnProProValLeuLeuThrProGluGlnIleGln 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     205 LysThrGluProTyrAlaAsnIleLysAlaAlaLeuGluAspIleThrGlnGluSerAla 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28 AlaLeuAlaGlnGlnAsnAsnProAlaAsnIleIleAsnHisValProAlaHisAspThr 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 AlaArgLeuAsnAlaAlaGlyLeuAsnAlaLysProGlnSerGlnAlaLeuAspValVal 87
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Matches:
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR PELLORATION NUMBER: 60/207,727
PRIOR PELLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PLING DATE: 2000-10-23
PRIOR PELLING DATE: 2000-11-27
PRIOR PELLING DATE: 2000-11-27
PRIOR RPLICATION NUMBER: 60/253,625
PRIOR RPLING DATE: 2000-12-22
PRIOR RILING DATE: 2001-2-12
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FSSESEG for Windows Version 4.0
LEWITH: 2571
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RGANISM: Haemophilus influenzae
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CGCGTTATCCTCTTTATTGACGAAATTCATACTATGGTCGGCGCGGGGTAAAACC	ValGlyTyrTyrAspIleAspLeuSerIleIleArgAsnSerIleGlyGluValAspVal 	IlelleHisAspLeuGlyGluProValTyrIleAspTyrArgAlaValGluValArgGly	GluGlyAlaAspaspLysAlaPhe	GluValProLeuLeulleGlyAspValPheHisHisGlyLysTyr::::::	GluThrLysLysAsnLeuIleGluAsnAlaSerAlaGluHisGlyTyrPheAspGlyArg 	TrpLeuAspArgSerValAspValIleLeuProAspAsnThrAlaAspValSerLeuIle		CAGTTACCAGATAAAGCCATTGATTTG TYrAspThrGlyThrGlnTyrArgPheAspGluValValValPhePheThrIleAspProLys	CAG	CAGTTACCAGATAAAGCCATTGATTTG TYASPThrGlyThrGlnTyrargPheaspGluValValPhePheThrIleaspProLys TyraspThrGlyThrGlnTyrargPheaspGluValValPhePheThrIleaspProLys ThrasnGlnLeuThrThraspProAspLysLeuProValLysargGluLeuLeuGluGluGlu :::	CAGTTACCAGATAAGCCATTGATTTG TYAASPThrGlyThrGlnTyrArgPheaspGluValValPhePheThrIleaspProLys TyrAspThrGlyThrGlnTyrArgPheaspGluValValPhePheThrIleaspProLys ThrAsnGlnLeuThrThrAspProAspLysLeuProValLysArgGluLeuLeuGluGln :::	CAGTTACCAGATAAAGCCATTGATT:::  CAGTTACCAGATAAAGCCATTGATT:::  TYFASPThrGlyThrGlnTyFArgPheAspGluValValPhePheThrTleAspProLys  THASBGlnLeuThrThrAspProAspLySLeuProValLySArgGluLeuLeuGluGln  :::	CAGTTACCAGATAAGCCATTGATT:::  CAGTTACCAGATAAGCCATTGATT:::  TYFASPThrGlyThrGlnTyrArgPheAspGluValValPhePheThrTleAspProLys  THASnGlnLeuThrThrAspProAspLysLeuProValLysArgGluCauLeuCatGAAGCA  THASnGlnLeuThrThrAspProAspLysLeuProValLysArgGluCauLeuCatGAAGCA  TeuLeuThrValAsnMetGlyGluAlaTyrAsnLeuGlnAlaValArgAlaCatGAACGT  TeuLeuThrValAsnMetGlyGluAlaTyrAsnLeuGlnAlaValArgAlaLeuSerAsn  CGTATTATCCAATTAAAATTGGAACAACAAGCGTTACAAAA	1153 CAGTTACCAGATAAAGCCATTGATT:::   1153 CAGTTACCAGATAAAGCCATTGATT:::   1180	CAGTTACCAGATAAAGCCATTGATTTG TYAASPThrClyThrClnTyrArgPheaspGluValValPhePherhrIleaspProLys TYrAspThrClyThrClnTyrArgPheaspGluValValPhePherhrIleaspProLys ThrAsnGlnLeuThrThrAspProAspLysLeuProValLysArgCluLeuLeuGluGln ::::::::::::::::::::::::::::::::::::	CAGTTACCAGATAAAGCCATTGATTTG TYAASPThrGlyThrGlnTyrArgPheaspGluValValPhePheThrTleaspProLys TYrAspThrGlyThrGlnTyrArgPheaspGluValValPhePheThrTleaspProLys ThrAsnGlnLeuThrThrAspProAspLysLeuProValLysArgGluLeuLeuGluGluGlu :::	CGG
### ##################################	245 ValGlyTyrTy     868 GATGGTGCGA1	265 IleIleHisAs :::    922TTACATTG	285 GluGlyAlaAs :::     976 GATGCCGCACT	298 GluvalProLe ::: 1036 ACCATTGCGAI	313 GluThrLysLy     1096ACTGACCC		1153 CAG										
3 A	Oy 2 Db 8	Oy 2 Db 9	0y 2 0b 9	Qy 2 Db 10	Qy 3	•	rr an										

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1627 TTGCAACAAGTAAACTCACAAGTTGATAATAGTCATTACACAACAGCATCAATTGCA 1686
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                                                                                                                                                                                         APPLICANT: Haselbeck, Kacie L.
APPLICANT: Chisen, Kari L.
APPLICANT: 2yskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Carr, Grant J.
APPLICANT: Trawick, John D.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA, 0.11A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/201,078
PRIOR PILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-27
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                            RESULT 18
US-09-815-242-4761
US-09-815-242-4761
Sequence 4761, Application US/09815242
Parent No. US2002061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Staphylococcus aureus
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Qy Db	78 1687		
Oy Dp	91		
oy D	96	SerArgileGlyGluGlnSerProProLeuGlyLeuAspMetSerVallleGluGluThr 115 :::	
Oγ	116	ThrProLeuSerLeuGluGluLeuPheAlaGlnGluSerThrGlu 130	
q	1867		
Qy Dp	131	MetGlyIleAsnProAsnAspTyrIleProGluTyr	
οy	145	GuGlnProAsnSerGluValValValProProThr	
qq	1987	GTCACAACTGAAAAAGGTAATGGTATGGAGTGTTAGAACAAGATGTGATTACACCAACA 2046	
ογ	157	LeuGluproGluLysProGlyLeulleLysArgLeuTyrAlaArg 171 ::::::   :::     :::    :::	
DP DP	2047		
å å	172	ABABAGHURARANGSHURARARGARGARGARGARGARGARGARGARGARGARGARGA	
3	0	Val Deolard out to the books of the books of the control of the co	
g 4	2167	**************************************	
ò	195	213	
og Q	2227	ATTAAAACAAAAGCAATCAATGATATTAATCAAACTACACCTGCTACAACAAAAGCA 2286	
δý	214	AlaAlaLeuGlu 217	
QQ	2287		
οy	218	AsplleThrGlnGluSerAlaMetAspLeuAsnGlySerIleProArgLeuArgGln 236	
qq	2347	ပ္ပ	
ò	237	ThrAlaLeuValAlaAlaArgAlaValGlyTyrTyrAspIleAspLeuSerIle 254	
qq	2398	GCTAAAGTTTCTGGTGTTAAAGCAATTGAAGCGACAACGACTGCACAAAGATTTAGAAAGA 2457	
δ	255	a)	
qq	2458	:::::     GTTAAAAACGAAGAATCTCAAAAATTGAAAATTACTGACTCTACGCAAACAAA	
ò	257	257	
Op	2518	GATGCCTATAATGAAGTTAAAGAAGGTGCAAGAGGTAGAAAGCTCAAAAATGCTACAGTT 2577	
οy	258		
qq	2578	TCAAATGCAACAAATGAAGAAGTAGAGAAGCTGATGCAGCAGTAGATGCAGCTCAAAAG 2637	
δý	272	ProvalTyrIleAspTyrArgAlaValGluValArgGlyGluGlyAlaAspAspLys 290	
qq	2638	CAAGGTTTACATGACATCCAAGTTGATAAATCAAAACAGGAAGTTGCTGATACAAAATCA 2697	
Οy	291		
qq	2698	AAAGTATTAGATAAAATCAAATTCAAACACAGCAAAAGTTAAAACCTGCA 2751	

Oy 304 Db 2752	GlyaspValPheHisHisGlyLysTyrGluThrLysLysAsnLeuIleGluAsnAlaSer 3   1   1   1   1   1   1   1   1   1	323 2811
324	AlaGluHisGlyTyrPheAspGlyArgTrpLeuAsp 3	335
	GCTTCAACTACAGAAGAAAAACAAGCTGCATATACAGAATTAGATACTAAAAACCAAGAA 2	2871
336	ArgSerValAspValIleLeuProAspAsnThrAlaAspValSerLeuIleTyrAsp 3 ::::::	354 2931
355	ThrGlyThrGlnTyrArgPheAsp3	362
2932	AGTATTGCTGCAATTAATCAAGTTCAAGCTGCCACAACTAAGAAATGGGATGCAAAAGCG 2	2991
363	GluValValPhePheThrIleAspProLysThrAsnGlnLeuThr 3	377 3051
378	ThrAspProAspLysLeuProValLysArgGluLeuLeuGluGlnLeuLeuThrValAsn 3	397
3052	ACTGAAGAACAACAACAAGCAGCGAAAGACAAAGTGGATCAAGCAGTAGTTACTGCA 3	31.05
39	MetGlyGluAlaTyrAsnLeuGlnAlaValArgAlaLeuSerAsnAspLeuIleAlaThr 4	<del>,</del> !
3106	AACGCTGATATAGATAATGCTGCAGCAAACAATGATGTGGATAATGCA 3	3153
418	ArgTyrPheAsnMetValAsnThrGluIleValPheProGlu	431
432		146
3214	GCAAAACAAGCAATTGCAGATAAAGTACAAGCTCAAGAAACAGCAATTGATGGAAATAAC 3	3273
3274	SerSerArgThrGlu	459 3333
460	LeuGluProValIleGluThrValGluLeuThrAspGlyIleLeuMet 4	~
3334	::: GCTGATGCCGCAATAGATGCAGCACATACAAATGCGGAAGTTGAAGCGGCTAAAAAGCA 3	3393
476	AsplieSerProlleGluPhe	981
3394	GCAATTGCTAAAATTGAAGCGATTCAGCCAGCAACAACAACTAAAGATAATGCGAAAGAA 3	3453
487	LeulleGlnAspLysLeuAsnLeuValAlaAlaLysAlaArgHisLeuTyrAspMetPro 5	506
, ,	Section 100 to 11 Conditional Conditional Collection (Collection Condition Collection Condition Collection Col	
	GCTGAAGAAATTGCAGGGCTAATGCGGAC	່ ທີ
527	IJeSerAspAlaValSerAlaValAlaArgAlaIleLeuProAspGluSerGluAsnGlu 5	546
3544	AGATAATGCTGTGACAAAAAAAAAAAAAAAAAAAAAAAA	3603
547	]5	549
3604	CAACAGTTAAT 3	3663
550		099
3664	CAAATTGCAAGAGATT	3723
561	SerLysLysValProLeuTyrValPheValAla 5	878
3724	AGATGCAACAGATGAAGAAAAAAGCAGCACTGATGCT	3771
579	SerAspLysProArgAspGlyGlnIleGlyLeuGlyTrpGlySerAspThrGlyThrArg 55	869

US-09-914-168-2 (1-919) x US-09-815-242-8869 (1-7437)	Qy 2 SerLysProValLeuPhealaasnArgSerPheMetProValAlaLeuAlaAlaTyrLeu 21 :::	Qy 22 ProLeuMetThrSerGlnAlaLeuAlaGlnGlnAsnAsnProAlaAsnIle 38	Qy 39IleAsnHisValProAlaHisAspThrAlaIleAsnGlnAlaLysAlaGlyAsn 56 :: ::	Qy 57 ProproValLeuLeuThr	Oy 66 IleGlnAlaArgLeuAsnAlaAlaGlyLeuAsnAla	Qy 7890   Qy 7890   Qy 7890   Qy 7890   Qy 7890   Qy 78	Qy 91 95	Oy 96 SerArgileGlyGluGlnSerProProLeuGlyLeuAspMetSerValIleGluGluThr 115	Qy 116 ThrproLeuSerLeuGluGluLeuPheAlaGlnGluSerThrGlu 130	Oy 131 MetGlyIleAsnProAsnAspTyrIleProGluTyrGlnGly 144 ::	Oy 145GluGlnProAsnSerGluValValValWaProProThr 156	Oy 157 LeuGluProGluLysProGlyLeuIleLysArgLeuTyrAlaArg 171 :::::   :::    :::       Db 2047 GTTAAACCTCAAGCGAAACAAGATATTATCCAAGCAGGTTACAACCAAACAAA	Qy 172	Qy 180 ValProArgLeuLysAlaLysPheTyrGlnSerSerGlnSerGly 194 :::	Qy 195GluThrSerAlaIleGlySerSerHisGlnLysThrGluProTyrAlaAsnIleLys 213 :::	Oy 214 AlaAlaLeuGlu217	Oy 218AspIleThrGlnGluSerAlaMetAspLeuAsnGlySerIleProArgLeuArgGln 236	Qy 237 ThralaLeuValAlaAlaAalaValGlyTyrTyrAspIleAspLeuSerIle 254
Db 3772 GAAGCAAATACTGAAAATGGTAAAGCAAATCAAGCCATTTCAGCAGCAACTAACGCA 3831	Oy 599 LeuvalThrLysPheGluHisAsnLeuIleAsnArgAspGlyTyrGlnAlaGlyAlaGlu 618     :::           	Oy 619 LeuargLeuSerGluAspLysClyValLysLeuTyrAlaThrLysProLeuSer 637 	OY 638 HisProLeuAsnAspGlnLeuArgAlaThrLeuGlyTyrGlnGlnGluValPheGlyHis 657 	Oy 658 SerThrasnGlyPheAspLeuSerThrargThrLeuGluHisGluIleSerargSerIle 677	Oy 678 IleGlnAsnGlyGlyTrpAsnArg 685	RESULT 19 US-09-815-242-8869 : Sequence 8869, Application US/09815242	FACEUL NO. 2220220001505A1 GENERAL INFORMATION: APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.		APPLICANT: Yamamoto, Robert T. APPLICANT: XU, H. Howard TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes	REFERENCE: ELJ NT APPLICATION NT FILING DATE APPLICATION N			FRIOR FILLING DATE: 2000-11-2/ PRIOR FILLING DATE: 2000-12-22 PRIOR FILLING DATE: 60/269,308		LEWGYH: 7437 TYPE: DNA ORGANISM: Staphylococcus aureus FEATURE:	9(7437)		: 18.97% Mismatches: 2.79% Indels: 10 Gaps:

ΩD	2398 GCTAAAGTTTCTGGTGTTAAAGCAATTGAAGCGACAACGACTGCACAAGATTTAGAAAGA 2457	
Qy	255 IleArgAsn 257	Oy 507 AspAspArgValLeuAlalleAsnHisAspAspGlyValAs: ::: ::: !!!
g	:::::    2458 GTTAAAAACGAAGAAATCTCAAAAATTGAAAATATTACTGACTCTACGCAAACAAA	3514
οy	257 257	35.4
DP	2518 GATGCCTATAATGAAGTTAAACAAGCTGCAACAGCTAGAAAAGCTCAAAATGCTACAGTT 2577	5544 GIAGAIAAIGCIGIGACACAAGCAAAIAGCA
אַ הַ	258SerileGlyGluValAspValileIleHisAspLeuGlyGlu 271	
3 8	27.2 ProvaltvilleAsoTvrArdAlaValGluValArdGlvGluGlvGluGlvAraAscarive 290	Qy 550
연	CAAGGTTTACATGACATCCAAGTTGTTAAATCAAAAACAGGAAGTTGCTGATACAAAATCA	AAAA
οy	291	
QQ	2698 AAAGTATTAGATAAAATCAATGCAATTCAAACACAAAGGTAAAGTTAAACCTGCA 2751	DD 3/24 CAAGCTACGCCAGATGCAACAGATGAATGAAAACAGCGGC
Qy	304 GlyaspvalPheHisHisGlyLysTyrGluThrLysLysAsnLeuIleGluAsnalaSer 323	3772
Οy	AlaGluHisGlyTyrPheAspGlyArgTrpLeuAsp	Oy 599 LeuValThrLysPheCluHisAsnLeuIleAsnArgAspGl: 
q		e
οy	336 ArgServalAspValIleLeuProAspAsnThrAlaAspValSerLeulleTyrAsp 354	Oy 619 LeuArgLeuSerGluAspLysLysGlyValLysLeuTy:
Q	2872 GCAAGAACAAATCTTGATGCTGCAAATACAAACAGTGATGTAACAACAGCTAAAGACAAT 2931	
δŏ		3922
qq		Oy 658 SerThrAsnGlyPheAspLeuSerThrArgThrLeuGluHi
y g	363 GluValValPhePheThrIleAspProLysThrAsnGlnLeuThr 377 1   1   1   1   1   1   1   1   1   1	3961
3 8	Thrisen Droise of the Control of the Araclinian Control of the Con	Oy 678 IleGlnAsnGlyGlyTrpAsnArg 685
G 6	ACTGAAGAACAACAAGCAGCGAAAGACAAAGTGGATCAAGGCAGTAGTTACTGCA	Db 4005 ATTAGCAACAGCAGTTACAGAGGC 4028
οy	398 MetGlyGluAlaTyrAsnLeuGlnAlaValArgAlaLeuSerAsnAspLeuIleAlaThr 417	RESULT 20 US-09-815-242-4648
Op	3106 AACGCTGATATAGATAATGCTGCAGCAAACAATGATGATGATGATAATGCA 3153	; Sequence 4648, Application US/09815242 ; Patent No. US20020061569A1
οy	418 ArgTyrPheAsnMetValAsnThrGluIleValPheProGlu	GENERAL INFORMATION: FOR THE SELECTION OF THE SELECTION O
qq	3154 AAAACTACAAATGAAGCTACAATCGCAGCCATTACACCTGATGCAAATGTTAAACCAGGA 3213	; APPLICANT: Ohlsen, Karl L. ; APPLICANT: Zyskind, Judith W. ; ADPLICANT: Wall Daniel
å å		APPLICANT: Travick, John D.
3 2	CCARRACAROCANITOCAGATARARGIACAGACACAGARACARACARACAGATATAGAAATAACAGAAATAACAGAAATAACAGAAATAACAGAAATAACAGAAATAAACAGAAATAAACAGAAATAAAAAAAA	
g 90	3274 GGCTCAACAACTGAAGAAAAGCAGCTGCTAAACAACAACTTCAAAACTGAAAAAACAACA 3333	; TITLE OF INVENTION: LOGNILILICATION OF ESSENTIAL (; TITLE OF INVENTION: Prokaryotes ; FILE FEFERENCE: ELITAR.011A
δy	460 LeuGluProValileGluThrValGluLeuThrAspGlylleLeuMet 475	CURRENT APPLICATION NUMBER: US/09/815,242; CURRENT FILING DATE: 2001-03-21
qq	3334 GCTGATGCCGCCAATAGATGCAGCACATACAAATGCGGAAGTTGAAGCGGCTAAAAAAGCA 3393	; PRIOR FILING DATE: 2000-03-21 ; PRIOR FILING DATE: 2000-03-21 . DPIOR ADDITCATION MINDED. 6/206 049
Qy	476 AsplieSerProlleGluPhe	; PRIOR FILING DATE: 2000-05-23; PRIOR PRICATION NUMBER: 60/207,727; PRIOR FILING DATE: 2000-05-26
Qy		APPLICATION PELLING DATE:
g .	3454 GCAATTGCTACGAAAGCGAATGAACGTAAAACAGCAATCGCTCAAACGCAAGACATTACT 3513	FILING DATE: 2000-11-27

SinglnGluValPheGlyHis 657 roAspGluSerGluAsnGlu 546 ----- 3543 AAGTAACACCAACAGTTAAT 3663 ::: |||| |CAGCAGCAACTACTAACGCA 3831 |||| |||| |AAGCGGCTAAAGATGAAATT 3921 roLeuTyrValPheValAla 578 31ySerAspThrGlyThrArg 598 snArgSerIleLeuGlyArg 526 yrAlaThrLysProLeuSer 637 Genes in

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1614 GCAGCAGTACAACATGCCAAAGATTTAATTAACCAAACAGGTAATCCAACA---CTCGAT 1670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTTGAAAATCAAATGAATGCAGCAACTCGTGGCGAAGTAGCACAAAATTAACTGAG 1118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :::
GCACAAGCACTTAACCAAGCAATGGAAGCATTACGTAAT-------AGCATTCAA 1166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1437 CTTGAAAGTCAAATAAACAACGCAACTCGTGATGAAGTAGCGCAAAAATTAGCTGAA 1496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1269 CAAACTAGCAATCCA-----ACGCTTGATAAAGCACAAGTTGAACAATTGACA 1316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1317 CAAGGTGTTAACCAAGCTAAAGATAACCTACATGGTGATCAAAAACTTGCAGACGATAAA 1376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1377 CAACATGCAGTTACTGATTTAAATCAATTAAATAGTTTAAATAATCGCCAACGTCAAGCT 1436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACAGAA---TCTGGTAGCAAGTTTATCAATGAAGATAAGCCACAAAAAGATGCATACCAA 1613
                                                                                                                                                                                                                                                                                                                                                                                                                                        942 GCAGTGAATGACGCTAAAAACAACTTACATGGTGATCAAAAATTAGCTCAAGATAAGCAA 1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SerProProLeuGlyLeuAspMetSerVallleGluGluThrThrProLeuSerLeuGlu 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GluLeuPhealaGlnGluSerThrGluMetGlyIleAsnProAsnAspTyrIleProGlu 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlnSerGlyGluThr-----SerAlaIleGlySerSerHisGlnLys 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           223 ---SerAlaMetAsp------LeuAsnGlySerIleProArgLeuArgGln 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AsnSerIleGlyGluValAspValIleIleHisAspLeuGlyGluProValTyrIleAsp 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LeuAsp-----ValValAsnPheAspAspGlnSerProIleSerArgIleGlyGluGln 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------TyrGlnGlyGluGlnProAsnSerGluValValPro 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     155 ProThrLeuGluProGluLysProGlyLeuIleLysArgLeuTyrAlaArgLeuPheAsn 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            175 AspGlyValAsnLysValPro-----ArgLeuLysAlaLysPheTyrGlnSerSer 191
                                                                                                                                                                                                                                                                                                                                                                                                        64
                                                                                                                                                                                                                                                                                                                                                                                                    AlaIleAsnGlnAlaLys-----AlaGlyAsnProProValLeuLeuThrProGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlnIleGlnAlaArgLeu---AsnAlaAlaGlyLeuAsnAlaLysProGlnSerGlnAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      206 ThrGluProTyrAlaAsnIleLysAlaAlaLeuGluAspIleThrGlnGlu-----
                                                                                                                                                                                                                                       6077
184
135
345
281
48
                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4648
LENGTH: 6077
                                                                                                                                               TYPE: DNA
CRGANISM: Staphylococcus aureus
US-09-815-242-4648
                                                                                                                                                                                                                                  0.00938
131.50
33.76%
19.47%
2.78%
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                        Alignment Scores:
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Qy Db	277 1671	TyrargalaValGluValargGlyGluGlyAlaaspaspLysAlaPheThrThrValAla 296
δλ	297	AspGluValProLeuLeuIleGlyAspValPheHisHisGlyLysTyrGluThrLysLys 316
qq	1716	
Qy	317	AsnLeulleGluAsnAlaSerAlaGluHisGlyTyrPheAspGly 331
qa	1749	GATCAACAACAAGGAGTAACGACTGTTAATGCATTACCAAACTTAAATCATGCGCAACAA 1808
Qy	332	IleLeuProAspAsnThrAla
Dp	1809	CAAGCTTTAACTGATGCTATAAATGCAGCGCCTACAAGAACAGAGGTTGCACAA 1862
Οy	352	IleTyrAspThrGlyThrGlnTyrArgPheAsp 362
qq	1863	CATGTTCAAACTGCTACTGAACTTGATCACGCGATGGAAACATTGAAAAATAAAGTTGAT 1922
Qy	363	GluValValPhePheThrIleAspProLysThrAsnGlnLeuThrThrAspProAspLys 382
qq	1923	CAAGTGAATACAGATAAGGCTCAACCAAATTACACTGAAGCGTCAACTGAT 1973
Οy	383	LeuProValLysArgGluLeuGluGlnLeuThrVal 396
Dp	1974	AAAAAAGAAGCAGTAGCGTTACAAGCTGCAGAAAGCATTACAGAT 2024
δy	397	AsnMetGlyGluAlaTyrAsnLeuGlnAlaValArgAlaLeuSerAsnAspLeu 414
qq	2025	TGTAGAACAAGCATTAACTAAG 2
δ	415	leAlaThrArgTy
qq	2079	:::
Qγ	435	IleGlnAsnAspGlnValSerPheGluGlnSerSerSerSerArgThrGluPro 452
qq	2139	GCGAAACAAACTATTGACCAATTAGCACTTTAAATGCTGATCAAATTGCAACTAAA 2198
οy	453	AlaGlnValAspGluSerThrLeuGluProValIleGluThrValGluLeuThrAsp 471
qq	2199	CAAAACATTGATCAAGGGACGAAGTTTGAACCAATGGCTGAATTAGTAGTAGT 2249
οy	472	GlyIleLeuMetAspIleSerProIleGluPheSerAlaSerAsnLeuIleGlnAspLys 491
qq	2249	2249
Οy	492	LeuAsnLeuValAlaAlaLySAlaArgHisLeuTyrAspMetProAspAspArgValLeu 511
qq	2250	.::-111 
ΟŽ	512	AlaIleAsnHisAspAspGlyValAsnArgSerIleLeuGlyArgIleSerAsp 529
qq	2292	GCAGTCAATGAACATGCTAACGTTGAGCAAACTGTAGATTACACGCAAGCAGATTCAGAT 2351
Qy	530	AlaValSerAlaValAlaArgAlaIleLeuProAspGluSerGluAsn 545
QQ	2352	AAGCAAAATGCTTATAAACAAGCTATTGCAGAAGCTGAAAATGTATTAAAACAA 2405
Qy	546	547
qq	2406	AATTCGAATAAGCAACAAGTGGATCAAGCACTTCAAAACATTTTAAATGCAAAACAAGCA 2465
Οy	548	<pre>IleAspLeuProGluArgThrAlaLeuAla :::::</pre>
Op	2466	AAAACAAATGGTAAACATGA
Qy	568	SerLysLysValProLeuTyrValPheValAlaSerAspLysProArgAspGlyGlnIle 587
qq	2526	TTGAATGCATTA 2537

34

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4453 CTTGAAAATCAAATCAATAATGCAGCAACTCGTGGCGAAGTAGCACAAAAATTAACTGAG 4512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4336 GCAGTGAATGACGCTAAAAACAACTTACATGGTGATCAAAAATTAGCTCAAGATAAGCAA 4395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          102 SerProProLeuGlyLeuAspMetSerValIleGluGluThrThrProLeuSerLeuGlu 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GluLeuPhealaGlnGluSerThrGluMetGlyIleAsnProAsnAspTyrIleProGlu 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----TyrGlnGlyGluGlnProAsnSerGluValValValPro 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProThrLeuGluProGluLysProGlyLeuIleLysArgLeuTyrAlaArgLeuPheAsn 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LeuAsp------ValValAsnPheAspAspGlnSerProIleSerArglleGlyGluGln 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4396 CGTGCAACAGAACGTTAAATAACTTGTCTAACTTGAATACA---CCACAACGTCAAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48 AlaIleAsnGlnAlaLys-----AlaGlyAsnProProValLeuLeuThrProGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlnIleGlnAlaArgLeu---AsnAlaAlaGlyLeuAsnAlaLysProGlnSerClnAla
                                                                                                       APPLICANT: Cart. 3.
APPLICANT: Cart. 3.
APPLICANT: Cart. 5.
APPLICANT: Cart. 5.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011a
FILE REPERENCE: ELITRA.011a
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ. ID NOS: 14110
SOFTWARE: FELSED FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9477
184
135
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281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches:
Indels:
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Matches:
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                       Ohlsen, Kari L.
Zyskind, Judith W.
Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.018
131.50
33.76%
19.47%
2.78%
                                                                                         Trawick, John D.
                                                                  Daniel
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
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LENGTH: 9477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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QQ	4663		0
δ	175	AspGlyvalAsnLysValProArgLeuLysAlaLysPheTyrGlnSerSer 191	
QQ	4711	::   CAAGGTGTTAACCAAGCTAAAGATAACCTACATGGTGATCAAAAAACTTGCAGACGATAAA 4770	0
oy g	192	GinserGlyGlutnr	c
3			<b>o</b>
g g	206	ThrGluProTyrAlaAsnIleLysAlaAlaLeuGluAspIleThrGlnGlu 222	0
οy	223	SerAlaMetAsp	
qq	4891	GCACAAGCGCTTGATCAAGCAATGCAAGCATTACGTAATAGTATTCAAGATCAACAACAA 4950	0
QY Dp	237	ThralaLeuValalaalaArgalaValGlyTyrTyrAspIleAspLeuSerIleIleArg 256 	7
O D	257	ASnSerIleGlyGluValAspValIleIleHisAspLeuGlyGluProValTyrIleAsp 276 ::::::	4
δy	277	ValArgGlyGluGlyAlaAspAspLysAlaPhe	
g	5065	AAATCACAAGTTGAACAATTAACACAAGGAGGAAACAACTGGAAAA 5109	Ø
o o	297	AspGluValProLeuLeuIleGlyAspValPheHisHisGlyLysTyrGluThrLysLys 316	8
ò	317	AsnLeuIleGluAsnAlaSerAlaGluHisGlyTyrPheAspGly 331	
g	5143	::: GATCAACAAGAGGAGTAACGACTGTTAATGCATTACCAAACTTAAATGCGCAACAA 520	2
δ	33	51	
QQ	5203	525	9
ò.	3	m	
QQ	5257	3atcacgcgatggaaacattgaaaa	9
Oy Dp	363	GluvalvalPhePheThrIleAspProLysThrAsnGlnLeuThrThrAspProAspLys 382 :::	7
Οy	383		
qq	5368	::    ::	8
οy	397	AsnMetGlyGluAlaTyrAsnLeuGlnAlaValArgAlaLeuSerAsnAspLeu 414	
qq	5419	CCAACTAATGGTTCAAATGCGAATAAAGACGCTGTAGAACAAGCATTAACTAAG 547	2
ò	415	IleAlaThrArgTyrPheAsnMetValAsnThrGluIleValPheProGluArgGluGln 434	
QG	5473	CTTCAAGAAAAG	2
ò	435		
q	5533	GCGAAACAAACTA	2
δy	453	AlaGlnValAspGluSerThrLeuGluProValIleGluThrValGluLeuThrAsp 471	
QQ	5593		æ
ò	472	GlylleLeuMetAspIleSerProIleGluPheSerAlaSerAsnLeuIleGlnAspLys 491	

qq	5643 5643	643
οy	51	11
qq	ACGCAATTGAATCAATCTAGGATCAATTĞCAACAA 56	685
δy	52	53
qα	:::::: ACTGTAGATTACACGCAAGCAGATTCAGAT 57	745
Oy	530 AlaValSerAlaValAlaArgAlaIleLeuProAspGluSerGluAsn 54	5
qq	GAAGCTGAAAATGTATTAAAACAA 57	667
ΟŻ	luval 54	47
qq	5800 AATTCGAATAAGCAACAAGTGGATCAAGCACTTCAAAACATTTTAAATGCAAAACAAGCA 58	859
δy	548 IleaspLeuProGluargThralaLeualaasnargLysThrProAlaaspValTyrGln 56'	29
qq	GGTAAACATGACATCGACCAA 5	919
δλ	<pre>ProLeuTyrValPheValAlaSerAspLysProArgAspGlyGlnIle 58</pre>	87
QQ	5920 TTGAATGCATTA 59.	931
Qy	588 GlyLeuGlyTrpGlySerAspThrGlyThrArgLeuValThrLysPheGluHisAsnLeu 60°	0.7
q	5	937
ΟŊ	- i	27
qq		973
οy	628 ValLysLeuTyrAlaThrLysProLeuSerHisProLeuAsn 641	41
qa	5974TCACACGATTTAAATCCAACAAATGTA 60	9009
Qy	642	51
qq	9	048
οy	652 GlnGluValPheGlyHisSerThrAsnGlyPheAspLeuSer 66	65
qq		6108
Qy	666 ThrargThrLeuGlu	4
qq	61	168
Qy	680 AsnGlyGlyTrpAsnArgThrTyrSerLeuArgTyrArgLeuAspLysLeuLysThrGln 69	66
QQ	62	228
Qy	700 AlaProProGluThrTrpGlnAspLeuProValAspPheValAsnGlyLysPro 71	17
qq	TAAGAAAGCATTAAATGGTGAAGAAAGATT 62	261
Οý	31yvalAlavalHisLysThrvalAlaAsp 73	34
qq	6262 AATAATCGTAAGTCTGAAGCATTACAAAGATTGGAT 62	297
QY	75	54
QQ	6298 CAATTAACACATCTAAACAATGCTCAAAGACAATTAGCAATCCAACAAATTAATAATGCT 63	357
Qy	755 GlyLeuValSerAspAlaAsnMetAlaIleAlaArgAlaGlyIleSerGlyValTyrSer 77.	74
qq		399
Qy	AsnArgAlaHisGlnMetThrGlyGlyIleGlnAla 79	94
qq	6400 AAATTAGATAATGCAATGGGTGCAGTACAACAATATATTGACGAACAGCACCTT 64	453

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RESULT 22
US-08-781-986A-59
US-08-781-986A-59
Sequence 59, Application US/08781986A
Sequence 59, Application No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                            6604 ATCGATGCTCAAAATGCATTAAATGGAGACCCAAAACCTTGCAAATGCCAAAGCA 6663
                             795 GlyTyrIleTrpSerAspAsnPheAsnHisValProTyrArgLeuArgPhePheAlaGly 814
                                                                                                             6508 TATGATAATGCAATTGCGAATGCACCACATGAG------TTAGATAAA---
                                                                                                                                                   TyrLeuThrGlyGlyGlnValLeuAlaValGlyThrAlaGluTyrAsnTyrGluPheMet
                                                                                                                                                                                                                              855 LysAspLeuArgLeuAlaValPheGlyAsp-----IleGlyAsnAlaTyrAspLys---
                                                                           815 GlyAspGlnSerIleArgGlyTyrAlaHisAspSerLeuSerProIleSerAspLysGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDGS version 6.2
SOFTWARE: ASCLI Text
CURRENT APPLICATION NOMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION NOMBER:
CLASSIFICATION NOMBER:
APPLICATION NOMBER:
APPLICATION NOMBER:
APPLICATION NOMBER:
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1118
324
271
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ...JARESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ength:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFRENCE/DOCKET NUMBER: PB24
TELECOMMUNICATION INFORMATION:
TELEPAN: (301) 309-8504
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACIENISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 31096 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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131.50
33.45%
20.25%
2.78%
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                                                                                                                                                                                                                                                                                                            872 ---GlyPheThrAsn 875
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-781-986A-59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111 ::: :::111::: 29566 29519 AATAAAGCTGAACCAACCAACTAACACT--- 29566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29492 -----CTTGATCACGCGATGGAAACATTGAAA 29518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29261 GGTAATCCCAACACTCGACAAATCACAAGTAGAACAATTGACACAAGCAGTAACAACTGCA 29320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29321 AAAGATAATCTACATGGTGATCAAAAACTTGCTCGTGATCAACAACAAGAGGAGTAACAACT 29380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29429 GATGCTATAAATGCAGGGCCTACAAGAAGAGGGTTGCACAACATGTTCAAACTGCTACT 29488
                                                                                                                                                                                                                                                                                                                                                  29093 AAATTAGCT---GAAGCAAAAAGCGCTTGATCAAGCAATGCAAGCATTACGTAATAGTATT 29149
                                                                                                                                                                                                                                                                                                                                                                                                                            29150 CAAGATCAACAACAAACAGAATCTGGT-----AGCAAGTTTATCAATGAAGATAAAA 29200
                                                                                                                     28996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerValAspValIleLeuProAspAsnThrAlaAspValSerLeuIleTyrAspThrGly 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                277 TyrArgAlaValGluValArgGlyGluGlyAlaAspAspLysAlaPheThrThrValAla 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          297 AspGluValProLeuLeuIleGlyAspValPheHisHisGlyLysTyrGluThrLysLys 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             357 ThrGlnTyrArgPheAspGluVal-----ValPhePheThrIleAspProLysThrAsn 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ValAsnLysValProArgLeuLysAlaLysPheTyrGlnSerSerGlnSerGlyGluThr 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 257 AsnSerIleGlyGluValAspValIleIleHisAspLeuGlyGluProValTyrlleAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      317 AsnLeuIleGluAsnAlaSerAlaGluHisGlyTyrPheAspGlyArgTrpLeuAspArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                197 SeralaileGlySerSerHisGlnLysThrGluProTyrAlaAsnIleLysAlaAlaLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GluAspIleThrGlnGluSerAlaMetAspLeuAsnGlySerIleProArgLeuArgGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       237 ThrAlaLeuValAlaAlaArgAlaValGlyTyrTyrAspIleAspLeuSerlleIleArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29381 GTAAATGCATTGCCAAACTTAAAT------CATGCACAACAAGATTAACT
                                                                                                                                                                                                                                    ValAsnPheAspAspGlnSerProlleSerArglle------GlyGluGlnSerPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  154 ---proproThrLeuGluProGluLysProGlyLeuIleLysArgLeuTyrAla----
GlnGlnAsnAsnProAlaAsnIleIleAsnHisValProAlaHisAspThrAlaIleAsn
                                                                              51 GlnAlaLys-----AlaGlyAsnProProValLeuLeuThrProGluGln1leGln
                                                                                                           28937 CAAGCTAAAGATAACCTACAGGGGGATGATCAAAAACTTGCAGACGATAAACAACATGCGGTT
                                                                                                                                                                                                                                                                          ------GAAAGCCAAATAAACAACGCAGCAACTCGTGGCGAAGTAGCACAA
                                         28877 CAAACTAACAATCCAACGCTTGATAAAGCACAAGTTGAACAATTGACACAAGCTGTTAAC
                                                                                                                                                                                             28997 ACTGATTTAAATCAATTAAATGGTTTGAAT---AATCCGCAACGTCAAGCACTT----
                                                                                                                                                                                                                                                                                                               104 ProleuGlyLeuAspMetSerVallleGluGluThrThrProLeuSerLeuGluGluLeu
                                                                                                                                                          68 AlaArgLeuAsnAlaAla---GlyLeuAsnAlaLysProGlnSerGlnAlaLeuAspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----TyrGlnGlyGluGlnProAsnSerGluValValVal-----
                                                                                                                                                                                                                                                                                                                                                                                           PheAlaGlnGluSerThrGluMetGlyIleAsnProAsnAspTyrIleProGlu---
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| ::: ||||::: ||||||
|GCTCAAATGCATTAAATGGAGACCAA 30850
                            ValasnProMetArgGlyTyrargGln 745
:::
NACACATCTAAACAATGCTCAAAGACAA 30544
                                                                                    ValSerAspalaAsnMetalaileala 765
:::::: |||:::
|GraaataaagcaTcTcGagcaaTTaAT 30604
                                                                                                                                                                                                                                                                SGINSErIleArgGlyTyrAlaHisAsp 825
| :::||| | |||||:::
| RATGCAATTGCGAATGCAGCACATGAG 30754
-----GAAGAAAGACTTAATAATCGT 30484
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Length: Matches: Conservative Mismatches: Indels: Gaps:	168-2 (1-919) x US-09-815-242-4780 (1-/302)  LeualaginginasnasnProalaasnileileasnHisValProalaHisAspThrala 4 ::::::             ATTAGTGCAACGAATAACCCTGAAATGAATCCTGATACAATTAACCAAAAAGGGAGCCAA 3	nproprovalLeuLeuThrProGluGlnIleGlnAla 6	ArgLeuasnalaalaglyLeuasnalaLysProginSerGinAlaLeuaspValValas 8 :::		GCGATGGGTAATTTGAAACATGCA	LeupheAlaGlnGluSerThrGluMetGlyIleAsnProAsnAspTyrIleProGluTyr	GluProGluLysPro	LeuPheAsnAspGlyValAsnLysValPrOArg	erSerGlnSerGlyGluThrSerAlaIleGlySerSer     ::          ::: ACTAATGCTAATGCAGCAAC	AlaAsnIleLysAlaAlaLeuGluAspIleThrGlnGlu ::::::          GTTCAAGCAGCACTAAACCAATTGAATCAA	SerIleProArgLeuArgGlnThrAlaLeuValAlaAla ::::::     GATAATAAAGTTGCTCAAGCAAAAGAGTCAGCGAAA	AGTAACTTGAATAATGGGGAATCAACTGCAGCAACTAGTGAA	Ileasp	sAspLeuGlyGluProValTyrIleAspTyrArgAlaValGluVal     TCAACTT	ysalaPheThrThrValAlaAspGluValProLeuLeu 	eGlyAspValPheHisHisGlyLysTyrGluThrLysLysAsnLeulleGluAsnAla       :::
scores: 0.0138 131.00 nilarity: 32.94% Similarity: 17.64% n: 1077%	168-2 (1-919) x US-09-8 LeuAlaGlnGlnAsnAsnProAl :::::: ATTAGTGCAACGAATAACCCTGA	IleAsnGlnAlaLysAlaGlyAsn :::              GTGAACAGTGCGAAGTCTGCA	ArgLeuAsnAlaAlaGlyLeuAsnAlaLysProGl :::           AAATTAGCAGCAACAAAACAAACTGCGAAATCAGA	PheAspAspGlnSerProlleSerArgll ::::: ::: aATGCACAACGAACTGCGGCAAATGCTGA	MetSerValIleGluGluThrThrProLeuSerLeu :::             :: ACAGCGGCTAAAAATAAAGCAACATCGTTAAACACA	LeuPheAlaGlnGluSerThrG       CTGCTGAAAGGATAATACGA	GlnGlyGluGlnProAsnSerGluValV. :::       :GCGGATCAACCAAAACAACGAGCG-	G1	LeuLysAlaLysPheTyrGlnS ::: ATT		SeralaMetaspLeuAsnGly :::              GCTAAAATGACTTGAATGGT	3 ArgAlaValGlyTyrTyr        :: 7 CGTGCATTAGCTTCATATAGT		3 AspvalllelleHisAspLeu ::: ::      7 AATACAGCAATGGGTCAACTT	3 ArgGlyGluGlyAlaAspAspLysAl     :::   ::: 8CAAAATGGTATAAATGACCAA	11
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pρ	Db 4219 GATGCTGACCAAGGTAAGAAAGATGCTTACACAAATGCTGT	FACGAATGCT 4269
Qy	323 SerAlaGluHisGlyTyrPheAspGlyArgTrpLeuAs	pArgSerVal 338
QQ	4270 CAAGGTATTTTAGATAAAGCACACGG	ACAAGT
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ò	395	yGluAlaTyr 402
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qq	4645	4
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QQ	4705 GC	4
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Dp	4765 GC	CACCACAAAAA 4824
ογ	495	yrAspMetPro 506
qq	4825 ACAGCATTAAAACAACAAGTGAA	CTGATCTGAAA 4884
Oy	507	LeLeu 524
QQ	Db 4885 AATAGTGCTACATCACTTAATAGTGGATCAATTAAAACAAGCAATTGCTGATCAT	TTGCTGATCAT 4944
QΥ	Оу 525	GlyArgile 527
qq	4945	AAGGTGCTTAT 5004
QY	Qy 528 SerAspAlaValSerAlaValAlaArgAlaIleLeuProAspGluSerGluAsnGluVal	
qq	5005	20
QY	Oy 548 IleAspLeuProGluArgThrAlaLeuAlaAsnArgLysThrProAlaAspVal	565
qq	5059	51
٥y	Oy 566	575
qq	5119	
Qy	576	28
qq	5179	
QY	588	9
Op	5239 GTAACT	SCAATGAATCAA 5298

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PheGluHisAsnLeuIleAsnArgAspGlyTyrGlnAlaGly---

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TrpGlnAspLeuProValAspPheValAsnGlyLysProSerGlnGluAlaLeuLeuAla 724
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                                                                                                                                                          AspLeuArgLeuAlaValPheGlyAspIleGlyAsnAlaTyrAspLysGlyPheThrAsn 875
                                                                                                                                                                                                                 GGAAACATCAATCAAGCGCACACTGTAGCTGAAGTAACGCAAGCCATTCAAACCGCTCAG
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                                                                                                                                                                                                                                                                                                                            ----GCACAAAAAGGTGCTGTTACT
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                                                                                                           -GATAAA 6078
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TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/2191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/259,308
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-26
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
NUMBER OF SEQ ID NOS: 14110
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US-09-815-242-8898
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 8898
LENGTH: 18846
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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LOCATION: (1)
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ACAGCGGCTAAAAATAAAGCAACATCGTTAAACACAGCGATGGGTAATTTGAAACATGCA 6138
                                              MetSerValIleGluGluThrThrProLeuSerLeu------
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                                                                                                                                                       PheAspAspGlnSerProIleSerArgIleGlyGluGlnSerProProLeuGlyLeuAsp 108
                                                                                                                                                                                                                 AAATTAGCAGCAGCAAAACAAACTGCGAAATCAGATATCGGTCGTTTGACAGACTTGAAC
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Yamamoto, Robert T.
Xu, H. Howard
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GTAACAGATGCTAAAAACAATGCAAACCAAACATTATCTACGTTA----

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AlaArgAlaGlyIleSerGlyValTyrSerPhe---

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GACACTACACTTGGCAGT 6096 AspThrLysIleGlyAla 881 GAACTGAATACAGCGATG - - - GGTAACTTGAAAAATAGCTTGAAT

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442	<pre>varxsiiiiCutiteValFneFroGluArgGluGInIleGlnAsnAspGlnValSerPhe ::::::</pre>	Db 5	
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02	nMetGlyGluAlaTyr	Qy	
6816	GCACAAAACAAGATTTAACATCACAAATCGAAGGCGCAACA	Db	
394	lLysArgGluLeuLeuGluGlnLeuLeu	Qy	
6756	6718 AGACAAGCAADATCAGATGCGAAAGCAAACTTAGGTACA	Db	
377	yrArgPheAspGluValValPhePheThrIleAspProLysThrAsnGlnLeuThr	Qy	
6717	AAGCTGCATTAAATCAAGTAACGACTGCTAAGAATGCTTTAAACGGTGACGCAAATGTA	рь	
357	allleLeuProAspAsnThrAlaAspValSe	Qy	
6657	GATAAA	Db	
338	GluHisGlyTyrPheAspGlyArgTrpLeuAspArgSerVa	Qy	
6606	C	Db	
322	pValPheHisHisGlyLysTyrGluThrLysLysAsnLeuIleGluAsnAl	Qy	
6555	GTATAAATGACCAAAACACTGTTAAACAACAAGTGAACTT	Db	
302	lyGluGlyAlaAspAspLysAlaPheThrThrValAlaAspGluValProLeuL	9	
ŰΪ	84 AATACAGCAATGGGTCAACTT	рь	
282	lllelleHisAspLeuGlyGluProValTyrIleAspTyrArgAlaValGlu	Qy	
4	AATGCAACGACAGTAGCAGGCGTAACTGCTGCACAAAATACTGC	Db	
62	spgargasnSerIleGlyGluv	οy	
6423	TTAGCTTCATATAGTAACTTGAATAATGCGCAATCAACTGCAGCAACTAGTCA	Ф	
249	rgAlaValGlyTyrTyr	Qy	
w	07 GCTAAAAATGACTTGAATGGTGATAATAAAGTTGCTCAAGCAAAAGAGTCAGCGAA	Db	
2	LeuAsnGlySerIleProArqLeuArqGlnThrAlaLeuValAlaA	9	
ω i	62 GCGAATGAAACAGAAGTTCAAGCAGCACTAAACCAATTGAATCAA-	DЬ	
٠ د	sThrGluProTyrAlaAsnIleLvsAlaAlaIeucluAsnIle⊤hrcln	9	
	38 ATTACTAATGCTAATGCCAAC	DЬ	
Š :	uLysAlaLysPheTyrGlnSerSerGlnSerGlyGluThrSerAlaIleGlySer	9	
	08TATGATACTGCGGTTACACAAGCAGAA	DЬ	
o i	63 GlyLeuIleLysArqLeuTyrAlaArqLeuPheAsnAspGlyValAsnLysValDroAr	Ş	
N .	ACAAGCG	DЬ	
62	GluGlnProAsnSerGluValValValProProThrLeuGluProGluLysP	γo	
$\vdash$	GTGTCAATTACACAGAT	Db	
142	heAlaGlnGluSerThrGluMetGlyIleAsnProAsnAs	Qy	

Qγ	Qy Db	Db	Qy	Db	Qy	Db	Qy	Db	Qy	망	Qγ	Db	Qy	Db	Qy	Дb	Оу	Db	Qy	Db	VO	Db	Qy	Db	Qγ	Db	Qy	da	Оу	Db	Oy	Db	VQ	Db
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ArgThrTyrSerLeuArgTyrArgLeuAspLysLeuLysThrGlnAlaProRroGluThr 704 :::	ArgThrLeuGluHisGluIleSerArgSerIleIleGlnAsnGlyGlyTrpAsn 684 :::    ::::::::::::::::::::::::::::::	GTAAATCAAGTG 7	isSerThrAsnGlyPheAspLeuSerThr 666	ACCAATTAAGTCATTTAAATAATGCTCAA	7 650	ACTGCGCTTAATGGTGCACAAAACTTAGCGAATAAAAAGCAAGAAACGACT 7	GluAspLysLysGlyValLysLeuTyrAlaThrLys 634	AGTCAGCCGACACTTGATCCATCTGCAGTAACACA	T WATTWATTWATCH TO TO THE TOTAL TO THE TOTAL TOT	775	616	CTTCGAAATAGTATTGCGAATAAAGATGATGTAAAAGCGAGTCAACCATATGTTGATGCA 7695	PheGluHisAsnLeuIleAsnArgAspGlyTyrGlnAlaGly 616	TGATA	rArgLeuValThrI	AAGTATTACTGGTCAAATTGATAGCGCGACACAA 7	PheValAlaSerAspLysProArgAspGlyGlnIle 587	CGAAGCAACAAGCTAAAGATGCATTACGTCAAATG 75	roLeuTyrVal 575	 	spLe	ACTGATGCATATAATGCTGCGAAAAACATTGTAAATGGTTCGCCTAATGTGATT 7395	LeuProAspGluSerGluAsnGluVal 54	TAT 7	GlyArgIle 527	::: :::::    TCAATTAAAACAAGCAATTGCTGATCAT 7	spAspArgValLeuAlaIleAsnHisAspAspGlyValAsnArgSe	ACAGCATTAAAACAACAAGTGAACGCTGCGCAACGTGTATCAGGTGTAACTGATCTGAAA 722	sAlaArgHisLe	GCTAAAACTGAAGCTATACAAGCTATCGATAACTTGACACATTTGAATACACCACAAAAA 7161	SerAlaSerAsnLeuIleGlnAspLysLeuAsnLeu	::: :::::: GCGAACTTACAACGC 7	ValIleGluThrValGluLeuThrAspGlyIleLeuMetAspIleSerProIleGluPhe 4	::::    CTGAATCTTACTTAAATAAGATCACGGTGCGAATAAAGATAAGCAAGC

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                                                                              APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Ess
TITLE OF INVENTION: Identification of Ess
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,24:
CURRENT FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/101,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/207,727
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PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
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                                                 APPLICATION NUMBER: 60/253,625 FILING DATE: 2000-11-27
FILING DATE: APPLICATION
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Best Local Similarity:
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US-09-815-242-4174
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NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 4174
LENGTH: 3552
TYPE: DNA
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Patent No. US20020061569A1
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PRIOR FILING DATE: 2000-05-23
PRIOR PPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
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                                                                            NAME/KEY: CDS
                                                                                                                   ORGANISM: Staphylococcus
                                                                                                                                       TYPE: DNA
                                                                                                  FEATURE:
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                                                                                                                                                                                                                                                                                             FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
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                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/253,625
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TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes

FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT APPLICATION NUMBER: US/09/815,242

PRIOR APPLICATION NUMBER: 60/201,078

PRIOR PRILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR PILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR APPLICATION NUMBER: 60/259,308

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

NUMBER OF SED ID NOS: 14110

SOFTWARE: FastSEQ for Windows Version 4.0

ORGANISM: Staphylococcus aureus

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APPLICANT: Ohlsen, Kari L.
APPLICANT: Ohlsen, Kari L.
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Garr, Grant J.
APPLICANT: Yanamoto, Robert T.
APPLICANT: Xu, H. Howard
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15	.452 ATAGTTAACAAAACAATCACAGCTGAGGTTCTGGCCATAGATGAATACACGGGTAAAACT	Db 1,	
ري در در	526 ArgIleSerAspAlaValSerAlaValAlaArgAlaIle	Qy	_
14	392 ATTGATTCAAAAACTGCTGAAATCAAATTTGTCAAAAATATGAACCGAGATTCTACTT	Db 1:	_
л S	506 ProAspAspArgValLeuAlaIleAsnHisAspAspGlyValAspArgSerTleTeugl	Qy	
	332 AACAAAGCTGCCTCAAATGTCAAATATGTCATGGGACGTAACGATGGTGGA	Db 1	
505		Qy	
	296 ATCCTG	Db 1	
492	473 IleLeuMetAspIleSerProIleGluPheSerAlaSerAsnLeuIleGlnAspLysLeu	Qy	
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472	453 AlaGlnValAspGluSerThrLeuGluProValIleGluThrValGluLeuThrAspG	Qy	
12	203 GTAATAAATGTAAGAGAAGGAATTGCATCCGTCCTGCTTCCAAGACA	Db 1	
70 453	rArqThrGlup	Qy	

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; FEATURE:
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. LOCATION: (387)...(5777)
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Patent No. US20020115078A1
GENERAL INFORMATION:
APPLICANT: Kleanthous, Harold
                                                                                TITLE OF INVENTION: Identification of Polynucleotides
TITLE OF INVENTION: Encoding No. US20020115078Alel Helicobacter Polypeptides
TITLE OF INVENTION: Genome
FILE REFERENCE: 06132/041002
CURRENT APPLICATION NUMBER: US/09/881,752A
CURRENT APPLICATION NUMBER: US/09/881,752A
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 08/833,457
PRIOR FILING DATE: 1997-04-01
NUMBER OF SEQ ID NOS: 370
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 307
LENGTH: 5832
TYPE: DNA
ORGANISM: Helicobacter pylori
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AGGGTTTTAGATCAAGGGAATATTATCGCTACGAGTGCA----
                                GluThr-----LysLysAsnLeuIleGluAsnAlaSerAlaGluHisGlyTyrPheAsp
                                                                      AGCGTGAATGAAATCATCACCGCCATTGACACGAAAGAATTAGACATCCACGCAAAGATT
                                                                                                         ThrValAlaAspGluValProLeuLeu---IleGlyAspValPheHisHisGlyLysTyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - AAATCGCTCAGTGAAATCATTAAAGGCAAGCAGGGGCGTTTCAGGCAAAAC
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CT 3968	39 LeuglyTrpGly	Oy 58 Db 390	
AT 39	9 CGCACCCCAGTAACTTGTAAAGCGCCCAAAGGGCGTGTGCGCGAAATGCTATGGCTTG	Db 384	
< C	4 TyrValPheValAlaSerAspLysProArgAspGlvGlnIle	S	
	2 ProAlaAspValTyrGlnSerLysLysVal	Oy 56	
7	GTTTTATTAGAAGATGTGATCGATCCCATTACGAATGAAATCTTGCTTTATGCGGAC	37	
r 561	luValIleAspLeuProGluArgThrAlaLeuAlaAsnArqL	Qy 5	
C 37	ATTGCGGTGGGGAGTGAGCTGATTGAACCTTTAGAAGAGAGCGTATTTTTGGG	36	
544	spAlaValSerAlaValAlaArgAlaIleLeuProAspGluSerGlu	0у 5	
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sp 50	91 LysLeuAsnLeuValAlaAlaLysAlaArgHisLeuTyrAspMetProAspA	Оу 4 Db 35	
ACA 3560	01 TTGAATGTCTTAGAATACTTCAATTCCACGCATGGCGCTAGAAAGGGCTTAGCGGAT	Db 35	
Asp 490	leLeuMetAspIleSerProIleGluPheSerAlaSerAsnLeuIleGln	Oy 4	
GG 35	::: CTAACTTTAAAGAG	Db 34	
hr 470	56AspGluSerThrLeuGluProValIleGluThrValGluLeu	Oy 4	
TT 34		Db 33	
- 455	45 SerSerSerArgThrGluProAlaGlnVal	Qy 4	
CA 33	21 GAAATGATGACCGCTATCGCGCAAGATAAAGAGGGCTTTAACTCTATTTATATGATG	Db 33	
444	30 ProGluArgGluGlnIleGlnAsnAspGlnValSerPheGluGln	0у 4	
AAA 33	73AATAAGATCATTGACACTTGGACTGAAGTCAATGACAAAATGAGT	Db 32	
Phe 429	10 LeuSerAsnAspLeuIleAlaThrArgTyrPheAsnMetValAsnThrGluIleVal	0у 4	
32	37 TACGATCAAGGGCTGCTCACTGACCAAGAGCGTTAC	Db 32	
Ala 409	90 LeuGluGlnLeuLeuThrValAsnMetGlyGluAlaTyrAsnLeuGlnAlaValArg	Оу з	
CAA 32		Db 31	
Leu 3	72 LysThrAsnGlnLeuThrThrAspProAspLysLeuProValLysArgGlu	Оу з	
CCA 31	29 GCGACTAAGGCTGGTATTTCTATCTCTATGGAGGATATTATCAC	Db 31	
Pro 371	55ThrGlyThrGlnTyrArgPheAspGluValValPhePheThrIleAs	Оу з	
TAT 31	ົດ	Db 3(	
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AGTT 3068	009 TGGAACAGACCCATGAAGAAAAAGATATTGGCGTGCTTGTGGATTATGTGCATAAA	Db 3	
354	spValSerLeuIleTyrAsp	Oy	
TTG 30	958 GGCCCATGATCATTAAGTCCATTTTGCCTGATTTTATCCCTACGGAT	Db 2	
344	lyArgTrpLeuAspArgSerValAspVa	Oy	

RESULT		О <sub>У</sub>	Db .	Qy	Db	Qy			VΩ	Db	Qy	Db	Qy	DЬ	Qy	DЬ	Qy	DЬ	γQ	Db .	2 5	<u> </u>	0	Db 49	) Db	Qy	Db	Qy	Db	Qy	DЬ	QУ	Db
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APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2001-02-1 NUMBER OF SEQ ID NOS: 14110
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TYPE: DNA
ORGANISM: Helicobacter pylori
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175 AspGlyValAsnLysValProArgLeuLysAlaLysPheTyrGlnSerSerGlnSerGly 194
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FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
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                                                                                                                                                                                                                                                                                                                                                                                                                  LeuAsnAlaLysProGlnSerGlnAlaLeuAspValValAsnPheAspAspGlnSerPro 94
                                                                                                                                 CTTTTAGGTAAGCGCGTGGATTTTTCAGGC-----AGAAGCGTGATTGTGGTTGGG
                                                                                                                                                                                                                                                          ThrThrProLeuSerLeuGluGluLeuPheAlaGlnGluSerThrGluMetGlyIleAsn 134
                                                                                                                                                                                                                                                                                                         AATGCGGTTAAAGGGGCTAACAAACGCCCTTTA----
                                                                                                                                                                                                                                                                                                                                               IleSerArgIleGlyGluGlnSerProProLeuGlyLeuAspMetSerValIleGluGlu 114
                                                                                                                                                                                                                                                                                                                                                                                         -----AGGATGTTGCAAGAAGCCGTGGATGTGCTTTTTGATAACGGCCGCAGCACT 5106
                                            CCTAATCTCAAAATGGATGAATGCGGGTTGCCTAAAAACATGGCGTTAGAACTCTTCAAA 5301
                                                                       ProThrLeuGluProGluLysProGlyLeuIleLysArgLeuTyrAlaArgLeuPheAsn 174
                                                                                                                                                                         ProAsnAspTyrIleProGluTyrGlnGlyGluGlnProAsnSerGluValValValPro 154
                                                                                                                                                                                                                  -----AAATCGCTCAGTGAAATCATTAAAGGCAAGCAGGGGGCGTTTCAGGCAAAAC
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Yamamoto, Robert T.
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Trawick, John D.
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Zyskind, Judith W.
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7249 CATAAGGTGCATAAGGGGGGAAGTATCGCTGATATTATC-----CAAGAGGGCTGG 7299
                                                                             7192 ---TTAGCCGGCGTTGGCGGTAAGATTGAGGGGAAAGTGTATTTGCCTTATGCTAGTGGG
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                            726 ValAlaValHisLys-----ThrValAlaAspAsnLeuValAsnProMetArgGlyTyr 743
                                                                                                                709 ProvalAspPheValAsnGlyLysProSerGlnGluAlaLeuLeu------AlaGly 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6862 ATTGGGGAGCCTGGAACGCAGCTCACTTTAAGGACTTTCCATGTGGGCGGGACAGCGAGC
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                                                                                                                                                                                    689 LeuArgTyrArgLeuAspLysLeuLysThrGlnAlaProProGluThrTrpGlnAspLeu 708
                                                                                                                                                                                                                                                            669 LeuGluHisGiuTleSerArgSerTleTleGlnAsnGlyGlyTrpAsnArgThrTyrSer 688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6565 GAT----ATTGCGGTGGGGAGTGAGCTGATTGAACCTTTAGAAGAGCGTATTTTTGGGCGC 6621
                                                                                                                                                                                                                                                                                                                                                    649 GlyTyrGlnGlnGluValPheGlyHisSerThrAsnGlyPheAspLeuSerThrArgThr 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            619 LeuArgLeuSerGluAspLysLysGlyValLysLeuTyrAlaThrLys-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  593 ---SerAspThrGlyThrArgLeuValThrLysPheGluHis-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   545 -----AsnGluValIleAspLeuProGluArgThrAlaLeuAlaAsnArgLysThr 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 529 AspAlaValSerAlaValAlaArgAlaIleLeuProAspGluSerGlu------ 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6274 GATAGCGGCGCAAGGGGTAGCGCGGCGCAAATCCGTCAGCTTTCAGCGATGAGGGGTCTT 6333
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                                                                                                                                                       TTAAGG---AGAAGCGATATTGTCAAG------CCAAGCGAA------ 7191
                                                                                                                                                                                                                                                                                                                                                                                                                            ------ProLeuSerHisProLeuAspGlnLeuArgAlaThrLeu 648
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Qy	Qу	0-Sn	Allgamer Pred. Ne Score: Percent Best Loc Query Ma DB:	;; US-C	; NUI ; SEQ ; SEQ					RESI US-: ; Si ; Pi	Db	Qy	DЬ	Qy	ф	Qy	Db -	00	B 15	Db	Qу	Db	Оy	. Dp	Qy
85 As	65 GJ 11 260 C <i>t</i>	9-914-16		4 2 3	NUMBER OF SOFTWARE: EQ ID NO	PRIOR FI PRIOR FI	CURRENT APE CURRENT FII PRIOR APPLI	TITLE OF	APPLICAN APPLICAN	ULT 31 09-974-30 equence 1 equent No.	7669 F	864 F	7621 (	849 -	7561 /	834 (	01	815	7465	05	781	7357	764		744
pValValAsnPheAspAspGlnSer	ln1leGlnAlaArgLeuAsnAlaAlaGlyLeuAsnAlaLysProGlnSerGlnAl 	58-2 (1-	cores:	DNA DNA SM: Bacillus 300-1524	Fast 1524	FILING DATE: 2000-1 APPLICATION NUMBER: FILING DATE: 2001-0	WI APPLICATION NUMBER: UNIT FILING DATE: 2001-10 APPLICATION NUMBER: 09/	REFERENCE: 10085.500-US	PPLICANT: Berka, Randy M. PPLICANT: Clausen, Ib Gro ITLE OF INVENTION: Methods	300-1524 1524, Appli 10. US2002014	AAGGTGGGT	- n	GCCACATG		AGTGAAGTGAGCACTAATAGCGTGATTTCTAAACCCACGACTAAC	GlyTyrLeuThrGlyGlyGlnValLeuAlaValGlyThrAlaG	GGTAGGGAAGCCGCTCGCCATTATATCGCTAGGGGTTCTGAGATCTTGATTGA	il vAsnci	ASPASNPNEASNHISValProTyrArgLeuargPhePheAla ::: GAAAAA	GTTTTAGAGGCTAACCATTTAGAGCGCACCCATGGGATCAAAAAGGGCG	GlySerAsnArgAlaHis-	ATTGCGCAAGATGTGTATGCCAAAGAAAAAGGCGTAATCAAATAC-	IleAlaAı	AATGTGCCTAATCGCATCCCTTATGCGAGCGAATTGCTAGTCAAGGAT-	ArgGlnArgTyrSerLeuGluValGlySerSerGlyLeuValSerAsnAlaAsnWe+al
AsnPheA	AlaAr    TGCCG	919)	ty:	lus li		TE: 20	ATION N DATE: CON NUM	10085	a, Randy usen, Ib ION: Met	524 , Application 20020146721A1	T 767	у 866	GGATC		GAGCA	uThrG	AGCCG	n ser I	1eAsnH	AGGCTA	snArgA	AAGATG	b	CTAATO	rgTyrs
eAspAs	gLeuAs    ::  TTATC	x US-0	0.0074 127.00 35.72% 18.24% 2.69%	icheni	DS: 8481 for Windows		UMBER 2001 IBER: (	Expre:	ndy M. Ib Grot Methods		7		CTTACA	TyrA	CTAATA	lyGlyG	CTCGCC	learac	isVale	ACCATI	laHis-	TGTAT	1	GCATC	erLeu
pGlnSe	nAlaAl :   :: CGCGAC	09-974-	4	formi	٧e	279	000			060/sn			ACACCO	snTyr(	GCGTGA	lnVali	ATTAT		roTyr	TAGAG	Gln	CCAAA	MaGly	CTTAT	3lu <b>Va</b> l
ProI 	laGlyLo	300-15	Leng Matc Cons Mism Inde Gaps	ts.	rsion	52	9/974,		Monito	74300			GGATCCTTACAACACCCCTATCATTGCGGACTTT	luPhe	ATTTCT,	SeuAla	ATCGCT	,	ArgLeu	GGCACC	GlnMetThrGlyGlyIleGlnAlaGlyTyr	GAAAAA	AlaGlyIleSerGlyValTyrSerPheGlyAs	GCGAGC	GlySer
leSerAr	euAsnA ;;; GCTCGA	24 (1	Length: Matches: Conservativ Mismatches Indels: Gaps:		4.0		300		toring				ATTGCG	MetLys	AAACCC	ValGly	AGGGGT	GGCTTG	ArgPhe	CATGGG	GlyGly	GGCGT	GlyVal	GAATTO	SerGl
gIle(	LeuAsnAlaLysProG ::: TGCTCGACGCATATAG	-2545)	tive:					,	Multiple				III GACTTI	AspLeu	III ACGACT	ThrAla		GOUTTETTTECE	PheAla	GGGATCAAA	'IleGl	ATCAA	Tyrse	CTAGTC	/LeuVa
lyGluG	roglns :::  TAGAAT		2545 168 161 338 255						ລ				AAA	ArqLe	ð	Glu	ATCTT	GTGAT		AAAGGG	AlaGl	ATAC	rPheG1	CAAGGA	Seras
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ProPro	AlaLeu ::: .GGTATG			*									GG	TyrAsnTyrGluPheMetLysAspLeuArqLeuAlaValPheGlv	CGA		PIGITESETASPLYS	GTGATAGCTGATGATAAT	G1	::: ATATGGTGAG			pAsnAlaTy	ASIMETALA      AATGACCCT	nMa+ A
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456 1122	laGlnValAsp     \ATGGGTGTTT	437 1069	Db Db
1068	TYPPHEASHMETVALASHYNTGIUILEVALPHEPROGUARGGUGINILEGIN 	1012	B 8
0	GGCGACAATTATCACGAGGCGCCGATCCTCGGT	979	₽ B
418	IleAlaThrArg	399	Qy
978	CTC	949	В
398	roValLysArgGluLeuLeuGluGl	379	Qy
948	ACGGATGACTTGTTTGCG	931	Db
378	lValPhePheThrIleAspPr	359	Qy
930	GATGTCATGATCAAAACAGACATC	907	Db
358	rLeuIleTyrAspThr	339	Qy
906	::: GAGATC	850	Db
338	${\tt GluAsnAlaSerAlaGluHisGlyTyrPheAspGlyArgTrpLeuAspArgSupersCluster}$	319	δ
849	TCTTTG	832	ДЪ
318	alProLeuLeuIleGlyAspValPheHisHisGlyLysTyrGluThrLysLysAsnLeu	299	Qy
831		790	Вρ
298	aValGluValArgGlyGluGlyAlaAspAspLysAlaPheThrThrValAlaAspC	279	Qy
789	GCGCCGCTTGAAGTCAGCCTCGATTCCCTCGGATAT	754	Ф
278	IleGlyGluValAspValIleIleHisAspLeuGlyGluProValTyrIleAspTyrArg	259	Qy
753	GAGCTTGCGACGATTACGACAGAA	718	DЬ
258	LeuValAlaAlaArgAlaValGlyTyrTyrAspIleAspLeuSerIleIleArgAsnSer	239	Oy
717	GCGGAAAAAACTGAAAGAAAGCTTGAAGAATTTAAAGAACAGGCT	658	Db
238	IleThrGlnGluSerAlaMetAspLeuAsnGlySerIleProArgLeuArgGlnThrAla	219	Qγ
657	GTCA	610	₽
218	isGlnLysThrGluProTyrAlaAsnIleLysAlaAlaLeuGluAsp	199	Qy
609	  GTCGGCGAAAAGACGGCG	571	DЬ
198	rSerGlnSerGlyGluThrSerAla	179	οy
570		523	рь
178	aArgLeuPheAsnAspGlyValAsn	(J)	Оу
UI	CTTACC	487	Db
158	nSerGluValValValProProThrLeuGlu	139	Qy
486	 ACAGATGTCGAATACTAT	427	В
138	nGluSerThrGluMetGlyIleAsnProAsnAspTyr	125	Qγ
	CAGCTG	376	ф
N	AspMetSerValIleGluGluThrThrProLeuSerLeuGluGluLeuPhe	105	Qy
375	AGCTTGAA-AACTACGAGGCCGATGATATTATCGGCACCCTTGCCAAATCAGCGGAAAAA	317	Db

2079	AGCGTTCACGAACGATATGGACGTTCACACAAAAACGGCGATGGACGTTTTTT	2023	Db
751	spAsnLeuValAsnProMetArgGlyTyrArgGlnAr	733	Qy
2022	GCGGATTACTCACAGATCGAGCTGAGGGTTCTCGCCCACATTTCAAAGGATAAAAATTTG	1963	Db
732	isLysThrVal	722	Qy
1962	: : :	1903	Дb
721		714	Qy
1902	AGACGGGAAGGCTCAGCTCAACCGATCCGAATCTGCAAAATATACCGATCCGCCTTGAG	1843	ф
713	GlnAlaProProGluThrTrpGlnAspLeuProValAspPheVal	699	Qy
1842	TTAACA	1783	Db
869	ysLeuLysThr	688	Qy
1782	AGGGCTT	1723	Db
687	-GlnAsnGlyGlyTrpAsnArgThrTyr	675	Qy
1722	GTCAT	1666	Db
674	nGlyPheAspLeuSerThrArgThrLeuGluHisGluIleSer	655	Qу
1665	AAACTCGGGCTGCCTGTCGTCAAAAAAACGAAAAACG	1630	DЪ
654	SerHisProLeuAsnAspGlnLeuArgAlaThrLeuGlyTyrGlnGlnGluVal	635	Qy
1629		1576	Db
634	aGluLeuArgLeuSerGluAspLysLysGlyValLysLeuTyrAlaThrLys	616	Qy
1575	TGTCCGCTAAATTAGCGGAATACGAGAAAAAAATCCACGAGTCAGCA	1528	Db
615	ValThrLysPheGluHisAsnLeuIleAsnArgAspGlyTyrGlnAla	599	Оу
1527	: ATCGATCGGTGTCCAAGTCGATGTCGACAGACTGAAAAAAATGGGTGAAGAA	1468	Db
598	${\tt sProArgAspGlyGlnIleGlyLeuGlyTrpGlySerAspThrGlyThrArg}$	579	Qy
1467	TTTGAAGCGCTCGAAATGCCCCTCGCCACATTCTCGGT	1429	Db
578	lnSerLysLysValProLeuTyrValPheValAla	559	Qy
1428	;AACTG	1393	Дb
558	uProAspGluSerGluAsnGluValIleAspLeuProGluArgThrAlaLeuAlaAsn	539	Qy
1392	NAAGGCGAAGGCGATATCGCTGCTGCGCGAAAAGCTC	1348	Д <b>b</b>
538	uGlyArgIleSerAspAlaValSerAlaValAlaArgAlaIle	519	Qy
1347	AAAGGAGCGAAACAGGCGGTTCCGGATGAGAAGGAGCTTGCCGACCAT	1300	Db
518	rgValLeuAlaIleAsnHisAspAspGly	505	Qy
1299	GAAGCGGTCTA	1243	Dъ
504	AsnLeuIleGlnAspLysLeuAsnLeuValAlaAlaLysAlaArgHisLeuTyrAsp	485	Qy
1242		1183	DЪ
484	etAspIleSerProIleGluPheSerAla	471	Qy
1182	::::: GATGCAAAACGTGCGGCGGTCGCTTTGCGCTGGCGGGGCATTGAACTGAAAGGCGCTGAG	1123	Db
470	roVal	457	Qγ

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Percent Similarity:
Best Local Similarity:
       US-09-914-168-2
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PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 3311
LENGTH: 11185
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3311, Application US/09880107
Patent No. US20020142981A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Gene Expression Profiles in FILE REFERENCE: 44921-5028-WO CURRENT APPLICATION NUMBER: US/09/880,107 CURRENT FILING DATE: 2001-06-14 PRIOR APPLICATION NUMBER: US 60/211,379 PRIOR FILING DATE: 2000-06-14
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Vockley, Joseph (
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
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APPLICANT: Vockley, Josep
APPLICANT: Scherf, Uwe
                                                                                                                                                              OTHER INFORMATION:
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126.50
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19.84%
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                                            Conservative: Mismatches: Indels:
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Matches:
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                          TATCTGTCTACTACACCTTTTCCATCACAGCATCGTACAGAAATAGAATTGTTTCCTTAT
                                                                                                                    ValSerLeuIleTyrAspThrGlyThrGlnTyrArgPheAspGluValVal------
                                                                                                                                                                                                                                                                            TTTGACCAAATTCCTGAAGTCATTACGGTGTCAAAGACTTCAGAAGACACCATCCAC---
                                                                                                                                                                                                                                                                                                                                                                                                    GTTTCTGAATTGGTAACCACAGGTCACTATGGATTCACCTTGGGAGAAGAGGATGATGAA 1940
                                                       PhePheThrIleAspProLysThrAsnGlnLeuThrThrAspProAspLysLeuProVal
                                                                                                                                                                                 AspGlyArgTrpLeuAspArgSerValAspValIleLeuProAspAsnThr---AlaAsp
                                                                                                                                                                                                                                            GlyLysTyrGluThrLysLysAsnLeuIleGluAsnAlaSerAlaGluHisGlyTyrPhe
                                                                                        ATGGATGACTGGGAAGAGAGACAAACTAGTGGTAGGATAACGGAAGAGTTTCTTGGCAAA
                                                                                                                                                                                                                                                                                                                AlaAspGluValProLeuLeuIle----
                                                                                                                                                                                                                                                                                                                                       GAC----AGAACACTTACAGTT------GGATCTGATGAGAGC------ACCTTGATC
                                                                                                                                                                                                                                                                                                                                                                 AspTyrArgAlaValGluValArgGlyGluGlyAlaAspAspLysAlaPheThrThrVal 295
                                                                                                                                                                                                                                                                                                                                                                                                                                 IleGlyGluValAspValIleIleHis-----AspLeuGlyGluProValTyrIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTGGTAACTGCAAGAATGATCCTGGAATCCAAAACTGAAAAGAAAATGGTA---AGCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LeuValAlaAlaArgAlaValGlyTyrTyrAspIleAspLeuSerIleIleArgAsnSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACATCTATGGAAATCTTAAAGCACATTCCTTCCAAGGAATTCCCTGTAACTGAAACACCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SerAlaMetAspLeuAsnGlySerIleProArg------LeuArgGlnThrAla 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---LysAlaAlaLeuGluAspIleThrGln------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GluThrSerAlaIleGlySerSerHisGlnLysThrGluProTyrAlaAsnIle-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---GGAAAGCTAGACATATCAGAAATTAAGGAAGAAGTGCTCCAGAGTACA----- 1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AspGlyValAsnLysValProArgLeuLysAlaLysPheTyrGlnSerSerGlnSerGly 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGGATGACTACTCACCTTCTGCTTCAGGACCTCTT-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProThrLeuGluProGluLysProGlyLeuIleLysArgLeuTyrAlaArgLeuPheAsn 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProProLeuGlyLeuAspMetSerValIleGluGluThrThr-----ProLeuSerLeu 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTACACCAATCATCCCTTTAGTTGATGAATTACCTGTC----ATTCCAACAGAGTTC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATCCTCGCAGAAACTGCATCACCCAGTTTATCCAAAGGAACCACAAATGGTTTCTGATAGA 1397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----ACAACTGTTTCCCCTTTAATTATGCCTGATAATAATGGATCATCC
                                                                                                                                                                                                                ACTCATTTAGAAGACTTGGAGTCAGTCTCAGCATCC-------
-LeuLeuGluGlnLeuLeuThrVal--
                                                                                                                                                                                                                                                                                                           -----GlyAspValPheHisHis
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708	9 LeuArgTyrArgLeuAspLysLeuLysThrGlnAlaProProGluThrTrpGlnAspLeu 	Qу 68
688 3218	TCTTCCCATACCATTCCTCTTTCTGTAATTCCCAAGACAGAC	QУ 6/1 Db 3171
1	GTGGAAGGATTAGCATTTGTTAGTTATAGTAGCACCCAAGAGCCTACTATGTAGAC	66 311
660 3110	2 GlnGluVal	Qy 65 Db 305
651 3050	2 AlaThrLysProLeuSerHisProLeuAsnAspGlnLeuArgAlaThrLeuGlyTyrGln (	Ľω
631 3017	ArgLeuSerGluAspLysLysGlyVal	5 2
619 2957	2 LysPheGluHisAsnLeuIleAsnArgAspGlyTyrGlnAlaGlyAlaGluLeu	Qy 60 Db 289
601 2897	2 ProArgAspGlyGlnIleGlyLeuGlyTrpGlySerAspThrGlyThrArgLeuValThr (	Qy 58 Db 283
581 2837	7GlnSerLysLysValProLeuTyrValPheValAlaSerAspLys	Qy 56 Db 277
566 2777	3 ArgThralaLeualaAsnArgLysThrProAlaAspValTyr	Qy 55 Db 271
552 2717	3 AlaValAlaArgAlaIleLeuProAspGluSerGluAsnGluValIleAspLeuProGlu	
532 2660	HisaspaspGlyValasnargSerIleLeuGlyargIleSeraspalaValSer:::   ::: ::   ::: :::   ::: :::   ::: :::   ::: :::   :::: :::    :::: :::   :::::   :::::   :::::   :::::   ::::	Qy 515 Db 2601
514 2600	LysalaargHisLeuTyraspMetProAspAspArgValLeuAlaIleAsn:::	Qy 498 Db 2541
497 2540	8 SerProIleGluPheSerAlaSerAsnLeuIleGlnAspLysLeuAsnLeuValAlaAla .	Qy 47 Db 250
477 2501	8 SerThrLeuGluProVall1eGluThrValGluLeuThrAspGlyIleLeuMetAspIle	Oy 45 Db 248
457 2480	8 ASPGINVAlSerPheGluGlnSerSerSerSerArgThrGluProAlaGlnValAspGlu:::	Qy 43 Db 242
437 2420	TyrPheAsnMetValAsnThrGluIleValPheProGluArgGluGlnIleGlnAsn	Qy 419 Db 2361
418 2360	GlyGluAlaTyrAsnLeuGlnAlaValArgAlaLeuSerAsnAspLeuIleAlaThrArg :::	Qy 399 Db 2301
2300	1 TCTGGTGATAAAATATTAGTAGAGGGAATTTCCACAGTTATTTAT	Db 224

Db 3219					<u> </u>		112				-	
GTTAGTACCTTCTGTTCCATCAGAA	475	83 Ala	72 4704 CC	58 4644	45 4584	25 4524	12 4470	09-914-168-2 (1-919)	Scores: milarity: Similarity: h:	729 3288 3288 3288 3288 3288 3288 3288 32	709 3246	3219
3245 728 3287 3287  4643 4583 4751 102 4751		PheAspAspGlnSerProIleSerArgI	AlaAlaGlyLeuAsnAlaL 	ProValLeuLeuThrProGluGlnIleG          CTGTGACCCTGTCACAGGATTCTGCAO	GlnAlaLysAlaGlyAsnP 	31nGlnAsnAsnProAlaAsnIleIleA :::    :: DACGGGGATATGAAGGCCAGTACTGTGA	yr[	(1-	Length: Matches: Conservative: Mismatches: Indels: Gaps:	AsnLeuValAsnPro 739 :::::!   US/09954531  US/09954531  ss for Identifying Anti-Canc Sets R: US/09/954,531 2-05-02 US/60/233,133 9-18 US/60/234,009 US/60/234,009 US/60/234,567 US/60/234,567 US/60/234,567 US/60/234,567 US/60/234,567 US/60/234,567 US/60/234,567 US/60/234,567	31yLysProSerGlnGluAlaLeuLeuA  } :::        :::  GTGAACCCTCTCAAGACATACTTGTC-	STGTTAGTACCTTCTGTTCCATCAGAA-
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444	AsnAspGlnValSerPheGluGln	437	λλ
436 5656	GCCACCTATGTCTGAGGAG	424 5597	
423 5596	aValArgAlaLeuSerAsnAspLeuIleAlaThrArgTyrPheAsnMetVal ::: !!           ::: !! CACTTTAAAAGAAGGCAATGACATACTCGATGAAGCCAACCGTCTTGCAGATGAAATC	37	
405 5536	ysArgGluLeuLeuGluGlnLeuLeuThrValAsnMetGlyGluAlaTyrAsnLeuGln    :::	98	, P 5
385 5497	hePheThr     TATTTGCA	366 456	Db Dy
65	ValSerLeuIleTyrAspThrGlyThrGlnTyrArgPheAspGluValVa	346 5453	ρ υ
345 5452	yrPheAspGlyArgTrpLeuAspArgSerValAspValI1eLeuProAspA	28 93	96
327 5392	H1sGlyLysTyrGluThrLysLysAsnLeuIleGluAsnAlaSerA :::       :::   :::   GAAAATGAAGAAATGGAGAAGGATCTCCGGGAAAAACTGGCTGJ	08 36	р <sub>О</sub>
307 5335	AlaPheThrThrValAlaAspGlu ::: ::: TTGGTAGCTGCAGAAGCCCTTCTGAAAAAA	90 76	B 3
289 5275	uProValTyrIleAspn G	270 5234	8 8
269 5233	CTTC/	74	р 9
252 5173	uArgGloThrAlaLeuValAlaAlaArgAlaValGlyTyrTyr     :::   \$AATGAAACTCTAGGAACTCGA	4 3	Фb
232 5140	AlaMetAspLeuAsr 	16 81	β Q
215 5080	GLnL: :::: GAGA	196 5036	gb Qy
195 5035	\rgLeuLysAlaLysPheTyrGlnSerSer 	176 4976	рb
175 4975	ThrLeuGluProGluLysProGlyLeuI      ::  CAGCGGGCCCCAGAGAGGCTTA	N U	Db Qy
155 4924	TyrIleProGluTyrGlnGlyGluGlnProb 	on ω	P 04
137 4864	LeuPheAlaGlnGluSerThrGluMetGlyIleAsn	123 4805	Оy
122 4804	ProProLeuGlyLeuAspMetSerVallleG	5 0	Db Oy
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ValAlaAspAsnLeuValAsnProMetArgGlyTyrArgGlnArgTyrSe              :::	7	Qy
2 PheValAsnGlyLysProSerGlnGluAlaLeuLeuAlaGlyValAlaValHisLysThr	712 6569	Qy Db
12 ArgLeuAspLysLeuLysThrGlnAlaProProGluThrTrpGlnAspLeuProVal 	692 6524	Qу
2 GluIleSerArgSerIleIleGlnAsnGlyGlyTrpAsnArgThrTyrSerLeuAr	67 647	Qу Db
32 GlnGluValPheGlyHisSerThrAsnGlyPheAspLeuSerThrArgThrLeuGluHis :::   :::  0 AAGGAATTGATAAACCAAGCT	6440	ф
9 4	6389	aa Aa
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33 AlaWalalaArgAlaIleLeuProAspGluSerGluAsnGluValIleAspLeuProG ::::::::::::::::::::::::::::::::::::	533 6113	рь Оу
3 IleAsnHisAs     ::: 3 ATAGAAAATGC	51 605	Qy Db
93 AAGAAGTTAGCAAATGATGTAAAAAGAAAATGAAGACCATCTAAATGGCTTAAAAACCAGG	599	Db
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05MetProAspAsp	50 593	ду Ф
	587	Db 43
ACTGCAGCCTTCAAAGCTTACAGCAATATT	5813	Db Db
85AspLysLeuAsnLeuYa	4 8	Qy
65 GluThrValGluLeuThrAspGlyIleLeuMetAspIleSerProIleGluPheSerAl :::             62GCTGTCCTTGATGGAATCCTTGATGAGGGCTAAAAACATCTCCTTCAATGC	4 E 57 E	Qy dd
45 SerSerSerSerArgThrGluProAlaGlnValAspGluSerThrLeuGluProVal	57:	da Vy
57	56.	Db

US-09-914-168-2 (1-919) x US-09-782-378A-23 (1-10302)  QY 146 GlnProAsnSerGluValValValProProThrLeuGluProGluLysProGlyLeuIle 165	ignment Score ed. No.: ore: rcent Similar st Local Simi ery Match:	PRIOR FILING DATE: 2000-10-02  NUMBER OF SEQ ID NOS: 27  SOFTWARE: Patentin version 3.0  SEQ ID NO 23  LENGTH: 10302  TYPE: DNA  ORGANISM: Homo sapiens  ORGANISM: Homo sapiens	APPLICANT: Hearing, Patrick  APPLICANT: Bahou, Wadie  APPLICANT: Sandalon, Ziv  APPLICANT: Gnatenko, Dmitri  TITLE OF INVENTION: Adenoviral Vectors  FILE REFERENCE: STONYB-04970  CURRENT APPLICATION NUMBER: US/09/782,378A  CURRENT FILING DATE: 2001-02-12  DBIOS APPLICATION NUMBER: 50/237 7/7	692 SULT 3 -09-78 Sequen Patent	GTGCCCAGCACACACCATTCGACGTCTCCTCCAGGGT LeuThrGlyGlyGlnValLeuAlaValGlyThrAlaGluTyrAsnT ::: :::	799 6779 819	6668 CTCTGGGATGTTGGATCTGGAGTTGGACGTGTAGAGTACCCAGATTTGACTATTGATGAC 779 AlaTyrGlySerAsnArgAlaHisGlnMetThrGlyGlyIleGlnAlaGlyTyrIleTrp :::	CTCTTT ValSerAspAlaAsnMetAlaIleAlaArgAlaGlyIle ::: ATTGACTTTCTGGCTATAGAAATGCGTAAAGGCAAAGTC
430 ProGluArgGluGlnIleGlnAsnAspGlnValSerPheGluGlnSerSerSer	Db 6289 ATCTGTTGGTTAACAAAGGCTGAGCATGCAAAAGAGATCAACCACCGAATTGGGA 6348  Oy 400 GLUALATYRASHLEUGLNALAVALARGALEUSERASHASPLEUILEALA	Db 6172 CTGGCAGTTTAAACCAACGCTGGGATGCAATTGTTGCAGAAGTGAAAGGATAGGCAG 6228  Qy 374 AsnGlnLeuThrThrAspProAspLysLeuProValLysArgGluLeuLeuGluGlnLeu 393 :::	337 ServalAspvalIleLeuProAspAsnThrAlaAspValSerLeuIleTyrAsp	HILLY VA AACAGA AACAGA UThrLy : : : : CTTAGA	5818 GGACCTGAAGCCATTCAGATCAGAGATACACTTACTCAGCTGAATGCAAAATGGGACAGA  285	Qy 259 IleGlyGluValAspValIIeIleHisAspLeuGlyGluProValTyrIleAspTyr 277 :::       Db 5758 CTTGGAGAGAGTTGCAGTCATTCATGAAAAACAGCCAGATGTCATCCTTGAAGCCTCT 5817  Qy 278ArgAlaValGluValArgGly	Op 242 AlaargalaValGlyTyrTyrAspIleaspLeuSerIleIleArg	5545 ATCCCTATTCAACAGAGGAAAATGGGTCAACTTGCTTCTGGAATTAGATCACTTCTT  205 LysThrGluProTyralaasnIleLysAlaAlaLeuGluAspIleThrGln

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6769

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APPLICANT: Stam, Lynn

APPLICANT: Bachmann, Jane
APPLICANT: Bachmann, Jane
APPLICANT: Kandar, Kim
APPLICANT: Kandar, Kim
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE
FILE REFERENCE: 31133B
CURRENT APPLICATION NUMBER: US/10/108,605
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US 09/761,142
PRIOR FILING DATE: 2001-01-16
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Best Local Similarity:
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PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 361
SOUTWARE: Patentin Ver. 2.1
SEQ ID NO 102
LENGTH: 14155
TYPE: DNA
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                                                                                                                                                                                   9501 CTTTTCAACTGGAGCGAAGCTTCACAAGCCAAGTCCGCTGACGTTGAGCGCCGCAATGTG
                                                                                                                                                                                                                                                         9441 AACAAGAGCCTCAATGCCCTCAAGAATGATATTGGAGAATTCAGCGACCATCTGGAAGAT
                                                                                                                                                                                                                                                                                                                                                                                                        9321 CACATTTTGGGACAAATCAACGGAACCAGTATCGAACTTACACCCAATGAACAAGTCCTG
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{\tt AlaSerAlaGluHisGlyTyrPheAspGlyArgTrpLeuAspArgSerValAspValIle}
                                                              LeuIleGlyAspValPheHisHisGlyLysTyrGluThrLysLysAsnLeuIleGluAsn
                                                                                                             GCCAACCAGAAGGCCTTTGACAACTCTAAATTCGACACCGTTTCGGAGCAA------
                                                                                                                                                                                                                                                                                                                                                                         AlaArgAlaValGlyTyrTyrAsp-----
                                                                                                                                                                                                             Leu-----GlyGluProValTyrIleAspTyrArgAlaValGluValArgGly---
                                                                                                                                                                                                                                                                                             ---IleAspLeuSerIleIleArgAsnSerIleGlyGluValAspValIleIleHisAsp
                                                                                                                                                                                                                                                                                                                                GAAAAGGCGAGGAAACTCTATGAAGAAGTGAACACTCTAGTTCTGCCCATCAAGGCGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                 GluSerAlaMetAspLeuAsnGlySerIleProArgLeuArgGlnThrAlaLeuValAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGTGTCCTGGAGGACTTTAACAGTGTAACCCTGGCCTTCTTCACCAGTCAAAAATTGAAC
                                                                                                                                            -GluGlyAlaAspAspLysAlaPheThrThrValAlaAspGluValProLeu 301
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                                       -AAGCTACAGGCAGAGAAGAAC------
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RESULT 35 US-10-108-605-102

Sequence 102, Application US/10108605 Patent No. US20020160934A1 GENERAL INFORMATION:

APPLICANT: Broadus, Julie

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7297 GACAGACAGAACGCCTTGGAGGCT

7320 721

AsnGlyLysProSerGlnGluAla

657	HisProLeuAsnAspGlnLeuArgAlaThrLeuGlyTyrGlnGlnGluValPheGlyHis	638	Qy
10439	CAATTGGATGACGTAGAAGGATCCGTTTCGAAGCTAAACGAATTGGCA	10392	B 2
0	GATCTGACCAATAAGGACGTTTCTCAAGCTAACAAA	ى د	B B
617	wValThrLysPheGluHisAsnLeuIleAsnArgAspGlyTyrGlnAlaGlyAla :::	598	Qγ
597 10355	AlaSerAspLysProArgAspGlyGlnIleGlyLeuGlyTrpGlySerAspThrGlyThr:::	578 10302	9d 6A
577 10301	LysThrProAlaAspValTyrGlnSerLysLysValProLeuTyrValPheVal :::	10248	ρ δ
0 5	spGluSerGluAsnGluValIleAspLeuProGluArgThrAlaLeuAlaAsnArg       ::: :::        CTGAGTCGCAGAGGATATGTGGAAGAATTCAAATGCCAAT	4 0	da Oy
539 10202	AsnArgSerIleLeuGlyArgIleSerAspAlaValSerAlaValAlaArgAlaIleLeu	520 10149	Ф
519 10148	ASPASPATGValLeuAlaIleAsnHisAspAspGlyVal	507 10089	ду О
506 10088	TCTGCAGAAGGTACAA	503 10029	₽ 6
502 10028	eulleGlnAspLysLeuAsnLeuValAlaAlaLysAlaArgHisLeu 	483 9972	4d 6d
482 9971	LeuThrAspGlyIleLeuMetAspIleSerProIleGluPhe	469 9912	g Qy
468 9911	erThrLeuGluProValIleGluThrValGlu                    ::: 	451 9852	g Q
450 9851	SerPheGluGlnSerSerSerSerArgThr :::     ::: GCGGCCGAATTGGCCATTAAGGCCCAAGAT	435 9792	g Vy
434 9791	WETVALASnThrGluIleValPheProGluArgGluGln	420 9744	g Q
9743		9743	DЪ
419	.euGlnAlaValArgAlaLeuSerAsnAspLeuIleAlaThrArgTyr	400	VΩ
399 9743	ProAspLysLeuProValLysArgGluLeuLeuGluGlnLeuLeuThrValAsnMetGly	380 9696	B 5
379 9695	AspGluValValPhePheThrIleAspProLysThrAsnGlnLeuThrThrAsp	362 9651	g Q
	ATCAAAGATGCTGGCAAT	9633	ф
61	uProAspAsnThrAlaAspValSerLeuIleTyrAspThrGlyThrGlnTyrArgPhe	34	γ
9632		9632	В

		GENERAL INFO APPLICANT: APPLICANT: APPLICANT: APPLICANT: TITLE OF IN FILE REFERE CURRENT APP CURRENT A	
	6 8-880-1 ce 1, Application US/09808880 ation No. US20030027287A1	SULT 36 -09-808- Sequence Publicat	RE US ;
	3 LysGluGluGlyAsn 907 ::: :::       8 CGGTTCAAGGGTAAT 11192	903 11178	Qy Db
902		883	Qy
11177		11142	Db
882	6 GlyAsnAlaTyrAspLysGlyPheThrAsnAspThrLysIleGlyAlaGly	866	Qy
11141		11112	Qy
11111	6 ThralaGluTyrAsnTyrGluPheMetLysAspLeuArgLeuAlaValPheGlyAspIle	1108	Qy Db
845	6 SerLeuSerProIleSerAspLysGlyTyrLeuThrGlyGlyGlnValLeuAlaValGly	820	Qy
11081		1102	Db
825	7 TyrargLeuargPhePheAlaGlyGlyAspGlnSerIleargGlyTyrAlaHisAsp	807	Qy
11021		10962	Db
806	2   IleGlnAlaGlyTyrIleTrpSerAspAsnPheAsnHisValPro	792	Qy
10961		10902	dd
791	2 ValTyrSerPheGlyAspAsnAlaTyrGlySerAsnArgAlaHisGlnMetThrGlyGly	772	Qy
10901		10842	Db
771	2 GlySerSerGlyLeuValSerAspAlaAsnMetAlaIleAlaArgAlaGlyIleSerGly	752	Qy
10841		10782	dd
751	6CeuValAsnProMetArgGlyTyrArgGlnArgTyrSerLeuGluVal	736	Qy
10781		10722	Db
735	7 ProSerGlnGluAlaLeuLeuAlaGlyValAlaValHisLySThrValAlaAspAsn	717	Qy
10721		10665	Db
716	7 LysThrGlnAlaProProGluThrTrpGlnAspLeuProValAspPheValAsnGlyLys	697	Qy
10664		10614	Db
696	8 IleGlnAsnGlyGlyTrpAsnArgThrTyrSerLeuArgTyrArgLeuAspLysLeu :::	678	Qy
10613		10554	Db
677	8 SerThrasnGlyPheaspLeuSerThrArgThrLeuGluHisGluIleSerArgSerIle ::::::::	658	Qy
10553		10497	Qy
10496	0 GAGGATATCGAGGAACAGCAGCACCGTGTGGGCAGTCAGAGCCGGCAGTTGGGCCAG	10440	ф

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PRIOR FILING DATE: 1999-02-16
PRIOR APPLICATION NUMBER: 60/106,100
PRIOR FILING DATE: 1998-10-29
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 50937
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Best Local Similarity:
Query Match:
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; OTHER INFORMATION: Description of Artifical Sequence: Recombinant DNA
US-09-808-880-1
                                21597 GCTGCCGACACCGGTGCGGTGATCGACCCCGTACACGCGCAGCTGTGGGGGCTTCGGCCGT 21656
                                                                                                          21546 GAGTCGGCGCGCGTCTG-----TGGCTGGTCACGGAAGCTGCCGTCGTGATCGGT 21596
                                                                                                                                                                                 21486 GCGGGTCTGGCGGCATCGCTGGCGTTGGCCCAGGCGTTGATCGATGTCGGCGGGTCCGGT 21545
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ORGANISM: Artificial Sequence
                                                                             249
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                                                                                                                                 230 ---SerIleProArgLeuArgGlnThrAlaLeuValAlaAlaArgAlaValGlyTyrTyr 248
                                                                                                                                                                                                                                                                                             194 GlyGluThrSerAlaIleGlySerSerHisGlnLysThrGluProTyrAlaAsnIleLys 213
                                                                                                                                                                                                                                                                                                                                                                  174 AsnAspClyValAsnLysValProArgLeuLysAlaLysPheTyrGlnSerSerGlnSer 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126 GlnGluSerThrGluMetGly------Ile 133
     262 ValAspValileIleHis--
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                                                                                                                                                                                                                     AlaAlaLeuCluAsp------IleThrGlnGluSerAlaMetAspLeuAsnGly----- 229
                                                                         AspIleAspLeuSerIleIleArgAsnSerIle---
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554 ThrAlaLeuAlaAsnArgLysThrProAlaAspValTyrGlnSerLysLysValProLeu 573	Qy
GTCC	Db
540 ProAspGluSerGluAsnGluValIleAspLeuProGluArg 553	Qy
522 SerIleLeuGlyArgIleSerAspAlaValSerAlaValAlaArgAlaIleLeu 539	ОУ
507AspaspargValLeuAlaIleAsnHisAspAspGlyValAsnArg 521	Db Qy
492 LeuAsnLeuValAlaAlaLysAlaArgHisLeuTyrAspMetPro	Оу
2 GlyIleLeuMetAspIleSerProIleGluPheSerAlaSerAsnLeuIleGlnAs    :::	Qy Db
54	Qy Db
437 AsnAspGlnValSerPheGluGlnSerSerSerArgThrGluProAlaGlnVal 455 :::	Db Qy
417 ThrargTyrPheAsnMetValAsnThrGluIleValPheProGluArgGluGlnIleGln 436 ::::::         22152ATCCATGCGCCGACCGTGGTCGAGTTCGCCTCGGTGGCCGAG 22193	Qy Db
397 AsnMetGlyGluAlaTyrAsnLeuGlnAlaValArgAlaLeuSerAsnAspLeuIleAla 416         :::     ::       22122 ACGACCGGCGAACACCCGCTGCGCGCGCGCTC	Qy Db
387 ArgGluLeu	Дb
0 6	Qy Db
350 SerLeuIleTyrAspThrGlyThrGlnTyrArgPheAspGluValValPhePhe 367 :::	Qy Db
36 A 00 C	Db Qy
5	Db
2183/ TACGTACCCAGGCTGGTGCGTTCAGGCGGCAGTGCACACTCGGGTGCG	Q 5
298 GluValProLeuLeuIleGlyAspValPheHisHisGlyLysTyrGluThrLys 315	P 09
280ValGluValArgGlyGluGlyAlaAspAspLysAlaPheThrThrValAlaAsp 297	Qy Db
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                              NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/10107649
Publication No. US20030044949A1
GENERAL INFORMATION:
ADDITION: BOAT TOWN
                                                                                                          APPLICANT: Sloma, Ålan
TITLE OF INVENTION: Polypeptides Having Gamma-Glutamyl
TITLE OF INVENTION: Transpeptidase Activity And Nucle
FILE REFERENCE: 10157.200-US
CURRENT APPLICATION NUMBER: US/10/107,649
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: 60/279,374
PRIOR FILING DATE: 2001-03-27
PRIOR FILING DATE: 2001-03-27
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                                                  {\tt ThrArgTyrPheAsnMetValAsnThrGluIleValPheProGluArgGluGlnIleGlnIneGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluI
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                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09738877
Patent No. US20020015970A1
                                                                                            APPLICANT: MUTTAY, Richard
APPLICANT: Watson, Susan
APPLICANT: Watson, Susan
APPLICANT: Watson, Susan
APPLICANT: Watson, Richard
TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF ANGIOGENESIS, COMPOSITIONS,
TITLE OF INVENTION: SCREENING FOR ANGIOGENESIS MODULATORS
FILE REFERENCE: A-69806/DJB/JJD
CURRENT APPLICATION NUMBER: US/09/738,877
CURRENT FILING DATE: 2000-12-15
PRIOR APPLICATION NUMBER: US 09/637,977
PRIOR FILING DATE: 2000-08-11
                                                    PRIOR APPLICATION NUMBER: US 60/148,425
PRIOR FILING DATE: 1999-08-11
PRIOR APPLICATION NUMBER: PCT/US 00/22061 PRIOR FILING DATE: 2000-08-11 NUMBER OF SEQ ID NOS: 4
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Best Local Similarity:
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; ORGANISM: Homo
US-09-738-877-2
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                                                                                        ThrGlnGluSerAlaMet--
                                                                                                                                                                          CTTGTAACCACTTGTCAAGCCGAAACCTTAGCTGGGGTAAAATCA-----CAGGAGATG
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		NG DATE: 2000-08-11 JCATION NUMBER: US 60/148,4	
		FILE REFERENCE: A-69806/DJB/JJD CURRENT APPLICATION NUMBER: US/09/738,877 CURRENT FILING DATE: 2000-12-15 PRIOR APPLICATION NUMBER: US 09/637,977	
AND	OMPOSITIONS,	Welss, Stephen J. Glynne, Richard Glynne, Richard GNZENTION: NOVEL METHODS OF DIAGNOSIS OF ANGIOGENESIS, C INVENTION: SCREENING FOR ANGIOGENESIS MODULATORS	
		APPLICANT: Murray, Richard APPLICANT: Watson, Susan	_
		ULT 39 09-738- equence atent N	RES US- ; S
		CTGGCTGATACTGATGCCTC	DЬ
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	1e 762	erSerGlyLeuValSerAspAlaAsnM	Qy
	- 5091	5053GAAAGAATAGAGAAGTCACTAGTTGAACCGAAAGAAGAT	рь
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	۳ دا	euArgTyrArgLeuAspLysLeuLysThrGlnAlaProProGluThrT	Qy
	C 4974	4915 AAGACCATGACTGTTGAGGTAGAAGGTTCCACTGTAAATGATCAGCAGCTGGAAGAGGTC	Db
	h 686	667 ArgThrLeuGluHisGluIleSerArgSerIleIleGlnAsn-GlyGlyTrpAsnArgTh	Оу
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	:p 591	572 ProLeuTyrValPheValAlaSerAspLysProArgAspGlyGlnIleGlyLeuGlyTr	Qy
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: PACES: 52-62
: DATE: 1997-01-01
: DATABASE ACCESSION NUMBER: U81607
: DATABASE ENTRY DATE: 1997-06-26
US-09-738-877-1
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PRIOR FILING DATE: 2000-08-11
NUMBER OF SEO ID NOS: 4
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
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                                             3471 AAAGTAGATGCTCAGGAGGCAAAAACTGAGCCTTTTACACAAAGGGAAGGTGGTGGGGCAG 3530
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TYPE: DNA

ORGANISM: Homo sapiens

PUBLICATION INFORMATION:

AUTHORS: Nauert et al.

TITLE: Gravin, an autoantigen recognized by serum from myastheinia gravis

JOURNAL: Curr. Biol.

VOLUME: 7
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                                                                          179 LysValProArgLeuLysAlaLys------PheTyrGlnSerSerGlnSerGLyGlu 195
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                               196 ThrSer----
                                                                                                                                   159 ProGluLysProGlyLeuTleLysArgLeuTyrAlaArgLeuPheAsnAspGlyValAsn 178
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                                                                                                                                                                                                                                                                         123 LeuPheAlaGlnGluSerThrGluMetGlyIle---AsnProAsnAspTyrIleProGlu 141
                                                                                                                                                                                                                                                                                                                                         119 -----SerLeuGluGlu 122
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                                                                                                             ---GAAGCGTCGGGTCTGAAGAAGAG------ACGGATGTAGTGTTG 3470
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4476 ·G	Db
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434GlnIleGlnAsnAspGlnValSerPheGluGlnSerSerSerSerArgThro	Qy
4356 AGCAGTTTGGAAGGAAGCCCTCCCTCCCTGCCTAGGTCAAGAGGGAAGTATGCAACCAA	Db
433438	Qy
4296 GTCAGTAAGCAGCTCCTCCAGACACTGAAATCTCCCCCATACATCATCCATC	Db -
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395 ThrValAsnMetGlyGluAlaTyrAsnLeuGlnAlaValArgAlaLeuSei	g 4g
4182 CCCGTGGAGAGAGATGGTAGTTCAAGTCGAAAGGGAGAAAACAGAAG	) B
384 ProValLysArgGluLeuLeuGluGlnLeuLeu 3	γQ
4122 GCTGAATGTAAAAAGGATGATGCTCTTGAACTGCAGAGTCACGCTAAGTCTCCTCCAT	Db
383	Qy
4062 ATAACAGTCAGTCGGGAAAAGGTCACTGAAGTTGCCCTTAAAGGTGAAGGACAGAAGAA A	DЬ
376 LeuThrThrAspProAspLysLeu	0у
4011 ACCAAAGACGTACCATTTTTCGAAGGACTTGAGGGGGTCTATAGACACAGGC 4	Db
361 PheAspGluValValPhePheThrIleAspProLysThrAsnCln 2	Qy
3951 GTATCCATTCTGTCAAAGACTGAGGGGACTCAAGAGGCTGA	Db
349 ValSerLeuIleTyrAspThrGlyThrGln	Qy
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                                                                                                                                                             tAlaIleAlaArgAlaGlyIleSerGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTCCTCCCATCTGAGGAAGAGGGAGGTGGAGCTGGA-ACAAAGTCTGTGCCAGAA----
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                                                                                                                    AGCCCTGGCTGATACTGATGCCTCAGGA
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SEQ ID NO 3439
LENGTH: 6608
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ORGANISM: Homo sapiens
                                       LysValProArgLeuLysAlaLys-----
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AAAGTAGATGCTCAGGAGGCAAAAACTGAGCCTTTTACACAAGGGAAGGTGGTGGGGCAG
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                                                                                                                            ProGluLysProGlyLeuIleLysArgLeuTyrAlaArgLeuPheAsnAspGlyValAsn 178
                                                                                                                                                                                                                                                                 AAAGTGAAAGAGGAATCCCAGCTGCCTGGCACCGGTGGGCCAGAAGATGTGCTTCAGCCT
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472	${\tt AlaGlnValAspGluSerThrLeuGluProValIleGluThrValGluLeuThrAspGly}$	453	Qy
4475	TCAAGTTCAGAGCTCTGAGGCATCATTCACTCTAACAGCGGCTGCAGAGGAGGAAAAG	4416	рь
452	GlnIleGlnAsnAspGlnValSerPheGluGlnSerSerSerArgThrGluPro	434	Оу
4415	AAGGAAGCCCTCCTCCCTGCCTAGGTCAAGAGGAGGCAGTATGCACCAAA	4356	Db
433		433	Qy
4355	AGCTCCTCCAGACAGTGAATGTGCCCATCATAGATGGGGCCAAAGGAAGTC	4296	Db 4
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4181	ATGTAAAAAGGATGATGCTCTTGAACTGCAGAGTCACGCTAAGTCTCCTCCATCC	4122	рb
383		383	Оу
4121	TAACAGTCAGTCGGGAAAAGGTCACTGAAGTTGCCCCTTAAAGGTGAAGGGACAGAAGAA	4062	Db
383	rThrAspProAspLysLeu	376	Qy
4061	AGGACTTGAGGGGTCTATAGACACAGGC	4011	Db
375	luValValPhePheThrIleAspProL	361	Qy
4010	CCATTCTGTCAAAGACTGAGGGGACTCAAGAGGCTGACCAGTATGCTG	3951	Db
360	rGlyThrGlnTyrAr	349	Qy
3950		3924	Db
348	eAspGlyArgTrpLeuAspArgSerValAspValIleLeuProAspAsnThrAlaAs	329	Qy
9	GAAACTAAAGAACAATCAAAGATGGAAGACACTCTAGAGCAT	3879	Db
328	nLeuIleGluAsnAlaSerAlaGluF	309	οy
3878	CAGTTCCTGCACAGAAAGAGAGGCCTCCAGCACCTTCCAGTTTTGTGT	3819	Db
308	ysAlaPheThrThrValAlaAspGluValProLeuLeuIleGlyAspValPh	289	Qy
œ (	ATGAGGTCGCATCTGGTACCCAGTCAGGGGGCA	7	Db .
00	vGluProValTvrIleAspTvrArqAlaValGluValArqGlvGluGlvAlaAs	269	Q V
7	CAGGCACAACCCAGAAAGACGAGATTGTGGAA	N	g .
268	spIleAspLeuSerIleIleArqAsnSerIleGlvGluValAspValIleIleHisAs	249	Q Y
248 3728	GlySerILeProArgLeuArgGInThrAlaLeuValAlaAlaArgAlaValGlyTyrTyr	3705	B 5
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228	ThrGlnGluSerAlaMet	220 3645	B 5
3644	CACTTGTCAAGCCGAAACCTTAGCTGGGGTAAAATCACAGGAGAT	3591	Db
219	laLe	204	Qy
3590	CCCCAGAAAGCTTTGAAAAAGCTCCTCAAGTCACAGAGAGCATAGAGTCCAG	3531	DЬ
203	ThrSerAlaIleGlySerS	196	Qy

	tAlaIleAlaArgAlaGlyIleSerGly 771    :::    AGCCCTGGCTGATACTGATGCCTCAGGA 5351	762 5324	Qу
5323	GAAAAAGGTGATGATGTTGATGACCCTGAAAAGCAGAACTC	5283	σb
762	luValGlySerSerGlyLeuValSerAspAlaAsnMe	745	Qy
5282	::: ::: ::: :::	5244	Db
745	ysThrValAlaAspAsnLeuValAsnProMetArgGlyTyrArgGl	725	Qy
5243	GATGATGGTCATGCCTTGTTAGCA	5220	Db
725	G1	705	Qy
5219	GTCCTCCCATCTGAGGAAGAGGGAGGTGGAGCTGGA-ACAAAGTCTGTGCCAGAA	5166	Db
705	TyrSerLeuArgTyrArgLeuAspLysLeuLysThrGlnAlaProProGluThrTr	686	Qy
5165	AGACCATGACTGTAGGTAGAAGGTTCCACTGTAAATGATCAGCAGCTGGAAGAGGTC	5106	Db
686	rgThrLeuGluHisGluIleSerArgSerIleIleGlnAsn-GlyGlyTrpAsnArgTh	667	Qy
5105	CAA	5061	DЬ
666	isSerThrAsnGlyPheAspLeuSerThr	650	Qy
5060	GCACAGGATGAAACACCAATTACTTCAGCCAAAGAGAGTCAGAGTCAACCGCAGTGGGA	5001	Db
649	rHisProLeuAsnAspGlnLeuArgAlaThrLeuGly	630	Qy
5000	GCTGACAGCCAGGACGGGACAGGAAACGGAGAAAGAAGGAAG	4941	Db
629	pGlyTyrGlnAlaGlyAlaGluLeuArgLeuSerGluAspLysLysGlyValLys	610	Qy
4940	GAAGAAACAGCCACGAAATGTTGACGTCTGAGTTACAGACACAAGCTCACGTGATAAAA	4881	Db
609	spThrGlyThrArgLeuValThrLysPheGluHisAsnLeuIleAsn	594	Qy
4880	   AAAAGCAGTAAACTTGTCCAAAACATCATCCAGACAGCCGTTGACCAGTTTGTACGTAC	4821	Db
593	GlySer	592	Qy
4820	AAAGTGAGTGTAGCAATTGAGGATTTAGAGCCTGAAAATGGGATTTTGGAACTTGAGACC	4761	Db
591	rр	572	Qy
4760	ACCACATCACTGAAGTGGAAGTCAGATGAAGTCGATGAGCAGGTTGCTTGC	4701	Db
571		553	Qy
4700	::: GAGAGAAA	4656	Db
552	laValAlaArgAlaIleLeuProAspGluSerGluAsnGluValIleAspLeuProGlu	533	Qy
4655	ACAGGGCCCGACTGTCAGGCAAAATCGACACCAGTGATAGTATCT	4611	Db
532	oGlyValAsnArgSerIleLeuGlyArgIleSerAspAlaValSer	513	Qy
4610	TTTGCCGCTCATCCAGGGAAGATGCTGTGCCC	4578	Db
512	LeuTyrAspMetProAspAspArgValLeuAla	493	Qy
S	ATTTAGTTCTGGAAGAGAAATCCTCTGAAAAAAATGAAGAC	w	Db
92	pLysLeu	473	Qy
4535	::: :::	4476	Db

Job time : 556 secs

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Command line parameters:

-MODEL-frame+_p2n.model -DEV-x1h
-O-/Cgn2_1/USP70_Spool/US09914168/runat_28042003_151615_6799/app_query.fasta_1.1095
-DB-EST -OFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=b1ts -START=1 -END=-1 -MATRIX=bLosum62 -TRANS=human40.cdi -LIST=45
-DCCALIGM=200 -THR_SCORE-PCt -THR_MAX=100 -THR_MIN=0 -ALIGN=40 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09914188_@CGN_1_1_1477_@runat_28042003_151615_6799 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WARIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Fgapop 6.0 , Fgapext
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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22 Z	BH137735 ENTNI81TF	z	AK014398 Mus muscu		₹	34 Mus		ľΩ	9	772 A	ഗ	1 AL546	1769 Mus	159 Hom	476.	musc	60284975	Homo sap	Ŧ	GthEST			60147	_	_	2ea		AT28265.	BC025329 Homo sapi	,D39	AY108685 Zea mays	AV557254	Home	Mus	Mus musc	-		AF161466 Homo sapi	Z (	BE459389	363592 SWOV	2509 1D2 cDNA	320 AG-ND-16	BQ506223 EST613638	ı <del>(i</del>

## ALIGNMENTS

RESULT 1

BQ506223C

LOCUS

DEFINITION

EST613638 Generation of a set of potato cDNA clones for microarray analyses mixed potato tissues Solanum tuberosum cDNA clone STMGI92

ACCESSION

VERSION

BQ506223.

VERSION

BQ506223.

GG1:21922105

KEYWORDS

SOURCE

ORGANISM

EUKARYOta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

REFERENCE

1 (bases 1 to 792)

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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                               478 GTTTTCAACAGAGTCAATGCTCGTGCTAGAAAAGGATTGGTATTAGGTCCTATGCGTCTT
                                                                                                                                                                                                                   529
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CTTGGTGGAACCAATAGTGTAAGAGGATAT-
                                                      AlaGlyGlyAspGlnSerIleArgGlyTyrAlaHisAspSerLeuSerProIleSerAsp
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                                                                                          CTCCTAAGCTTCTCTGGTGGTCATGTGGTCGGTAATTTTCCACCTCATGAAGCATTTGTG
                                                                                                                                                                         AsnPheAsnHisValProTyrArgLeuArg------
                                                                                                                                                                                                          GTGTTTGTTTTCAACATGGATCAGGGACTTCCT---
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                                                                                                                                                                                                                                                         TTACTTGCCAAA-----CTTGAGACTGTCTATACTGGTTCTGGTGACCCTGGTTCTTCA
                                                                                                                                                                                                                                                                                  AlaIleAlaArgAlaGlyIleSerGlyValTyrSerPheGlyAspAsnAlaTyrGlySer 782
                                                                                                                                                                                                                                                                                                               ATAAGGGACTACTACAGTAGTCCACTTACTGCAAGTGGCAACACTCATGAT---GATATG
                                                                                                                                                                                                                                                                                                                                        TyrArgClnArgTyrSerLeuCluValGlySerSerGlyLeuValSerAspAlaAsnMet 762
                                                                                                                                                                                                                                                                                                                                                                     GCCGGAATCATATTTCAGCGTGCTGGTGCTCGGGATGACAAGGGGGAATCCTATT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           On Jun 10, 2002 this sequence version replaced gi:21365092 Other_ESTs: EST613637 Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cdna@resgen.com
Seq primer: T7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Karamycheva,S.A.

Generation of a set of potato cDNA clones for microarray analyses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone is available through the Research Genetics, contact the Research Genetics for further information 1-800-711-6195 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2002 CO Jun 10, 2002 E)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Buell,C.R., Hart,A., Baker,B., Tanksley,S., Fry,W.,
Restrepo,S., Griffiths,H., van der Hoeven,R., Tsai,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       236
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ע
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/clone="cmucro."
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/cultivar="Kennebec or Binjte
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                                                                                    Scores:
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Seq primer: M13 Rev
Class: BAC ends.
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                                                                                                                           146
                                                                                                                                                                                                                                                                                                                                                                                                 bjloftus@tigr.org
                                                                                                                                                                                          /organism="Anopheles
/strain="PEST"
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3.86e-06
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                                                                                                                                                                                                                                                                                                                                                                                                                       This clone is from an A. gambiae BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M University BAC Center University, College Station, Texas 77843-2123, USA using a HindIII
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjloftus@tigr.org
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Eukaryota; Metazoa; Arthropoda; Nematocera;
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Shetty, J., Malek, J., Koo, H.,
Direct Submission of BAC-end
Unpublished (2001)
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AG-ND-161M3.TR ND-TAM Anopheles
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/clone="AG-ND-161M3"
/clone=lib="ND-TAM"
/note="Vector: pECBAC1; S
a 182 c 183 g 138
                                                          Length:
Matches:
Conservative:
                                        Mismatches:
                    Indels:
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138 t
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BF942509
BF942509.1
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Institut National de la Recherche Agronomique
Centre INRA de Nancy, 54280 Champenoux, France
Tel: +33 383 39 40 80
Fax: +33 383 39 40 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identification of symbiosis-regulated genes in Eucalyptus globulus-Pisolithus tinctorius ectomycorrhiza by differential hybridization of arrayed cDNAs Plant J. 25 (3), 1-12 (2001) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BE942509 620 bp mRNA linear EST 2: 1D2 cDNA library of 4-day-old Eucalyptus globulus bicostata-Pisolithus tinctorius ectomycorrhiza Pisolithus tinctorius cDNA 5' similar to outer membrane protein, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plant J. 25 (3), 1-
Contact: Martin FM
                                                                                                                                                                                                                                                            Email: fmartin@nancy.inra.fr
Insert Length: 620 Std Error:
Seg_primer: CapFinder 5'CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Voiblet, C., Duplessis, S., Encelot, N. and Martin, F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Boletales; Sclerodermataceae; Pisolithus.

1 (bases 1 to 620)
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/Clone lib="CDNA library of 4-day-old Eucalyptus bicostata-Pisolithus tinctorius ectomycorrhiza" /tissue_type="mantle and Hartig net hyphae" /dev_stage="symbiotic, 4 days after contact"
                                                                                                                                                                                                              Location/Qualifiers
                                                                                                           /db_xref="taxon:37468"
                                                                                                                                   /strain="441"
                                                                                                                                                              /organism="Pisolithus tinctorius"
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US-09-914-168-2 (1-919)
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Smith College Department of Biological Sciences Department of Biological Sciences, Clark Science College, Northampton, MA, 01063, USA
                                                                                                                                                                       Eukaryota; Metazoa; Nematoda; Onchocercidae; Onchocerca.

1 (bases 1 to 423)
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423 bp mRNA linear EST 06-JAN-1999
SWOVL2CAS01E04SK Onchocerca volvulus L2 larvae cDNA (SAW98MLW-OVL2)
Onchocerca volvulus cDNA clone SWOVL2CAS01E04 5', mRNA sequence.
                                                                Contact: Steven A. Williams
Molecular Parasitology
                                                                                                                                                                                                                                       Onchocerca volvulus
                                                                                                                                                                                                                                                                                                                            Onchocerca
AI363592
                                                                                                          Unpublished (1999)
                                                                                                                                 Genes expressed in L2 larvae
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                                                                                                                                                                                                                                                                Onchocerca volvulus.
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/note="Organ: ectomycorrhiza; Vector: pBluescript; Site_1:
ECORI; The CDNA library was constructed from 1 ug total
ectomycorrhiza RNA using the SMART cDNA library
Construction kit (#K1051-1 Clontech, Palo Alto, CA, USA)
according to the manufacturer's instructions. cDNAs were
cloned into EcoRI digested pBluescript."
a 175 c 167 g 126 t 1 others
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Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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Fax: 4135853786
Email: genome@si
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primer: pBluescript SK
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/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
Xho I; Filarial nematode parasite of humans. mRNA was
prepared from approximately 9,000 L2s isolated from
infected mosquitoes from Kumba, Cameroon and converted to
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/clone_lib="Onchocerca
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Alcala, J., Vrebalov, J., White, R., van der Hoeven, R.S., Holt Liang, F., Hansen, T.S., Craven, M.B., Bowman, C.L., Ronning, C. Nierman, W., Fraser, C.M., Martin, G.B., Giovannoni, J.J. and T.
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Clemson University
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                                                                                                                                                                                                -GAAGAAGGCACAGTTGGCTCTGGCCGGTCTTATGCAGTTGGCTGTGGA
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/tissue_type="fruit"
/dev_stage="immature green (5-35 days p
/lab_host="SOLR"
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/clone="cLEM6L23"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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Mus musculus (strain:C57BL/6J) adult male lung cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library
                                                                                                                                                                                                                                                                                                                Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamcto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AK004785
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                                                                                                                                                                                    Nature 409 (6821),
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Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Akahira, S., Akimura, T.,
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RIKEN full-length enriched
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    Aono, H., Arai, A.,
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoha Kanagawa 30-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9212, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Please visit our web site (http://genome.gsc.riken.go.jp/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="data source:MGD,
evidence:ISS
                                                                                                                                                                                                                                                                                                                                   /translation="mkmadakokrneqlkrwigsetdleppvvkroktkvkfddgavf
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SAPTAVT I PVAPTVVNAAAPSTTTLTTTTAGTVSEVRERRRSYLTPVRDEESESQRKA
RSRQARQSRRSTQGVTLTDLQEAEKT I GRSRSTRTREQENEEKEKEEKEKQDKEKQEE
                                                               SDIEEKENRESSSLRTSSSYTRRKWEDDLKKNSSINEGSTYHRSCSFGRRQDDLISCS
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/db_xref="GI:12836228"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             myosin phosphatase,
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1. .3015
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/clone_lib="RIKEN_full-length enriched mouse cDNA library"
                                                                                                                                 EISASKEAQKEKDTAGVMRSASSPRLSSSLDNKEKEKDNKGTRLAYVTPTIPRRLAST
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                                                                                                                                                                                                    ESLEHEKADEEEEGKKDESSCSSEEDEEDDSESEAETDKTKPMASVSNAHTSSTQAAP
                                                                                                                                                                                                                                    LGYLEELQKKQTLLHSEKRDKKSPLIESTANMENNQPQKAFKNKETLIIEPEKNASRI
                                                                                                                                                                                                                                                                       IQAGYDVNIKDYDGWTPLHAAAHWGKEEACRILVDNLCDMETVNKVGQTAFDVADEDI
                                                                                                                                                                                                                                                                                                      {	t RQGVDIEAARKEEERVMLRDARQWLNSGHISDVRHAKSGGTALHVAAAKGYTEVLKLL}
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-GlnLeuArgAlaThrLeuGlyTyr 650 :::    :::    ACGACTAGCCAGTACATCTGACATT 1533	ACGAGACTTGCGTATGTCACCCCTACAATCCCGAGACGACTAG	643 1474	Qу	
AGGAGAAAGATAACAAAGGA 1473	TCCAGTCCGAGACTCTCGTCCTCTTTGGATAATAAAGAAAAGGAGAAAGATAACAAAGG	14	Db	
642	ThrLysProLeuSerHisProLeuAsnAsp	633	Qy	
GluAspLysLysGlyValLysLeuTy1Ala 632 	LeuArgLeuSer	619 1354	Оу	
	TACGGTGCCTGAA	1336	Db	
3lyTyrGlnAlaGlyAlaGlu 618	${\tt LeuValThrLysPheGluHisAsnLeuIleAsnArgAspGlyT}$	599	Qy	
CGAAAGACTGGCAGT 1335	GATGAGTCTCCTGCATCCTGGAGGTTAGGGCTTCGAAAGACTCGGCAGT	1288	Db	
		582	Οv	_
	CCTGTTAAAAAGTTTCCAATATCGACTACAAAAATTTCTCCCCAAAGAAGAGAAGAAAAA	1228	Db	-
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CT		1153	Дb	
ProAspGluSerGluAsnGlu 546	IleSerAspAlaValSerAlaValAlaArgAl	527	Qy	-
GCTCAT 1152		1147	Db	
AsnArgSerIleLeuGlyArg 526	/ AspAspArgValLeuAlaIleAsnHisAspAspGlyValAsnArgSer	507	Qy	
AAT 1146	GCAGAGACAGATAAGACAAAGCCCATGGCTTCTGTAAGCAAT	1105	Db	
ArgHisLeuTyrAspMetPro 506		487	Qy	
	GACGAGGAGGACGATGACGAGGAGGACGATGATTA	1078	Db	
eGluPheSe	ValGluLeuThrAspGlyIleLeuMetAspIleSerProIl	467	Qy	
 TGTTCCAGTGAGGAG 1077	GCTGATGAGGAGGAAGAAGCAAGAAGGACGAGTCGAGCTGTTCCAGTGAGGAG	1024	Db	
LeuGluProValIleGluThr 466		447	Qy	-
	:::	970	DЬ	
		427	Qy	
	0 CAGAAGGCTTTTAAAAACAAGGAAACGTTG	940	Db	
		407	Qy	
	5 TCTCCACTGATCGAGTCCACAGCAAATATGGAAAACAATCAACCA	895	Db	
GluAlaTyrAsnLeuGlnAla 406		387	Qy	
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:::::::: \GCAGATGAAGACATTTTGGGA 834	8 ACCGTCAACAAAGTGGGCCAAACAGCCTTTGATGTAGCAGATGAAGACATTTTGGGA	778	Db	
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  GACAATCTGTGTGATATGGAG 777	8 GCTCATTGGGGTAAAGAAGAAGCATGTCGGATTTTAGTGGAGAATCTGTGTGATATGGAG	718	Db	_
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DIGGACACCICTICATGCIGCA 717	8 CAGGCAGGCTATGATGTTAATATTAAAGATTATGATGGCTGGACACCTCTTCATGCTGCA	65	дь	_

IPMNAKDLEEALEMGVDWSLREGYAMAEDKEHCEEYGRMLQADPNKVSARAKKRGLPQ LGTLGAGNHYAEIQVVDEITEWGVVVMIHGGSRGLGHQVATDALVA MEKAMKROKLIVNNRQLALSSNASPEVDDYLKGMAAAGNIAWVNRSSMTFLTRQAFAK VFNTTPDDLDLHVIYDVSHNIAKVEQHVVDGKERTLLVHRKGSTRAFPHHPLIAVDY OLTGQPVLLGGTMGTCSYVLTGTEQGMTETFGTTCHGAGRALSRAKGRRNLDFQDVLD KLADMGIAIRVASPKLVMEEAPESYKNVTDVVNTCHDAGISKKAIKLRPIAVIKG" ORIGIN  Alignment Scores: 0.00579 Length: 2049 Score: 124.00 Matches: 113	/organism="Homo sapiens" /db_xref="taxon:9606" /clone="cpcCHQ01" /clone="cpcCHQ01" /cell_type="cd34+ stem cells" /tisue_type="blood" 911608 911608 /codon_start=1 /product="HSPC117" /protein_id="AsF29081.1" /db_xref="G1:6841456" /translation="MSRSYUBLOFTEKINKNCWRIKKGFVPNWQVEGVFYVNDALEK /translation="MSRSYUBLOFTEKINKNCWRIKKGFVPNWQVEGVFYVNDALEK LMFEELRNACRGGGVGFDINCGVRLLRTNLDESDVQPVKEQLAQAMFDHIPVGVGSKGV	JOURNAL Submitted (23-JUN-1999) Shanghai Institute of Hematology, Shanghai Second Medical University, Rui-Jin Hospital, 197 Rui-Jin Road II, Shanghai 200025, P. R. China FEATURES Location/Qualifiers source 12049	Unpubl 3 (ba Ye,M., Fan,H	JOURNAL Genome Res. 10 (10), 1546-1560 (2000)  MEDLINE 20499367  PUBMED 11042152  REFERENCE 2 (bases 1 to 2049)  AUTHORS Ye,M., Zhang,Q.H., Zhou,J., Shen,Y., Wu,X.Y., Guan,Z.Q., Wang,L.,  Fan,H.Y., Mao,Y.F., Dai,M., Huang,Q.H., Chen,S.J. and Chen,Z.  TITLE Human full length from class team calls	REFERENCE 1 (bases 1 to 2049)  AUTHORS Chang, O.H., Ye,M., Wu,X.Y., Ren,S.X., Zhao,M., Zhao,C.J., Fu,G., Shen,Y., Fan,H.Y., Lu,G., Zhong,M., Xu,X.R., Han,Z.G., Zhang,J.W.,  Tao,J., Huang,Q.H., Zhou,J., Hu,G.X., Gu,J., Chen,S.J. and Chen,Z.  TITLE Cloning and functional analysis of cDNAs with open reading frames for 300 previously undefined genes expressed in CD34+ hematopoietic	2049 bp mRNA linear ns HSPC117 mRNA, complete cds. GI:6841455	Qy 668 ThrLeuGluHisGluIleSerArgSerIleIleGlnAsnGlyGlyTrpAsnArg 685	Oy 651 GlnGlnGluValPheGlyHisSerThrAsnGlyPheAspLeuSerThrArg 667 :::::::    :::::: Db 1534 GAAGAGAAGGAGAACAGAGAGTCTTCAAGTTTGCGAACAAGTTACTTAC
AAGAGGCCTTCCT avalArgAlaLeu	### STATE OF THE PROPERTY OF T	Qy 310 GlyLysTyrGluThrLysLysAsnLeuIleGluAsnAlaSerAlaGluHisGlyTyrPhe 329	Qy 290 LysalaPheThrThrValAlaAspGluValProLeuILeuIleGlyAspValPheHisHis 309	265	Qy 227LeuAsnGlySerIleProArgLeuArgGlnThrAlaLeuValAlaAlaArgAla 244   :::::::::::::::::::::::::::::::::::	Db 118 CAGTTCTTGGAGAAGATCAATAAAAACTGCTGGAGATCAAGAAGGGCTTCGTGCCCAAC 177  Qy 191 SerGlnSerGlyGluThrSerAlaIleGlySerSerHisGlnLysThrGluProTyrAla 210	1466 (1-2049)  JLEUTYFALAAFGLEUPHEASNASP GIIII	Percent Similarity: 34.46% Conservative: 71 Best Local Similarity: 21.16% Mismatches: 204 Query Match: 2.62% Indels: 146 DB: 11 Gaps: 25

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/organism="Zea mays"
/cultivar="Illinois High Oil"
/db_xref="taxon:4577"
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                                 Bolotin, A., Ehrlich, S.D. and Sorokin, A. Studies of genomes of dairy bacteria Lactococcus lactis
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Lactococcus lactis subsp. cremoris
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/tissue_type="embryo"
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/lab_nost="E. coli SOLE"
/note="07gan: embryo; Vector: pBluescript SK; Site_1: XhoI
/SIte_2: EcoRI; Library was prepared by Statagene using
the Uni-ZAP XR system (Stratagene BN937328-12). Clones
were picked by a Q-bot after blue/white selection
(ampicillin resistance - use 100 micrograms/microliter).
Developed from a pool of equal amounts of RNA from
developing embryos sampled at 14, 21, 28 and 35 days after
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90. This closed strain has been selected for high oil
concentration for 90 generations and originates from the
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382 LysLeuProValLysArgGluLeuLeuGluGlnLeuLeuThrValAsnMetGlyGluAla 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                267 HisAspLeuGlyGluProValTyrIleAspTyrArgAlaValGluValArgGlyGluGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               287 AlaAspAspLysAlaPheThrThrValAlaAspGluValProLeuLeuIleGlyAspVal 306
                                                                                                                                                                                                                                                                                                                                                                                                                                 GCCGACGAAGCCTATATTGGGATTGACCAGCAGACAGATAAA------
                                                                                                                                                                                     ATTCCAGAAACTTATGGGACTTTAAGTGAGCTATCAGAGCTTGCAGCA-----TTT
                                                                                                                                                                                                                                           LeuProAspAsnThrAlaAspValSerLeuTleTyrAspThrGlyThrGlnTyrArgPhe 361
                                                                                                                                                                                                                                                                                                           AATTATGATCGACGTCAATTTTCTGATATTCAAAATCATTTGTCAGGAATCGCACTGGTT 2057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTGAATTAAAT-----TTTGAATGGCGGGGTTTGCCAGTT------
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                                                                                                                         AspGluValValPhePheThrIleAspProLysThrAsnGlnLeuThrThrAspProAsp 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTGGAAGGGGCTCTACGTTTAGGCTATAAAACGGTCGGAATTTGTGATGTGGGAAACCTC
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High quality sequence stop: 3867.
Location/Qualifiers
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Tel: 33 1 34 65 25 16
Fax: 33 1 34 65 25 21
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best homologue in strain IL1403 is
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/strain="MG1363"
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Db	2151	GRANCTANA 21	59
 Qy	402	LeuSerAsnAspLeuIleAlaThrArgTyrPheAsn 4	21
Db	2160	TITAATTTACCAACCCTTCCTTTTCCAGCAGTTCGTTATCTGAAT 2	204
 Qу	422	ProGluArgGluGlnIleGlnAsnAspGlnValSer 4	41
 Db	2205	2	225
 Qy	442	$Phe Glu Gln Ser Ser Ser Arg Thr Glu Pro Ala Gln Val Asp Glu Ser Thr Leu Glu \ 4$	61
 Db	2225	2	225
Qy	462	.uThrValGluLeuThrAspGlyIleLeuMetAspIleSerProIleGlu 4	81
Db	2226	GTGCGTGATGGGCTTTCCTTTGACGAAAGTTTGACG 2	276
 Qy	482	4	89
 Db	2277		336
 Qy	490	euTyrAsp 5	0.4
Db	2337	TTTCCGCAAGCACTGACAAATCTGTCAGTATTAACAGCAAAAATTGCTTATCAATTT 2	393
 Qy	505	e E	24
 Db	2394	GATGAAAATTGGAACTTCCGAGATTTGATAAGAAAAGGGAAGCAGTTGAA 2	2444
Qy	525	rGlu 5	44
Db	2445	CATCTTCGAGAAGAAGCGATTTTAGGACTGTCTGCTCGACTTGAAGAAAAAAAA	504
 Qy	545	AsnGluValIleAspLeuProGluArgThrAlaLeuAlaAsnArgLysThrProAlaAsp 5	64
 Db	2505	GAT	2564
Qy	565	ValTyrGln	73
 Db	2565	TTCACCAAATGGGATTT 2	624
 Qy	574	GlyGln 5	86
Db	2625	GTTGCGCTATGCGCGTGAACAAGACATTTAT 2	684
Qy	587	ر.	99
Db	2685	TGCGGAATGGGGCTGGGTCGGCTGCTTTGGTTTGCCTATGTTTTGGGAATCACT 2	744
Qy	600	σ	13
Db	2745	CAGGTTGACCCTGTCAAACATAATCTTTTCTTTGAACGTTTTTTGAACCCAGAACGAGTG 2	804
Qy	614	GlnAlaGlyAlaGluLeuArgLeuSerGluAspLysLysGlyValLysLeuTyrAla 6	32
Db	2805	K)	864
Qy	633	ThrLysProLeuSerHisProLeuAsnAspGlnLeuArgAlaThrLeuGly 64	9
 рь	2865	N	924
Qy	650	TyrGlnGlnGluValPheGlyHisSerThrAsnGlyPheAsp 66	ü
DЬ	2925	AAAAGACAGGCGCTCAGAGATGTCGGTAAAGCCTTTGGGATGACCGAAGCTGAATTATCT 29	84
Qy	664	LeuSerThrArgThrLeu 67	2
Db	2985	AAT 3	044
 νQ	673	IleSerArgSerIleIleGlnAsnGlyGlyTrpAsnArgThrTyrSerLeuArg 69	ŏ

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REMARK
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AUTHORS
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                                                                                    Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 24 Row: h Column: 21
This clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene prediction, Similarity but not identity to protein This clone has the following problem: incomplete processing.
                                                                                                                                                                                                                                                                                                                             Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genom
                                                                                                                                                                                                                        Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M. Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D. Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey
                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (25-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                    Web site: http://www.hgsc.bcm.tmc.edu/cdna/Contact: amg@bcm.tmc.edu
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                                                                                                                                                                                                                                                                                                      Center code: BCM-HGSC
                                                                                                                                                                                                                                                                                                                      Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg,R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               house mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 2582)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        musculus,
/map~"FVB/N"
/clone~"IMAGE:4188839'
                             /db_xref-"taxon:10090"
                                                                          Location/Qualifiers
                                            /organism-"Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GI:15029980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2582 bp mRNA
Similar to KIAA0244 protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone IMAGE:4188839,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Euteleostomi;
; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTC 07-AUG-2002
                                                                                                                                                                                                                                      Muzny, D.M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                768
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              859
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             AACAGTAGCCCGTTATTTAAGTTTCCAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LysAlaLys-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (1-919) \times BC011226
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117.50
34.21%
18.83%
2.49%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (1-2582)
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/tissue_type="Salivary gland,
/clone_lib="NCI_CGAP_SG2"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
1 482 c 620 g 597 t
                                                                                      10 week old female
                                                                                      mouse"
```

GlyGluValAspValIleIleHisAspLeuGlyGluProValTyrIleAspTyrArgAla GATTTTAGTACAAGTCAAAATGTCTTAGAGGACTCGCTGAAGAACATGCTCAGCGATAAG ---ValGluValArgGlyGluGlyAla-----AspAspLysAlaPheThrThrValAla GGTGAAGTGAACGTGCCATCTCCTGAGTTAGATTGTCCACTTCTCTCAGAGACTAGTGCT ValAlaAlaArgAlaValGlyTyrTyrAspIleAspLeuSerIleIleArgAsnSerIle TCAGCATCTTCAGTTGATTCTTCAGTGTCGTCTTGTGCTGGAATGAAGGAGGAGGCT---SerAlaMetAspLeuAsnGlySerIleProArg-----LeuArgGlnThrAlaLeu CCTAAGGAGAGTAGAAGGAGTGGCCGGCATGCTGAACAGATGGACGTGGCGCCAGAAGTC GCAACTCTAAGCACAAAAAAGCCATCTGGGAAGACCTTATCTACCTCTAAAGTAGGGGTG ATGGCACAAGAACAAGTAAGAAGTTTGCGACAAAGCACTATTGCCAAGCGTTCAAATGCA ---LeuTyrAlaArgLeuPheAsnAspGlyVal------AsnLysValProArgLeu GTTGTTAAAGAAAGTGGTAATGATACCATTGATGAAGAAGTAGATTTAACCTAACAGG CCCAATTTCCAGATGCCTTGTTCAACAGTTGTTGGTCTTGACGATATTATGGATGAAGGA 297 GATCCTATGCTAGGATCTGCAAGTAACCAGTTCTGTTTTGCCTGTTTTGGATAGCAATGAT AspMetSerValIleGluGluThrThrProLeuSerLeuGluGluLeuPheAlaGlnGlu 127 AspGluValProLeuLleGlyAspValPheHisHisGlyLysTyrGluThrLysLys AAGCCAGCAGAAAGATGTCAGGGTAAAGAAGAAGTTTATGCCTCACTGAAATCTGAACAC AGTTTGAGGGACAGAGTAGAAGACAATTCAGTAAGATCACCAAGAAAATCACCTCGTTTA SerThrGluMetGlyIleAsnProAsnAspTyr---IleProGluTyrGlnGlyGluGln SerSerHisGlnLysThrGluProTyrAlaAsnIleLys--------GlnSerGlyGlu-----ThrSerAlaIleGly------ProThrLeuGluProGluLysProGlyLeuIleLysArg -------AlaAlaLeuGluAspIleThrGlnGlu-------GAGTTTGATCCCAAACATGCATGCAATAATCAG -PheTyrGlnSerSer------Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: - AGAGAAGATGAGCAGAGT SerGluVal 183 151 296 279 747 259 239 657 597 477 417 858 714 222 537 213 200 191 357 167 177

661	lnGluValPheGlyHisSerThrAsnGly	Qy
1746	93 CCCCAGGATCAAAACACAATGCAGATTTCCAAACCTTTAACTCATACTCATAGT	DЬ
641	erGluAspLysLysGlyValLysLeuTyrAlaThrLysProLeuSerHisProLeuAsn	Qy
1692	(TTGAAAAGAATG	DЪ
621	AsnArgAspGlyTyrGlnAlaGlyAlaGluLeuArgLeu	Qy
1662	1633AGTTGTAATTCTGGAGTTAAATCTGTGAAA	DЬ
601	AspThrGlyThrArgLeuValThr	Qy
1632	1609 GGTGATAAGGTTTGGAAGAGTCAG	В
581	lProLeuTyrValPheValAlaSerAspLys	Qy
1608	49 TCTGATGAGCCGGAACCCCAGCCTGATTCTCAGAGGCCAGTCAAAGTGAGAAAAAAAA	DЬ
561	nGluValIleAspLeuProGluArgThrAlaLeuAlaAsnArgLysThr	Qy
1548	16 ACTAAATCTAATGTCAAGGCTGTGAAGCGAAAT	B 3
>	rT)ofouglybraTlocorbenbleVelaraleVelbleVelbrableTlofougranen	Ş
ion I	56 ATGACCACAGAGACACCCAGAAAAACTGTGGCAGCAAAGCATGAAGTAGGTCATAGCAAA	Db
521	Arq	Q
1455		DЬ
508	AlaLysAlaArgH1sLeuTyrAspMetProAspAsp	Qy
1395	ATTACTCAAAGTATTAAAATGGAAACAGCCAATCTTCAGGATGATAGAAGTGGT	DЬ
493	leGlnAspLysLeuAsn	Qy
1335	AAAGCAA	Db
476	2 ProVallleGluThrValGluLeuThrAspGlyIleLeuMetAsp	Qy
1275	GTGCTTTTGAA	Db
461	31nSerSerSerSerArgThrGluProAlaGlnValAspGluSerThrLeuGlu	Qy
1215	56 CAGAGAAATGAGTTGGAAACACTGGGCTATGGTGAGGACACGGAGTCTAATGATGCTCAG	DЬ
441	GluArgGluGlnIleGlnAsnAspGlnValSer	Qy
1155	GATATTGTTGATAAACCTGAGAACTCACCT	рь
430	eulleAlaThrArgTyrPheAsnMetValAsnThrGluIleValPhePro	γQ
1113	AATGAAGGGGCAGAATGTCATTTGGAATTG	В
410	luGlnLeuThrValAsnMetGlyGluAlaTyrAsnLeuGlnAlaValArgAlaLeu	Qy
1077	CCGAATCTTCTGATGTGTCTAGTGACTCTGCTTGTGCCAATAAAAATAAGGCA	Вр
390	spProAspLysLeuProValLysArgGluLeuLeu	Qy
1023	1021GAA	Db
370	leAsp	Qy
1020	GGTGACCAGACGGCCGAG	Db
350		Qy
966	31/ ASTIGULAGUE	DP GA
,	Acal cut   col	?

DE AC	BC BC	Qy Db	Db			Db	Qy	da Qy	ДĎ	Оу	Db	 0v	Db	0v	Db	Qy	Db
DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL REMARK COMMENT	RESULT 11 BC032205 LOCUS	800 2103	2050	790	760	1971	741	740 1911	1857	721	1808	701	1768	682	1767	662	1747
Mus musculus, clone IMAGE:5342620, mRNA.  BC032205  BC032205.1 GI:21618986  HTC.  house mouse.  Mus musculus  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom  Musmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; M  I (bases 1 to 2607)  Strausberg, R.  Direct Submission  Submitted (06-JUN-2002) National Institutes of Health, Mammalia  Gene Collection (MGC), Cancer Genomics Office, National Cancer  Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590  USA  NIH-MGC Project URL: http://mgc.nci.nih.gov  Contact: MGC help desk  Email: cgapbs-remail.nih.gov		PASDPheAsmHisValProTyrArgLeuArgPhePheAlaGly 814 :::	COLYSCEASIBLIGATION OF THE COLYSCEAS OF		aAsnMetAlaIleAlaArgAlaGlyIleSerGlyValTyrSerPheGlyAspAsnAlaTy 780	 		TGAGCATCTTAAGGAGGACGATAAACTGAAGCCAAGAAAACCTGATAGGAACCTGCAGCC 1970	TAGO	aLeuLeuAlaGlyValAlaValH1sLySThrValAlaAspAsnLeuValAsnProMet 740	ACTTGGTGCATTCCAGTCAAAAA-CAGAGCCAGAAGCCTCAGCAGCAGCC		GGCTTCTCTAAGGAGCCTCCCCATCCTGTACAAACTGGAC1807		1767	PheAspLeuSerThrArgThrLeuGluHisGluIleSerArgSerIleIleGlnAsnGly 681	GATAAGCTTCAT 1767

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 SerThrGluMetGlyTleAsnProAsnAspTyr---IleProGluTyrGlnGlyGluGln 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               137 GATTTTAGTACAAGTCAAAATGTCTTAGAGGACTCGCTGAAGAACATGCTCAGCGATAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108 AspMetSerValIleGluGluThrThrProLeuSerLeuGluGluLeuPheAlaGlnGlu 127
SerAlaMetAspLeuAsnGlySerIleProArg------LeuArgGlnThrAlaLeu 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProAsn----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GATCCTATGCTAGGATCTGCAAGTAACCAGTTCTGTTTTGCCTGTTTTGGATAGCAATGAT 256
                                                                  CCTAAGGAGAGTAGAAGGAGTGGCCGGCATGCTGAACAGATGGACGTGGCGCCAGAAGTC 676
                                                                                                                                                          AAGCCAGCAGAAAGATGTCAGGGTAAAGAAGAAGTTTATGCCTCACTGAAATCTGAACAC 616
                                                                                                                                                                                                                                               GCAACTCTAAGCACAAAAAAGCCCATCTGGGAAGACCTTATCTACCTCTAAAGTAGGGGGTG
                                                                                                                                                                                                                                                                                                                                     ATGGCACAAGAACAAGTAAGAAGTTTGCGACAAAGCACTATTGCCAAGCGTTCAAATGCA 496
                                                                                                                                                                                                                                                                                                                                                                                   LysAlaLys--
                                                                                                                                                                                                                                                                                                                                                                                                                          AGTTTGACCGACAGAGTAGAAGACAATTCAGTAAGATCACCAAGAAAATCACCTCGTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---LeuTyrAlaArgLeuPheAsnAspGlyVal-----AsnLysValProArgLeu 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTTGTTAAAGAAAGTGGTAATGATACCATTGATGAAGAAGAATTGATTTTACCTAACAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCCAATTTCCAGATGCCTTGTTCAACAGTTGTTGGTCTTGACGATATTATGGATGAAGGA 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 56 Row: o Column: 24
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, GenomeScan gene prediction
This clone has the following problem: frame shifted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Young, A., 2hang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    990
                                                                                                                                                                                      -SerSerHisGlnLysThrGluProTyrAlaAsnIleLys------
                                                                                                                                                                                                                                                                                         ------GlnSerGlyGlu-----ThrSerAlaIleGly---
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/note="Vector: pCMV
'aq c 628 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="Mammary tumor. C3(1)-Tag model. Infiltrating
ductal carcinoma. 5 month old virgin mouse."
/cione_lib="NCI_CGAP_Mam6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /map-"FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:5342620"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organisme"Mus musculus"
/db_xrefe"taxon:10090"
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117.50
34.21%
18.83%
2.49%
                                                                                                              ------AlaAlaLeuGluAspIleThrGlnGlu---
                                                                                                                                                                                                                                                                                                                                                                                ---PheTyrGlnSerSer-------
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Matches:
Conservative:
Mismatches:
Indels:
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158
129
262
291
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20 рь Qy

В οy Ъ δô В δÃ рь 20 В QY В ð В Ş

В

102/ 1230 1215A1GAGECEGGAACCCCAGCCIGATTC1CAGAGGCCAGTCAAAGTGAGAAAAAAAAAACAA 102/	
542 GluserGluAsnGluValIleAspLeuProGluArgThrAlaLeuAlaAsnArgLysThr 5	
⊳	
Oy 522 SerIleLeuGlyArgIleSerAspAlaValSerAlaValAlaArgAlaIleLeuProAsp 541	
Db 1475 ATGACCACAGAGACACCCAGAAAACTGTGGCAAAGCATGAAGTAGGTCATAGCAAA 1534	
Qy 509ArgValLeuAlaIleAsnHisAspAspGlyValAsnArg 521	
Db 1415 TTAGAGCCCAAAAACATAAAACCCAAACACATAAAATCTGTAAACTCATTCTAAACAAAGC 1474	
Qy 494 LeuValAlaAlaLysAlaArgHisLeuTyrAspMetProAspAsp 508	
Db 1355 TTGAATATTACTCAAAGTATTAAAATGGAAACAGCCAATCTTCAGGATGATGAGAAGTGGT 1414	
Qy 477IleSerProIleGluPheSerAlaSerAsnLeuIleGlnAspLysLeuAsn 493	
Db 1295 CCGGAAGCTAGCACTTTAGAAAATACTATTTGTGATGTTCTTGACCAAAATTCAAAGCAA 1354	
Qy 462 ProValIleGluThrValGluLeuThrAspGlyIleLeuMetAsp476	
Db 1235 TTACAGAGCACAGAGTTCAATAAGTCAGATTTGGAAGGTAATGCTTGTGCTTTTGAA 1294	
Qy 442 PheGluGlnSerSerSerSerArgThrGluProAlaGlnValAspGluSerThrLeuGlu 461	
Db 1175 CAGAGAAATGAGTTGGAAACACTGGGCTATGGTGAGGACACGGAGTCTAATGATGCTCAG 1234	
Qy 431 GluArg	
GGATAT	
Qy 411 SerAsnAspLeuIleAlaThrArgTyrPheAsnMetValAsnThrGluIleValPhePro 430	
Db 1097 GAAAAGAATGAAGGGGCAGAATGTCATTTGGAATTG 1132	
Qy 391 GluGlnLeuLeuThrValAsnMetGlyGluAlaTyrAsnLeuGlnAlaValArgAlaLeu 410	
Db 1043 CCCGAATCTTCTGATGTGTCTAGTGACTCTGCTTGTGCCAATAAAAATAAGGCA 1096	
Qy 371 ProLysThrAsnGlnLeuThrThrAspProAspLysLeuProValLysArgGluLeuLeu 390	
Db 1040GAA 1042	
Db 986 GATCAAGAATCAGAGGAGGTGAAGTTTCCCTGCGAAGGTGACCAGACGGCCGAG 1039	
Qy 334 LeuAspArgSerValAspValIleLeuProAspAsnThrAlaAspValSer 350	
Db 926 GATCTTGTTTCGGGTGAACTGAATGACACCATTGAAGGAAAGGATGCAGGGGGAAAACCT 985	
snLeuIleGluAsnAlaSerAlaGluHisGlyTyrPheAsp(	
Db 878 AACAGTAGCCCGTTATTTAAGTTTCCAGTTAGAGAAGATGAGCAGAGT 925	
Qy 297 AspGluValProLeuIleGlyAspValPheHisHisGlyLysTyrGluThrLysLys 316	
Db 827 AGTGTGGAAGAGAAGAACATTGAGGCTCTGATGGAATGTAAAGCTAAGACT 877	
Qy 280ValGluValArgGlyGluGlyAlaAspAspLysAlaPheThrThrValAla 296	
Db 767 GGTGAAGTGAACGTGCCATCTCCTGAGTTAGATTGTCCACTTCTCTCAGAGACTAGTGCT 826	
Qy 260 GlyGluValAspValIleIleHisAspLeuGlyGluProValTyrIleAspTyrArgAla 279	
Qy 240 ValAlaAlaArgAlaValGlyTyrTyrAspIleAspLeuSerIleIleArgAsnSerIle 259	
bb 6// TCAGCATCTTCAGTTGATTCTTCAGTGTCTTGTGCTGGAATGAAGGAGGAT 733	

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                                                                                                                                                                                                                                                                                                                                                                                                                          TCGCCAAAGGAGAAGCAGCCGAAGTTTTTCTCTGGATGAGCCTCCATTGTTCATCCCAGA
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                                                                                                                                                                                                                                                 AAGCAAGCAATGTGGGTTTTGCAAAAAACCACATGGCAACAGGTTTATGGTCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGCTGTGGGGAAGGGCAGTAGCCAT-----GTGAAGGATGAGCATGACCATCCAGTCAG 1929
Strausberg,R.
Direct Submission
Submitted (06-JUN-2002) National Institutes of Health,
                                                          Eukaryota: Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                     Homo sapiens
                                                                                                                                BC032614
BC032614.1
                                                                                                                                                            Homo sapiens, :
IMAGE:5557263,
                                                                                                                                                                                          BC032614
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                                                                                                                                                                                                                                                                                                         AAAGAAGGGTCAGATCAGACCACCTCAATTGAAAGCAAATATATGTGGACTCC
                                                                                                                                 GI:21595728
                                                                                                                                                                           Similar to
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                                                                                                                                                              mRNA.
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5 interacting
                                                          Craniata; Vertebrata;
Catarrhini; Hominidae;
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                 SerLeuGluGluLeuPheAlaGlnGluSerThrGluMetGly
                                                                          Gln---
                                                                                                     CGCGTTTCCGAGAGGGTGTCCTTAGAAGACCAAAGTCCGGGGATGGCGGCAGAGGGGGAC 1317
                                                                                                                      GlnAlaLeuAspValValAsnPheAspAspGlnSerPro---IleSerArgIleGlyGlu 100
                                              CAGCTCAGCCTGCCTCCCCAAGGG-----ACCTCAGACGGCCCTGAGGACACCCC---
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Percent Similarity:
Best Local Similarity:
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CCCGCCCCGCCACTGCCTGCGAAGAAGAACCTTCCC-----ACTGCCCCTCCCAGACGC 125
                                                                                                                                                                                                                                                                                              ProLeuMetThrSerGlnAlaLeuAlaGlnGlnAsnAsnProAlaAsnIleIleAsnHis
                                                                                                                              GGCCCCCTCAGGGAGGAAGCGATGAAGCCAGGGGGCAGCCTCCAGTCCCTTGCAGCAGGTC 1203
                                                                                                                                                                                    ValProAlaHisAspThrAlaIleAsnGlnAlaLysAlaGlyAsnProProValLeuLeu 61
                                                                                                                                                                                                                                                             CCCATGATGACCTGCGAGAGACTC----
                                                               ThrProGluGlnIleGlnAlaArgLeuAsnAlaAlaGlyLeuAsnAlaLysProGlnSer 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clone distribution: MGC clone distribution information can be fount through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 69 Row: m Column: 12
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 13376344
This clone has the following problem: frame shifted.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Akhter, N., Ayele, K., Beckström-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Guptta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripo, S., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.
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Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing Center (NISC), Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tissue Procurement: ATCC/DCTD/DTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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/note="Vector: pC
1000 c 805
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/tissue_type="Skin, melanotic
/clone_lib="NIH_MGC_72"
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SerProProLeuGlyLeuAspMetSerValIleGluGluThrThrProLeu 118

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2169		DЬ
468	59 ThrLeuGluProValIleGluThrValGlu	Qγ
2109	AAGGCCCTGGTGGACCCCGCCTGCACTCCGAGGAG	Db
458	.ValSerPheGluGlnSerSerSerSerArgThrGluProAlaGlnValAspGluSer	Qy
2073	2062AGCACCGAGCTC	DЬ
438	rPheAsnMetValAsnThrGluIleValPheProGluArgGluGlnIleGlnAsnAsp	Qy
2061	AGAGCTACCTGCAG	DЪ
418	GluAlaTyrAsnLeuGlnAlaValArgAlaLeuSerAsnAspLeuIleAlaThrArg	Qy
2043	ATTCGCACCATGATGACCCAGCTC	В
398	pLysLeuProValLysArgGluLeuLeuGluGlnLeuLeuThrValAsnMet	δÃ
1998	CCTGGTGCAGGACTACAAGGTGTACAGCCTGGAGATGATGGCGCGCCAGACCTCC	Ъ
378	ArgPheAspGluValValPhePheThrIleAspProLysThrAsnGlnLeuThrThr	Qy
1941	GTGGAGCTGGCGCAGGACAAGGGCTCGTACTTTGGC	ф
359	eLeuProAspAsnThrAlaAspValSerLeuIleTyrAspThrGlyThrGlnTyr	9
1905	-CACGCTTTCCTCTCCAACAACCGCAAGCTGTACAAGAAGGTG	Db
340	AlaGluHisGlyTyrPheAspGlyArgTrpLeuAspArgSerValAspVal	Q
1863	10 ATCCTGGGCAAGGCTCGGCACCGGCTGAGCTTTGCCAGTTTTCAGCAGCATGTTC	DЬ
321	lleGlyAspValPheHisHisGlyLysTyrGluThrLysLysAsnLeuIleGluAsn	Qy
1809	AGGAGGAGCTGGAGCAGTTCAGCAGCCCCAGCGTGAAGAAGAAGACCCCTCCATG	DЬ
301	spLysAlaPheThrThrValAlaAspGluValProLeu	Qy
1749	TCATGGCCACCGACCAGGACTCCTACTCCACCAGC	В
281	spValIleIleHisAspLeuGlyGluProValTyrIleAspTyrArgAlaValGlu	9
1707		рь
261	spIleAspLeuSerIleIleArgAsnSerIleGlyGlu	Оу
1680	1654 CAGAGCTCTCCAGAGTTCAAGGGCTCC	DЪ
241	luSerAlaMetAspLeuAsnGlySerIleProArgLeuArgGlnThrAlaLeuValAla	ОУ
1653	IGCCCAGGCCACTGCCCATTCC	Db
221	isGlnLysThrGluProTyrAlaAsnIleLysAlaAlaLeuGluAspIleThrGln	οy
1620	CCCACGCCGGGTCCACCCAGAGAGGGCCAAAGCCCTGCTTCTCAGGCTGGGACT	Ъ
201	luThrSerAlaIleGlySer	Qy
1560	CCAGCTCCCTTAGAGAACGCTGAGCTCTGCACACAGGCGATGGCCTTG	Db
194	<pre>lproArgLeuLysAlaLysPheTyrGlnSerSerGlnSerGly</pre>	Qy
1512	GAAAAAACGGATCTCTCGACAACTGGCCTCGACCCTC	Db
174	roThrLeuGluProGluLysProGlyLeuIleLysArgLeuTyrAlaArgLeuPheAsn	Qy
4	GCCAGCGATCCTCACAGCATGCCAGAGCTGCCCAGGACAGCCAAACAACCC	В
154	AspTyrIleProGluTyrGlnGlyGluGlnProAsnSerGluValValValPro	Qy
1407	CGGGAGAGCACGGAGCAAGGCCAGGACACAGAGGTGAAA	рь

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Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Erika Asamizu
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Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design
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/clone_lib="Maize Mapping Project/DuPont Cornsensus
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   LeuPheAlaGlnGluSerThrGluMetGlyIleAsnProAsnAspTyrIleProGluTyr
                                                                                                              CAGCAGCGCCAGGAACCTGCTCCGTTGTCCAACGAGTGTCCCGTAGTTTCGTCACCCACT
                                                                                                                                                                                                                        GlnAlaArgLeuAsnAlaAlaGlyLeuAsnAlaLysProGlnSerGlnAlaLeuAspVal 86
                                                                                                                                                                                                                                                            AGCAGT - - - AGCAGTAGCAACTGCTCACTGCCCACCAATGTGGTTAATCCTATGCAACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                          MetProValAlaLeuAlaAlaTyrLeuProLeuMetThrSer----
                                         CCTCCGAAACCTGTTGAACAGCCTATAATCCATCAAATGACTAGCGCCAGTGTGTCCAAG
                                                                        ProProLeuGlyLeuAspMetSerValIleGluGluThrThrProLeuSerLeuGluGlu
                                                                                                                                               ValAsnPheAspAspGlnSerProIleSerArg------IleGlyGluGlnSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      melanogaster cDNA clone FBgn0003862 PID:g158818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: 394 row: D column: 9
High quality sequence stop: 543.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lawrence Berkeley National Labone Cyclotron Rd, Berkeley, CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Stapleton, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST
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pOT2 "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note- "Organ: embryo; Vector: pOT2; Site_1: EcoRI; XhoI; Sized fractionated cDNAs were directly ligat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="LD39445"
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/sex-"male and female"
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Strausberg, R.
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Strausberg, R.
Strausberg, R.

Direct Submission
Submitted (05-MAR-2002) National Institutes of Health, Mammallan
Submitted (05-MAR-2002) National Cancer
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Gene Collection (MGC), Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. CO
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 passed the following selection criteria: GenomeScan gene prediction
This clone has the following problem: frame shifted.
    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 42 Row: c Column: 5
This clone was selected for full length sequencing because it
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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BC025329
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                                                                                                                                                                                                                                                                                   /lab_host="DH10B-R"
/note="Vector: pOTB7"
696 c 759 g
                                                                                                                                                                                                                                                                                                                                                      /tissue_type="Muscle, rhabdomyosarcoma"
/clone_lib="NIH_MGC_17"
                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:4111278"
                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
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                                                                                                                                                                                                                           TTTTCTTGGCAATCCTATG------
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                                                                                                             -GGGCTTTTGAATGATGTTTCT----
- AATGTCGGGGGCCTCATCAGAAATGTTACACACGGAGTATCAAACTCTGC
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Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Baxter, E., Berman, B., Carlson, J., Champe, M., Chavez, C., Chew, M., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Miranda, A., Misra, S., Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Celniker, S., and Rubin, G.M.

BDGP/HHMI AT Drosophila EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BE491509 678 bp mRNA linear EST 19-AL AT28265.5prime AT Drosophila melanogaster adult testes poTB7 Drosophila melanogaster cDNA clone AT28265.5 similar to trx: FBann0008651 'transcription factor' located on: 3R 88B5-88B6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu hit genomic AE003704: arm:3R [10017332,10237903] estimated-cyto:8885-88C4: 04/09/2001 plate: AT.282 row: F column: 5 High quality sequence stop: 640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      One Cyclotron Rd, Fax: 510 486 6798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Stapleton, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2000)
On Dec 6, 2000 this sequence version replaced gi:11574810
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One Cyclotron Rd, Berkeley, CA 94720,
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                                                                                                                                                                                                                                                                                                                     /dev_stage="0-3 day old Ore-R males"
/lab_host="plates AT.10-AT.120: DH5-alpha. Plates
AT.121-AT.319: DH5-alpha TonA"
/note="Organ: ADULT testes; Vector: pOTB7; Site_1: EcoRI;
Site_2: Xho1; The mRNA for the testis library was made
from testes and seminal vessicles hand dissected from 6-3
                                                                                                                                                                                                                         Margaret Fuller. Sized fractionated cDNAs
ligated into pOTB7. Plasmid cDNA library
1 178 c 166 g 133 t
                                                                                                                                                                                                                                                                                                     day old Ore-R males. RNA kindly provided by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Drosophila melanogaster'
/db_xref="taxon:7227"
/clone="AT28265"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="male"
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NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalon@bcm.tmc.edu.
                                                                                                                                                                                                                                  Direct Submission
Submitted (27-AUG-2001) National Institutes of Health, Mammalian Submitted (27-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1673 bp
Homo sapiens, clone IMAGE:4153638,
BC013085
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A.M., Holloway, M., Te
Muzny, D.M., Gibbs, R.A.
                      Villaion, D.K., Luna, R.A., Hale, S.M., Hulyk, A.M., Holloway, M., Telford, B, Hodgson, A., Bo
                        Bouck,
                                            s.
                   Lu, X., Garcia,
, J., Yu, W.,
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through the I.M.A.G.E. Consortium/LLNL at: http://iseries: IRAK Plate: 19 Row: d Column: 10 This clone was selected for full length sequencing passed the following selection criteria: Hexamer franklysis Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 19 Row: d Column: 10 trequency ORF because it

552 clone has the following problem: incomplete processing Location/Qualifiers b 1p/19q Toss"NCI\_CGAP\_Brn67"
/clone\_lib="NCI\_CGAP\_Brn67"
/lab\_host="DH10B"
/note="Vector: pCMV-SPORT6"
/note="Vector: 427 g 353 t /clone="IMAGE:4153638" /tissue\_type="Brain, anaplastic /organism="Homo sapiens" /db\_xref="taxon:9606" .1673 oligodendroglioma with

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US-09-914-168-2 (1-919) x BC013085 Best Local Similarity: Percent Similarity: 0.197 110.00 34.53% 19.15% 2.33% (1-1673)Length:
Matches:
Conservative:
Mismatches: Gaps: Indels:

	) 214 100 2 (1 313) X BC013003 (1-10/3)	
Qy	31 GlnGlnAsnAsnProAlaAsnIleIleAsnHisValProAla 44	
В	296 GAAAAATCTGAGAAGGAAACTATTATGGCTCACCAGCCGACTGATGTGGAGTCCACTTTA 355	
Qy	45AsnGlnAlaLysAlaGly 55	
Db	:::         356 TTGCAGTTGCAGGAACAGAATACTGCCATCCGTGAAGAACTCAACCAGCTGAAAAAATGAA 415	
Qy	56 AsnProProValLeuLeuThrProGluGlnIleGlnAlaArgLeuAsnAlaAlaGlyLeu 75	
В	416 AACAGAATGTTAAAGGACAGGTTGAATGCATTGGGCTTT 454	
Qy	76 AsnAlaLysProGlnSerGlnAlaLeuAspValValAsnPheAspAsp 91	
Db	455 TCCCTAGAGCAGAGGTTAGACAATTCTGAAAAACTGTTTGGCTATCAGTCC 505	
Qу	92 GlnSerProIleSerArgIleGlyGluGlnSerProProLeuGlyLeuAspMetSerVal 111	
Db	506 CTGAGCCCAGAAATCACCCCTGGTAACCAGAGCGATGGAGGAAGGA	
Qy	112 IleGluGluThrThrProLeuSerLeuGluGluLeuPheAlaGlnGluSerThrGlu 130	
дb	566 GTGGAAGGCTCTGCCCCTGGCTCAGTGGAGGATCTCTTGAGTCAGGATGAAAATACACTA 625	
Qy	131 MetGlyIleAsnProAsnAspTyrIleProGluTyrGlnGlyGluGlnProAsnSerGlu 150	
Db	626 ATGGACCATCAGCACAGTAACTCCATGGACAATTTAGACAGTGAGTGCAGTGAG 679	
Qy	151 ValValValProProThrLeuGluProGluLysproGlyLeuTleLysArg 167	
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Db	737 TCGGAAGGCATCCCCCAGCATAGAGCGCTCCCGG	
Qy	188 TyrclnSerSerGlnSerGlyGluThrSerAlaIleGlySerSer 202	
DЬ	770AAGGGGAGCAGCGGGAATGCCAGTGAAGTGTCCGTGGCTTGCCTGACTGA	

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1513	90 TTGGCTAGTAGCTTGCAGGAAGAT	Db 14	
502	83 SerAlaSerAsnLeuIleGlnAspLysLeuAsnLeuValAlaAlaLysAlaArgHisLeu        :::    :::	Qy 4	Ω
1489	### CTCCTGGAGAGTGTCAGGCTG	Db 14	В
482	63 VallleGluThrValGluLeuThrAspGlyIleLeuMetAspIleSerProIleGluPhe	Qy 4	0
1447	88 CAGAAAGTGGCAGAGCTGTATTCTATCCATAACTCTGGAGACAAATCTGATATTCAGGAC	Db 13	
462	50 ThrGluProAlaGlnValAspGluSerThrLeuGluPro	Oy 4	۵
1387	28 ACAGTGGCCAGTGACCAGATAGAGATGAATCGCCTGAAGGCTCAGCTGGAGAATGAAAAG	13	-
449	34 GlnIleGlnAsnAspGlnValSerPheGluGlnSerSerSerSerArg	Oy 4	0
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433	28 ValPheProGluArgGlu	Qy 4	Ω
1267	20 GAAATGATAGGGGAGCGAAGAAGGAGTCACCATATGGAGCGAATT	Db 12	0
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1159	45GAGCAGCTTCTTGGT	11	
394	76 LeuThrThrAspProAspLysLeuProValLysArgGluLeuLeuGluGlnLeuLeu	Оу з	۵
1144	33CGTTTTGAACGG	Db 11	
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355	36 ArgSerValAspValIleLeuProAspAsnThrAlaAspValSerLeuIleTyrAspThr	Оу з	Ø
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1066		Db 10	0
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л	6 AspTvrArqAlaValGluValArqGlvGluGlvAlaAspAspTvsAlaPheThrThrVal	<b>N</b>	0
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275	56 ArgAsnSerIleGlyGluValAspValIleIleHisAspLeuGlyGluProValTyrIle	Qy 2	۵
964	44 GAAGAAGGTTATTCTGATG	Db 9	0
255	${\tt 36~GlnThrAlaLeuValAlaAlaArgAlaValGlyTyrTyrAspIleAspLeuSerIleIle}\\$	Qy 2	O
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erAsnLe        CCGCCT	uThrva	erSerSe :    CGTTCAG	AY104509 (1		/note-"this sequence assemblies resulting contigs to seed DuPon assembled by DuPont overgo addressing of Mapping Project" 418 g	/organism="Zea mays" /db_xref="MaizeDb:636() /db_xref="taxon:4577" /clone="pc0104742" /clone="bc0104742" /clone_lib="Maize Mapu	Qualif	2002) MO 6	1)	ey,M., ect/Du	noliop noliop , Andr	07587	mRNA	rGlnSe ::: TGAAAA	AATTGA	uValīl	pAlaVa     ::  TGCCAT
SerAsnLeuIleGlnAsp         AGCCGCCTGAGTAGCGGC	lGluLeu -AGGAC	rSerArg      CTCAGCT	1-1501)	Length Matche Conser Mismat Indels Gaps:	uence i lting f lting f DuPont Pont as pof E	mays" DB:636055" :4577" 42" ze Mapping	iers	Maize N		Morgar Pont Co	Eukaryota; virioipiantae; strep Spermatophyta; Magnoliophyta; L clade; Panicoidaae; Andropogone 1 (bases 1 to 1501)	!	1501 bp sequence	LysThrProAlaAspValTyrGlnSerLysLys     :::   ::: :::         AATTAAGATCAGACCTGGATGAAAAAAAAAAAAAAA	HIIIII	eAspLeu	lSerAla :::: TGCTAAC
SerAlaSerAsnLeuIleGlnAspLysLeuAsnLeuValAlaAlaLys 	ThrLeuGluProValIleGluThrValGluLeuThrAspGlyIleLeuMetAspIleSe	erSerSerArgThrGluProAlaGlnValAspGl 		Length: Matches: Conservativ Mismatches: Indels: Gaps:	/notce this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for overgo addressing of BACs in conjunction with the Mapping Project 418 g 286 t	055" ping Pro	Š	lapping ISA		Hainey, C.F., Dolan, M., Mido, G.H., Vogel, J.M., Whitsite Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.Vr Maize Mapping Project/DuPont Consensus Sequences for D Overgo Probes	Streptophyta; Em yta; Liliopsida; ppogoneae; Zea.		mRNA	570 1669		ProGlu	IleLeuGlyArgIleSerAspAlaValSerAlaValAlaArgAla     ::       ::::     ATCGATTACAGGATGCCATTGCTAAGGTAGAGGATGAATACCGAGGC
LeuAsni	GlyIleI      GGGTCG/	ProAlac :::  ATTTCGC		e: 533	of a pe appli e appli gs; thi of a cc conjur	Project/DuPont		Projec		and Tir	ida; Embr ida; Po a.		NA 1		р	ArgThr₽	GATGAAI
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Sh
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Gen
Center, Stanford University School of Medicine, Stanford, CA
Web site: http://www-shgc.stanford.edu i
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and My
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                                                                                                                                                                                                                                                                                                                                                                          clone distribution: MGC clone distribution information can be four through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov series: IRAK Plate: 32 Row: b Column: 11 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4557314 This clone has the following problem: frame shifted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (01-FEB-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                                                                                                                                                             /lab_host="DH10B"
/note="Vector: pBluescript"
445 c 472 g 463 t
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/clone_lib="NIH_MGC_96"
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/clone="IMAGE:4792831"
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619	rLysPheGluHisAsnLeuIleAsnArgAspGlyTyrGlnAlaG	600	Qy
	AAGAACTAGAAAAAAAAA	879	Db
599	pLysProArgAspGlyGlnIleGlyLeuGlyTrpGlySerAspThr	580	γ
878	AGGTGTTAGTATCCAAGCAAAATTCCATCATT	834	В
579	hrProAlaAspValTyrGlnSerLysLysValProLeuTyrValPheValAlaS	560	Qy
ū		00	Db
559	rGluAsnGluValIleAspLeuProGluArg'	540	γQ
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539	SerIleLeuGlyArqIleSerAspAlaValSerAlaValAlaArqAlaIle	522	γo
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501	AlaTleAsnHisAspAspGlvValAspArg	512	Ŷ
511 665	TCAGACC	498 609	Оу
808	ACCAGACGGCTGTGATGATAGAAATAGGGACAAACCTGTTGAACCAAACAGCCG	549	Db
497	GlnAspLysLeuAsnLeuValAlaAla	489	Qy
548	66-1	498	B 2
497	TGCTGGAGAACATCATGGAAAACAACACTCAGTGGCTAATGAAGCTTGAGAATT	n u	) F
468	ThrLeuGluProValIleGluThrValGlu	5	Qy
437	GTGTCCAATGCTGTGCAGAGGGACGCGCCGCTCGAATAAGATGACTCGGTGCAGAGGCTG	378	DЬ
458	GluGlnSerSerSerArgThrGluProAlaGlnValAspGluSer	443	Оу
377	TGCAGCTACACTTTCCTCCTGCCAGAGATGGACAACTGCCGCTCTTCCTCGAGCCCCTAC	318	Db
442	ValAsnThrGluIleValPheProGluArqGluGlnIleGlnAsnAspGlnValSerPhe	423	ργ
317	AACTTTCGGAAGAGCATGGACAGCATAGGAAAGAAGCAATATCAGGTCCAGCATGGGTCC	258	Db
422	ValArgAlaLeuSerAsnAspLeuIleAlaThrArgTyrPheAsnMet;	407	Qy
257		228	Ъ
406	ArgGluLeuLeuGluGlnLeuLeuThrValAsnMetGlyGluAlaTyrAsnLeuGlnAla	387	Qy
227	TTTACTCTGAGC	216	DЬ
386	PheThrIleAspProLysThrAsnGlnLeuThrThrAspProAspLysLeuProValLys	367	οy
215	CTAAGCTGCTGTTTATTACTGAAGAAAGAATGTGGCAGATTGTTTTC	168	DЬ
366	AlaAspValSerLeuIleTyrAspThrGlyThrGlnTyrArgPheAspGluValValPhe	347	Qy
167	43	108	Db
346	GlyArgTrpLeuAspArgSerValAspValIleLeuProAspAsnThr	331	Qγ
107	11 LYSTYTGLUTTICLYSLYSASTICULTEGLIASTIALAGCIUHISGLYTYTPINGASP	54	B 5
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 AspGlnLeuArgAlaThrLeuGlyTyrGlnGlnGluValPheGlyHisSerThrAsnGly
                                                                                                     CCCCAAACAGGGGAACAAGACCCTCAAGATGGCCCGCAAGACCAACATCAACATCAGCT
                                                                                                                                   {\tt AsnLeuIleAsnArgAspGlyTyrGlnAlaGlyAlaGluLeuArgLeuSerGluAspLys}
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Mammalia; Eutheria; Primates; Catarrhini;
1 (bases 1 to 758)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Tissue Procurement: DCTD/DTP/Gazdar
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/tissue_type="large cell carcinoma"
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/lab_host="Organ: lung; Vector: pCMV-SPORT6; Si
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US-09-914-168-2 (1-919) x BH770729 (1-1557)  Qy 181 ProArgLeuLysAlaLysPheTyrGlnSerSerGlnSerGlyGluThrSerAlaIleGly 200	Alignment Scores: 0.696 Length: 1557 Pred. No.: 105.00 Matches: 135 Score: 105.00 Matches: 135 Percent Similarity: 29.24% Conservative: 70 Best Local Similarity: 19.26% Mismatches: 200 Query Match: 2.22% Indels: 296 DB: 17 Gaps: 34	rce		E SE SM	RESULT 23 BH770729/C BH770729 BH770729 DEFINITION LLMGtag478 MG1363 Random Sequence Tag Library Lactococcus lactis subsp. cremoris genomic, DNA sequence. ACCESSION BH770729 VERSION BH770729.1 GI:20373686 VERSION GSS.	Db 514 AGAAGCCCGÁGCACACCGGTATGCCACTCGGGGGGGCAAACGGG 570  Qy 682 GlyTrpAsnArgThrTyrSerLeuArgTyrArgLeuAspLysLeuLysThr 698	QY 662 PheAspLeuSerThrArgThrLeuGluHisGluIleSerArgSerIleIleGlnAsnGly 681
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                                                                                                                                                                  1021 bp DNA line clone BAOAB004F03 of library BAOAB from strain Kluyveromyces lactis, genomic survey commat425271
                                        Kluyveromyces lactis
Eukaryota; Fung1; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales;
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AL425271.1 GI:12208465
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                    Souciet, J.L.,
   Bolotin-Fukuhara
                                                                                                           Kluyveromyces lactis.
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 Aigle,M., Artiguenave,F., B
mra,M., Bon,E., Brottier,P.,
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2 rue Gaston Cremieux, CP 5706, 91057 EWRY cedex, FRANCE. (E-mail:
seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic Inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.

Location/Qualifiers
AlaSerAsnLeuTleGlnAspLysLeuAsnLeuValAlaAlaLysAlaArgHisLeuTyr
                                                                                       CAAGAAGTGGTTCCTGAAAATGATGGC----
                                                                                                                                       IleGluThrValGluLeuThrAspGlyIleLeuMetAspIleSerProIleGluPheSer 483
                                                                                                                                                                                                               AGTAACAATAAATCAAAGTCTGCTGGTTCAGCAAAAGATGTCAAGGCTACAGAGCCAGTC
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Duchateau-Nguyen,G., Lemaire,M., Marmeisse,R., Montrocher,R.,
Robert,C., Termier,M., Wincker,P. and Wesolowski-Louvel,M.
Genomic exploration of the hemiascomycetous yeasts: 11.
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FEBS Lett. 487 (1), 3-12 (2000)
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/note="similar to Saccharomyces cerevisiae ORF YOR216c
/RUD3; suppressor of uso1-1 transport defect ]"
/evidence=not_experimental
/evidence=184 g 372 t 1 others
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/clone="BA0AB004F03"
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/strain≃"CLIB 210"
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                                                                       Contact: Maier, U. G.
Department of Cell Biology and Applied Botany
Philipps-University Marburg
Karl-von-Frisch-Strasse, D-35043 Marburg, Gerr
Tel: ++49 6421 282 2057
Fax: ++49 6421 282 1543
                                                                                                                                                           Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia 1 (bases 1 to 1364) Fraunholz, M., Duebel, J., Wastl, J., Zauner, S. and Mais EST Database of the cryptomonad alga: Guillardia thei
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/organism="Guillardia theta"
/strain="CCMP327"
/db_xref="taxon:55529"
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/lab_host="SOLR"
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Homo sapiens, clone IMAGE:3607338,
BC019335
BC019335.1 GI:17939559
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 18 Row: f Column: 1
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4758689
This clone has the following problem: frame shifted.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Lettlicia Hislao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
Info@bcgsc.bc.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (13-DEC-2001) National Institutes of Health, Mammaliar Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1867)
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/clone_lib="NIH_MGC_44"
/lab_host="DH10B.R"
/note="Vector: pOTB7"
/note="Vector: pOTB7" 292 t
                                                                                                                                                                                                                                                                                                                                                                      /organisme"Homo sapiens"
/db_xref="taxon:9606"
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Shevchenko,Y., Wetherby.K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Zhang,L.-H. and Green,E.D.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortiv
DNA Sequencing by: National Institutes of Health
Sequencing Center (NISC),
Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 1876)
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Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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/clone_lib="NHH_MGC_20"
/lab_host="DH10B-R"
/note="Vector: pOTB7"
/note="Vector: 561 g 292 t
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Indels:
GCTCCGTCTCCGCGGACA - - - GAGCGCGCG
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418 1082	tGlyGluAlaTyrAsnLeuGlnAlaValArgAlaLeuSerAsnAspLeuTleAlaThrAr:	398 1040
398 1039	oAspLysLeuProValLysArgGluLeuLeuGluGlnLeuLeuThrValAsnMe 	380 983
380 982	eAspProLysThrAsnGlnLeuThrThrAspPr :::	369 923
369 922	1	364 863
364 862	AlaAspvalSerLeuIleTyrAspThrGlyThrGln     	344 843
842		827
4	GluHisGlyTyrPheAspGlyArgTrpLeuAspArgSerValAspValIleLeuProA	Ν
324 826	PValPheHisHisGlyLysTyrGluThrLysLysAsnLeuIleGluAsnAlaSerAl::: :::           GCTGGCTGAATCTAGGCGGCAGTACGAAGAGAAAAACAAAGAATTTGAAAGGGAAAAAACA	305 767
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290 706	uProValTyrIleAspTyrArgAlaValGluValArgGlyGluGlyAlaAspAspLys	271 660
271 659	IleArgAsnSerTleGlyGluValAspValIleTleHisAspLeuGlyGl	255 620
25 <b>4</b> 619	uValalaA1aArgAlaValG1yTyrTyrAspIleAspLeuSerIle	239 563
239 562	7 5	220 503
220 502	ySerSerHisGlnLysThrGluProTyrAlaAsnIleLysAlaAlaLeuGluAspIleTh	200 452
200 451	-ProArgLeuLysAlaLysPheTyrGlnSerSerGlnSerGlyGluThrSerAlaIleGl	181 392
180 391	GlyLeuIleLysArgLeuTyrAlaArgLeuPheAsnAspGly-ValAsnLysVal	163 350
162 349	GlnGlyGluGlnProAsnSerGluValValValProProThrLeuGluProGluLysPro	143 317
142 316	LeuPheAlaGlnGluSerThrGluMetGlyIleAsnProAsnAspTyrIleProGluTyr	123 284
122 283	ProProLeuGlyLeuAspMetSerValIleGluGluThrThrProLeuSerLeuGluGluIIIII	103 240

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TCAGGAAGCGACAGGTCCAAGTACA 1763	1739	Db
nGlnGluValPheGlyHisSerThr 659	651	Qy
GGACGAGAAACCAATCAAGACAGAAGTTCCTGGTTCTCCAGCAGGAACTGAGGGCAACTG 173	1679	Db
sProLeuAsnAspGlnLeuArgAlaThrI	631	Qy
::: GAAGAAACAG	1658	Db
GlyTyrGlnAla	611	Qy
::	1644	Db
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a	571	Qy
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rGluAsnGlu 554	543	Qy
:: :::	1433	Db
eLeuGlyArgIleSerAspAlaValSerAlaValAlaArgAlaIleLeuProAspGluSe 543	523	Qy
:::        :::          :::	1373	Db
AsnHisAspAspGlyValAsnArgSerIl 523	514	Qу
TGGGTGCACCAGATGACA	1313	DЬ
sAlaArgHisLeu	496	Qy
	1302	Db
inLeu	476	Qy
GGAACAGGTTCAAAGCCAAATTCTTGAGAGCAGTTCTCTCCCTGAA 1301	1256	Дb
pGluSerThrLeuGluProValIleGluThrValGluLeuThrAspGlyIleLeuMetAs 476	456	Qy
CCAGAAATCCTCTGAAGACACTGCCCCATTCCTAGGAACCTTAGCAGGTGCTACCTATGA 125	1196	Db
SerSerSerSerArgThrGluPro	443	Qy
	1136	Db
GlnVal	437	Qγ
AATGTGGGGAAAAGAGAAATCTTGCACAATACTGAGAAAGAA	1083	Db
nThrGluIleValPhe	418	Qy

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TITLE
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                sProSerGlnGluAlaLeuLeuAlaGly-----
                                                                                                                       CTCCCCTGTCAAGCCCGCCTGCAACGTTTGGCCCTGCAAGGGACTCCGTGGACTTGGTTC
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                                                   ACGCCCTCCCGTCGGATCCACAGAAATGCCGATGGTCCGGGCCACCTTCTATGGTGAATT
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High quality sequence stop: (
Location/Qualifiers
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
http://image.llnl.gov
Plate: LLAM11008 row: h column: 14
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Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, I
cDNA Library Arrayed by: Incyte Genomics, Inc.
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Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/db_xref="taxon:9606"
/clone="IMAGE:4991293"
/clone=lib="NIH_MGC_10"
/cell_line="MGC36"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: No Site_2: SalI; Cloned unidirectionally. Primer: Oligo Average insert size 1.5 kb. Library prepared by Life Technologies."

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	AUTHORS	PUBMED REFERENCE	JOURNAL MEDLINE	TITLE		AUTHOR	MEDLINE PUBMED	JOURNAL	TITLE	REFERENCE AUTHORS	MEDLINE	JOURNAL	REFERENCE AUTHORS		4	$\mathbf{s}$				RESULT 29 AK013402	Db 93	Оу 790	Db 147	Qy 770	189	Qy 750	Db 234	Оу 732	Db 294
Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casawant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,	Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,	11076861	sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000) 20530913	Chazaki, Y. Muramatsu, M. Jroue, Y. Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system384-format	Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,	Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,	E 20499374 11042159	covery of ne	Hayashizaki ected cDNAs	, Shibata,K.	10349636	High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999)	Hayashizaki,Y.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	<pre>clone_lib:RIKEN full-length enriched mouse cDNA library clone:2810473H05. Mis_misculls</pre>	HTC; CAP trapper. Mus musculus (strain:C57BL/6J) 10, 11 days embryo cDNA to mRNA,	AK013402 AK013402.1 GI:12850738	PHOSPHOACETYLGLUCOSAMINE MUTASE (EC 5.4.2.3) (PAGM) (ACETYLGLUCOSAMINE PHOSPHOMUTASE) (N-ACETYLGLUCOSAMINE-PHOSPHATE MUTASE), full insert sequence.	Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2810473H05:homolog to	2- TAN- 200	CACGCGCCGCTGCCAGTCCTTGTGGAAGTGGGGCTTCAAGACCATGCCATTCCGGCTG 36	yGlyIleGlnAlaGlyTyrIleTrpSerAspAsnPheAsnHisValProTyrArgLeu 809	TACAGGGCCAG	Ası	::::::       :::::: ACGCGGGGCAGCGGGCTGATTGCG	uValGlySerSerGlyLeuValSerAspAlaAsnMetAlaIleAlaArgAlaGlyIleSe 770	GGTA	Met	GCCGGCCAACCCTGAGCTCCTCGCAGGCTGAAAGCCGCGGCGGCGCGCGC

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                                                                                                                                                                                                                                                                                                                                                                                                                        Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., BrownStein, M., Bult, C., Carnincl, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Salto, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Schrimi, L., Shibata, K., Shibata, Y., Shinagawa, A., Takahashi, F., Tanaka, T., Tayami, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tajima, Y., Toya, T., Yamamura, T., Yamanaka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
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                                                                                                                                                                                                                                                 /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:2810473H05"
/db_xref="NGD:MGI:1905665"
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                                                                                                                        /notes"data source:SPTR, source key:095394, homolog to PHOSPHOACETYLGLUCOSAMINE MUTASE (PAGM) (ACETYLGLUCOSAMINE PHOSPHOMUTASE)
                                                                                                                                                                                              /clone_lib="RIKEN full-length enriched
/dev_stage="10, 11 days embryo"
                                                                                                                                                                                                                                  /clone-"2810473H05"
                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
/translation="MDLEAVCKRSALHAKPQGLILQYGTAGFRTNAQHLDHIMFRMGL
                                                                                          putative,
                                                                       /codon_start=1
                                                                                                           (N-ACETYLGLUCOSAMINE-PHOSPHATE MUTASE)
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660 TCCAAGGCTTTCGTAGACCTTACGAATCAGGTTTCC---TGCAGTGGAGATGTAAAGAGG
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                                               AspLysAlaPheThrThrValAlaAspGluValProLeuLeuIleGlyAspValPheHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeuAsnGlySerIleProArgLeuArgGlnThrAla---LeuValAlaAlaArgAlaVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     {\tt GluProTyrAlaAsnIleLysAlaAlaLeuGluAspIleThrGlnGluSerAlaMetAsp}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTGGCCCCTTCCTGGGAGGAGCATGCCACCTGTCTGGCCAGTGCGGAGGAGCAG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SerGlu-----ValValValProProThrLeuGluProGluLysProGlyLeuIleLys 166
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                                                                                                                                                                                                                                                                                                                               AGGCCCAGCAGTGAGAAACTTTCA-----CAATCTGTGATAGATGGCGTGACTGTTTTA 539
                                                                                                                                                                                                                          GGAGGTCAATTCCATGATTACGGCCTGTTGACGACACCTCAGTTGCACTACATGGTGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -------GACGTGCGGCAAGTGCTTGCTGCCATCGTGGAGAAAGAAGCTGTGGAT
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                                                                                                             TGCCGGAATTCCGGAGGCCGGTATGGACAGGCCACCGTAGAAGGCTACTGCCAGAAGCTC
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RQVLAAIVEKEAVDLTOTAFVVI ARDTRRSSEKLSGVI LDGVTVLGGOFHDYGLLTTP
QLHYMYCRNSGGRYGQATVEGYCQKLSKAFVDLTNUSQSSDVKRSVKVDCANGIGA
LKLREMEHYFSRGLSVLLENDGTOGRLNHLCGADFVKSOQKPPQGIEMKSGERCCSFD
GDADRIYYYYCDADGHFHLIDGDKIATLISSFLKELLLEIGESVLGVVQTAYANGSS
TRYLEEVNKVPVYCTKTGVKHLHHKAQEFDIGVYFEANGHTALFSEAVEVKIKRAQ
ELDDGKGKAARTLASIIDLFNQAAGDAISDMLVYEAILALKGLTVQQWDAIYVDLPNR
QLKVKNADRRVLSTTDAERQAYTPPGLQEAINDLVKKYTLARAFVRPSGTEDIVRVYA
                                                                                                                                                                  -----ArgAlaValGluValArgGlyGluGly------AlaAsp
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35.21%
20.51%
2.16%
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Oy 547 ValileAspLeuProGluArgThrAlaLeuAla 557	477 IleSerProIleGluPheSerAlaSerAsnLeuI	413 ASPLEUIIEALAThrArgTyrPheAsnMetValAsnThrGluIleValPheProGluArg :::	Db 801	309 HisGlyLysTyrGluThrLysLysAsnLeu
AAAAGGTTTCATCCGAAAAACAAT lupheSerAlaSerAsn	47 411 83 428 137 448 191 191	ignment Scores:  ed. No.:  101.50  Matches:  reent Similarity:  44.518  Conservative:  30  st Local Similarity:  27.178  Mismatches:  17  Gaps:  10-9-914-168-2 (1-919) x AZ927049 (1-513)  372 LysThrAsnGlnLeuThrThrAspProAspLysLeuProValLysArgGluLeuLeuGlu  372 LysThrAsnGlnLeuThrThrAspProAspLysLeuProValLysArgGluLeuLeuGlu  373 LysThrAsnGlnLeuThrThrAspProAspLysLeuProValLysArgGluLeuLeuGlu  374 LysThrAsnGlnLeuThrThrAspProAspLysLeuProValLysArgGluLeuLeuGlu  375 AAAAATAAAAGCACCAAAAAGCAAGATGAAGTCATTGAA  376 GlnLeuLeuThrValAsnMetGlyGluAlaTyrAsnLeuGlnAlaValArgAlaLeu  377 LysThrAspLeuLeuThrVal	COMMENT Contract: Johnston M Contract: Johnston M Department of Genetics Washington University Medical School Washington University Medical School Box 88232, 4566 Scott Ave., St. Louis, MO 63110, USA Tel: 314 362 2735 Fax: 314 362 7855 Email: m]@genetics.wustl.edu Class: random plasmid subclone. Location/Qualifiers 1.513 /organism="Saccharomyces castellii" /strain="NRRL Y-12630" /clone="476.dis16c05.s1" /clone="476.dis16c05.s1" /clone="476.dis16c05.s1" /clone="A76.dis16c05.s1" /clone="Random genomic sequence" BASE COUNT 181 a 102 c 90 g 140 t	Saccharomyce Eukaryota; F Saccharomyce 1 (bases 1 Cliften, P.F. W.R. Water Surveying Sa comparative

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REMARK
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                                                                                                         US-09-914-168-2 (1-919) x BC028159 (1-2340)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
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                                                                                                                                                                                                             Best Local Similarity:
                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                        Score:
                                                                                                                                                                                                                                                                                                                    Alignment Scores:
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  858
                                                                                                                                                                                       Match:
                           84 LeuAspValValAsnPheAspAspGlnSerProIleSerArgIleGlyGluGlnSerPro 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           K NIH MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CONA Library Preparation: Life Technologies, Inc.
Sequencing Center (NISC),
Galthersburg, Maryland;
Galthersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nigri.nih.gov/
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Masseri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J.,
Pearson,R., Stentripop,S., Thomas,P.J., Touchman,J.M., Tsurgeon,C.,
Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A.,
CTGGATCACCTGAAT-----AGCAGTCCAGAGCTGGGAGCTGGAGACCAAAGCTCC 908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCCGCCAACAGAATTCTGTCA---AACCATCATCAGGGA 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Serles: IRAK Plate: 62 Row: 1 Column: 15
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, GenomeScan gene prediction
This clone has the following problem: frame shifted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens, Similar to KIAA0076 gene product, clone IMAGE:5240443, mRNA. BC028159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (08-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2340)
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                                                                                                                                                                                                                                                                                                                                                                                                     519
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/db_xref="taxon:9606"
/clone="IMAGE:5240443"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="Brain, fetal,
/clone_lib="NIH_MGC_121"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pCMV-SPORT6"
631 c 721 g 469 t
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101.00
32.90%
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420	AlaTyrAsnLeuGlnAlaValArgAlaLeuSerAsnAspLeuIleAlaThrArgTyrPhe	401	Ф
1769		1710	
400	2LysLeuProValLysArgGluLeuLeuGluGlnLeuLeuThrValAsnMetGlyGlu ::::::	382	Qy
1709		1653	Db
381 1652	ProLysThrAsnGlnLeuThrThrAspProAsp	371 1593	Оу
370	7 ThrGlnTyrArgPheAspGluValValPhePheThrIleAsp	357	Qy
1592		1533	Db
356	ServalAspVallleLeuProAspAsnThrAlaAspValSerLeuIleTyrAspThrGly	337	dd
1532		1479	Vo
336	AsnLeuIleGluAsnAlaSerAlaGluHisGlyTyrPheAspGlyArgTrpLeuAspArg	317	Qy
1478		1443	Db
316	GluValProLeuLeuIleGlyAspValPheHisHisGlyLysTyrGluThrLysLys	298	Qy
1442		1410	Db
297 1409	ValGluValArgGlyGluGlyAlaAspAspLysAlaPheThrThrValAlaAsp::::   :::   :::	280 1350	Оу
279	GlyGluValAspValIleIleHisAspLeuGlyGluProValTyrIleAspTyrArgAla	260	Qy
1349		1290	Db
259 1289	ValAlaAlaArgAlaValGlyTyrTyrAspIleAspLeuSerIleIleArgAsnSerIle	240 1278	Qy
239	ThrGlnGluSerAlaMetAspLeuAsnGlySerIleProArgLeuArgGlnThrAlaLeu ::	220	Qy
1277		1236	Db
219 1235	SerSerHisGlnLysThrGluProTyrAlaAsnIleLysAlaAlaLeuGluAspIle	201 1179	ФУ
200 1178	ProArgLeuLysAlaLysPheTyrGlnSerSerGlnSerGlyGluThrSerAlaIleGly	181 1137	Qy
180 1136	LysProGlyLeuIleLysArgLeuTyrAlaArgLeuPheAsnAspGlyValAsnLysVal:::	161 1122	Qy
160	ValValProGluProGlu	152	Qy
1121		1062	Db
151 1061	GlyIleAsnProAsnAspTyrIleProGluTyrGlnGlyGluGlnProAsnSerGluVal	132 1029	Qy
131	IleGluGluThrThrProLeuSerLeuGluGluLeuPheAlaGlnGluSerThrGluMet :::         :::         :::           :::	112	Qy
1028		969	Db
111	ProLeuGlyLeuAspMetSerVal	104	Qy
968		909	Db

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VERSION
KEYWORDS
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AK011769
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Wis musculus 10 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2610044J23:transformed mouse 3T3 cell double minute 1, full insert sequence.
Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Hazada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                     Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning
                                                                                                                                                                                                                                                                                                                                                                                         Carninci, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (strain:C57BL/6J) 10 days embryo cDNA to mRNA clone_lib:RIKEN full-length enriched mouse cDNA library
                                                                                                                                                                                                                                                                                                                                                       Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                      Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hune, D., Imotani, K., Ishi, Y., Itoh, M., Izawa, M., Kasukawa, T., Kotan, Y., Kojana, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Kurihara, C., R., Sakai, Y., Oka, C., Quackenbush, J., Salto, H., Salto, R., Sakai, K., Sano, H., Sasaki, D., Schriml, L., Shibata, K., Shibata, Y., Shipagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamanaka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC) RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama
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Please visit our web site (http://genome.gsc.riken.go.jp/)
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Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
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                                                      rAlaMetAspLeuAsnGlySerIle---ProArg------LeuArgGlnThrAl 238
                                                                                                                                                                                        sGlnLysThrGluProTyrAlaAsnIleLysAlaAlaLeuGluAspIleThrGlnGluSe 223
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/dev_stage="10 days embryo"
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KEYWORDS
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                                             /Clone="CS0DI032Y008"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6: Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive
                                                                                                                                                              /organism="Homo sapiens"
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lPheHisHisGlyLysTyrGlu----
                                                                                                TGAACAGCTGGGAGAAGATGTATAT--
                                                                                                                                                              -----AAGACCAGCTTGGCCAGCCTCTTTGCAGGGAAGCAAGAGAGGGACCTCCA
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                                                              yAlaAspAspLysAlaPheThrThrValAlaAspGluValProLeuLeuIleGlyAspVa
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Clemson University Genomics
Clemson University
100 Jordan Hall, Clemson, SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Development of a genetically and physically anchored EST resource for barley genomics: Morex unstressed seedling root cDNA library Unpublished (2001)
On Nov 16, 2000 this sequence version replaced ai:11185208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 800)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D.,
,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton
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800 bp mRNA linear EST 22-OCT-2001 HVSMEf0008L17f Hordeum vulgare seedling root EST library HVcDNA0007 (Etiolated and unstressed) Hordeum vulgare cDNA clone
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                                                           with water, nystatin and cefotaxime in covered crystallization dishes. Five-day old seedling roots were then harvested, total RNA was prepared, poly(A) RNA was purified, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids. These steps were performed in the TJ Close laboratory at the University of California. Riverside (Choi, Close, Fencon). Phagemids were plated and placed at the Clemson University Genomics Institute (CUGI)
                                                                                                                                                                                                                      /note-"Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1; Seeds were surface sterilized then germinated under axenic conditions in the dark at room temperature on filter paper
                                                                                                                                                                                                                                                                                                             /clone-"HVSMEf0008L17f"
/clone_lib-"Hordeum vulgare seedling
HVcDNA0007 (Etiolated and unstressed)
            preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oat
                                                                                                                                                                                                                                                                             /tissue_type="Seedling root"
/lab_host="TJC121"
                                                                                                                                                                                                                                                                                                                                                                /cultivar="Morex"
/db_xref="taxon:4513"
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                                                                                                                                                                                                                                                                       {\tt ArgLeuArgGlnThrAlaLeuValAlaAlaArgAlaValGlyTyrTyrAspIleAspLeu}
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	Alignment Scores:  1.37  Pred. No.:  10.00  Matches:  67  Score:  96  Conservative:  47  Best Local Similarity:  21.90%  Mismatches:  96  Query Match:  96  Gaps:  1041  Conservative:  47  Mismatches:  96  Gaps:  16	Alignment Pred. No.: Score: Score: Percent Si Best Local Query Matc	Alignm Pred. Score: Percen Best L Query DB:
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	/Lissue_type="neuropidsComma ceris" /lab_host="mul10B" /lab_host="mul10B" /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6		
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	GCGGCGGAAGGGGAC 25	39	Db
	LeuLeuIleGlyAsp 305	301	Qy
	GCGAACTGGCCGTCGGAGGTCGTCGACGACGTCCTGGACAAAGTGGCCGTGGCCTGTGAG 40	99	Db
	LysalaPheThrThr	286	Qy
		159	Db .
	HisAspLeuGlyGluProValTyrIleAspTyrArgAlaValGluValArgGlyGlu 285	267	Qy

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Meth. Enzymol. 303, 19-44 (1999)
                                   Submitted (18-AUG-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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100.00
32.41%
19.50%
2.12%
                                                                -----CACCAGCAGGGCCACAGAACT-----
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323 1456	304 GlyAspValPheHisHisGlyLysTyrGluThrLysLysAsnLeuIleGluAsnAlaSer :::	Ор
303 1405	286GlyAlaAspAspLysAlaPheThrThrValAlaAspGluValProLeuLeuIle	Qy Db
285 1345	278 ArgAlaValGluValArgGlyGlu	Db Qy
277 1285	LeuGlyGluProValTyr1leAspTyr :::         3TTGGTGAGCCCGAGTTCCACTACATCGCAGGGGCC	Db
260 1240 ·	241 AlaAlaArgAlaValGlyTyrTyrAspIleAspLeuSerIleIleArgAsnSerIleGly ::: ::	Db Qy
1189	TTGATGAAGGTTGTCAATGAAATGTGCCCCCAATATTACCAGGATTTACAACATTGGCAAA	Db 4
<u> </u>	:::       0 GAGATGACCACCACGGATGACCTGGATTTTAAGCACCACAACTATAAGGAAATGCGCCAG	g g
1069		OV D
231	231	Qy
231 1009	214 AlaAlaLeuGluAspIleThrGlnGluSerAlaMetAspLeuAsnGlySerIle	d dy
213 952	202SerHisGlnLysThrGluProTyrAlaAsnIleLys ::: ::	Db Qy
892		Db
0	86 LysPheTyrGlnSerSerGlnSerGlyGluThrSerAlaIleGlySer	Qy
185 832	172 LeuPheAsnAspGlyValAsnLysValProArgLeuLysAla :::	D Q
171 772	152 ValValProProThrLeuGluProGluLysProGlyLeuIleLysArgLeuTyrAlaArg :::	Дb
151 718	132 GlyIleAsnProAsnAspTyrIleProGluTyrGlnGlyGluGlnProAsnSerGluVal	D Qy
131 667	125 AlaGInGluSerThrGluMet	Db Qy
12 <b>4</b> 607	allleGluGluThrThrProLeuSerLeuGluGluLeuPhe                 :::::   GAAACATTAAAAATCACAGACTTCCAGCTGCAT	Db Qy
104 565	88 AsnPheAspAspGlnSerProIleSerArgIleGlyGluGlnSerProPro	дь Q <b>y</b>
87 505	71 AsnAlaAlaGlyLeuAsnAlaLysProGlnSerGlnAlaLeuAspValVal	gb dy
445	386 CCCAAGAAGGCCATCAAGCCCCAAGAAGGCTCCCAAGAGGGAGAAGTTAGTT	Dъ

uSerGluaspLysLysGlyValLysLeuTyrAlaThrLysProLeuSerHigPro 639	621 LeuS    : 2318 CTGG	Оy
GCTATGATATGGGAGCTACTCGGTGTGACTTCACCCTCACAAAGACCAA	67	Db
snArgAspGlyTyrGlnAlaGlyAlaGluLeuArg 620	609 AsnA	Qy
AGAACTGCATGGTT2	34	DЬ
lySerAspThrGlyThrArgLeuValThrLysPheGluHisAsnLeuIle 6	589 LeuG	Qy
TGAACCCTGGCGAATATGTGGTCACAGCCAAGGCGGAA 2233	2195 CTGA	рь
sLysValProLeuTyrValPheValAlaSerAspLysProArgAspGlydInIleGly 588	569 Lysi	Qy
AGCGATGGGGL	2162	Db
pLeuProGluArgThrAlaLeuAlaAsnArgLysThrProAlaAspValTyrGl	549 AspL	Qy
TTACAAGGGAAAGGGATTTCAAATGCTGTCATCTCTGTGGAAGGTGTTAACCATGACATC 2161	2102 TTAC	Дb
avalSerAlaValAlaArgAlaIleLeuProAspGluSerGluAsnGluValIle 548	530 Alav	Оу
GAGTCTCTGATTGTGTTCATGGAGCAGGTTCATCGAGGCATCAAAGGCATAGTGAGAGAT 2101	2042 GAGT	Db
lLeuAlaIleAsnHisAspAspGlyValAsnArgSerIleLeuGlyArgIleSerAsp 529	510 ValL	Qy
ATAACCG	1982 GTGG	Db
AAlaLysAlaArgHisLeuTyrAspMetProAspAsp	494 LeuV	Qy
CTAAACGATTTCAGCTACCTCCATACAAACTGCTTTGAGCTGTCCATCTAC 1981	1931 CTAA	Db
rolleGlu	474 LeuM	Qy
CAGAAGGAGGAGGCACCGTCAATGGGGCTTCCTGGCACACAGTGGCTGGAAGT 1930	1877 CAGA	Db
spGluSerThrLeuGluProValIleGl	454 GlnV	Оу
:   :::      CTCCACTCACCGCCTCATGACAGATGCCAGGAGGCGAGTGTG	1817 GCCT	Db
rSerSerSerArg	ers	Qy
CCAGGAGCACACCCAACACCTGATGATCATGTTTCCGCTGGCTG	1757 ACCC	ф
ProGluArgGluGlnIleGlnAsnAspGlnValSerI	429 Phep	Оу
ACAGGGGGTGAGCTGGTGGCATACCCCTATGACATGGTGCGGTCCCTGTGGAAG 1756	1697 CTAC	ДĎ
-LeuSerAsnAspLeuIleAlaThrA	410L	Qy
:::	1637 ACAG	Db
Asc	402 TyrA	Qy
GTCCCCAACCACTACATTGCCATCCCTGAGTGGTTTCTGTCTG	1577 GTCC	Db
gGluLeuLeuGluGlnLeuLeuThrValAsnMetGly(	383 Leup	Ωу
		Db
lvalPhePheThrIleAspProLysThrAsnGlnLeuThrThrAspProAsp	363 GluVa	Qy
AACAACTTTCCGGATTTAAACTCGCTGCTCTGGGAGGCAGAGGACCAG 1558	1511 AACA	DЬ
pasnThralaaspValSerLeuIleTyrAspThrGlyThrGlnTyrArgPheAsp 362	344 AspA	Qy
GAGTTGGGAGGCTGGTCCCTGGGACGTTGGACCCATGATGGCATCGATATCAAC 1510	1457 GAGT	DЪ
aGluHisGlyTyrPheAspGlyArgTrpLeuAspArgSerValAspValIleLeuPro 343	324 AlaG	Qy

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RESULT 37
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                                                                                                                                                                                                                                                                                                                    158
                                       116
392 ACTAGCGCCAGTGTGTCCAAGTGCTATGCCCAAAAGTCAACA--
                                                                                                                    98
                                                                                                                                                                                              80
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                                                                                                                                                                                                                                                                                                                                                                                                                                    23 LeuMetThrSerGlnAlaLeuAlaGlnGlnAsnAsnProAlaAsnIleIleAsnHisVal 42
                                                                                                                                                                                                                                                                                                                                                      ProAlaHisAspThrAlaIleAsnGlnAlaLysAlaGlyAsn------ProProVal 59
                                     ThrProLeuSerLeuGluGluLeuPheAlaGlnGluSerThrGluMetGlyIleAsnPro 135
                                                                            CCCGTAGTTCCGTCACCCCACTCCTCCGAAACCTGTTGAACAGCCTATAATCCATCAAATG
                                                                                                                                                         ACAAATCGGGTACTACCGATGCAGCAGCGCCAGGAACCTGCTCCGTTGTCCAACGAGTGT
                                                                                                                                                                                              GlnSerGlnAlaLeuAspValValAsnPheAspAspGlnSerProIleSerArg-----
                                                                                                                                                                                                                                        GTGGTTAATCCTATGCAACAACAAGCACCGTCAACCACCAGCAGCTCCACAACCAGGCCT
                                                                                                                                                                                                                                                                           {\tt LeuLeuThrProGluGlnIleGlnAlaArgLeuAsnAlaAlaGlyLeuAsnAlaLysProblem} \\
                                                                                                                                                                                                                                                                                                                  -----CATTTCTCCACAAGCAGCAGCAGTAGCAGTAGCAACTGCCTCACTGCCCACCAAT
                                                                                                                                                                                                                                                                                                                                                                                                 GTRATGGAACCTCAAGCWTTGGAGCAGCAG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : Bp 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)

By 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CNS013XL 969 bp DNA linear GSS 26-JUL-1999 Drosophila melanogaster genome survey sequence SP6 end of BAC BACN10705 of DrosBAC library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                               ---IleGlyGluGlnSerProProLeuGlyLeuAspMetSerValIleGluGluThr 115
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/note="end : SP6"
243 c 222 g
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/clone="BACN10105"
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/db_xref-"taxon:7227"
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                              245 ValGlyTyrTyrAspIleAspLeuSerIleIleArgAsn-----
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CTTGGTGCACGGTCTATTTCAACTCAAATCGTGAGGAACCGGATGAAGAGTGTCAGGAAT
                                                                                                                                                        ---ThrGluProTyrAlaAsnIleLysAlaAlaLeuGluAspIleThrGlnGluSerAla
                                                                                                                                                                                                                           SerGlyGluThrSerAlaIleGlySerSerHisGlnLys-------
                                                                                            MetAspLeuAsnGlySerIleProArgLeuArgGlnThrAlaLeuValAlaAlaArgAla 244
                                                                                                                              TCCACCGTCCCCAACCCGTCTCTGGCGGCCGCTTCCTCTGCGGTGACGCGATCCTCCGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (25-APR-2002) Maize Mapping Project, University Missouri, Columbia, MO 65211, USA
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Mapping Project"
3 323 c 371 g 368 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="MaizeDB:634674"
/db_xref="taxon:4577"
/clone="pC0083558"
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AK002434  LOCUS  AK002434  AK002434  AK002434  DEFINITION  Mus musculus adult male kidney cDNA, RIKEN full-length enriched library, clone:0610009009:DNA segment, Chr 15, Wayne State University 77, expressed, full insert sequence.  ACCESSION  AK002434  VERSION  AK002434  AK002434.1 GI:12832416	Qy 527 IleSerAspAlaValSerAlaValAla 535	Qy 507 AspAspArgValLeuAlaIleAsnHisAspAspGlyValAsnArgSerIleLeuGlyArg 526	Qy 487 LeuIleGlnAspLysLeuAsnLeuValAlaAlaLysAlaArgHisLeuTyrAspMetPro 506 ::: :::::::::::::::::::::::::::::::::	Qy 477 IleSerProIleGluPheSer	Qy 457 GluSerThrLeuGluProVallleGluThrValGluLeuThrAspGlyIleLeuMetAsp 476	Qy 437 AsnAspGlnValAsrPheGluGlnSerSerSerSerargThrGluProAlaGlnValAsp 456 ::: :::   :::    :::     ::: Db 749 TCCCCCGAGGTTGCAGAAAAAGAATCAGAAGCTGGTGGGAAGATGGGTGACCTAGAT 805	Qy 419TyrPheAsnMetValAsnThrGluIleValPheProGluArgGluGlnIleGln 436	Oy 405 GlnAlaValArgAlaLeuSerAsnAspLeuIle	Qy 385 VallysArgGluLeuLeuGluGlnLeuLeuThrValAsnMetGlyGluAlaTyrAsnLeu 404	Qy 380 ProAspLys	Qy 360 ArgPheAspGluValValPhePheThrIleAspProLysThrAsnGlnLeuThrThrAsp 379 ::: ::::::::::::::::::::::::::::::::	Qy 340 ValileLeuProAspAsnThrAlaAspValSerLeuIleTyrAspThrGlyThrGlnTyr 359	Qy 320 GluAsnAlaSerAlaGluHisGlyTyrPheAspGlyArgTrpLeuAspArgSerValAsp 339 :::::::	Qy 300 ProLeuLeuIleGlyAspValPheHisHisGlyLysTyrGluThrLysLysAsnLeuIle 319	Qy 282 ValArgGlyGlyGlyAlaAspAspLysAlaPheThrThrValAlaAspGluVal 299	QY 262 ValaspValIleIleHisAspLeuGlyGluProValTyrIleAspTyrArgAlaValGlu 281 :::
		REFERENCE AUTHORS	TITLE JOURNAL						TITLE JOURNAL MEDITOR		REFERENCE	JOURNAL MEDLINE	REFERENCE	TITLE TOURNAL MEDLINE PUBMED	REFERENCE	KEYWORDS SOURCE ORGANISM
Karco, H., Kawa Kurihara, C., Numazaki, R., Saito, H., Sai Schriml, L., S Sogabe, Y., Su Tanaka, T., Te Yasunishi, A.,	Carninci,P., Hara,A., Haya	11217851 5 (bases 1 t Adachi,J., Ai	and Hayashiza Functional ar Nature 409 (6 21085660	Ring, B., Ring Sato, K., Scho Toyo-oka, K., Wynshaw-Boris	Carninci, P., Fletcher, C., Hofmann, M., F	Kuehl,P., Lew Quackenbush,J Wagner,L., Wa	Aizawa,K., Iz Aizawa,K., Iz Saito,T., Oka Kadota,K., Ma	11076861 4 Kawai,J., Shi	RIKEN integra sequencing pi Genome Res. 1 20530913	Yamamoto,R., Fujiwake,S., Yoneda,Y., Is	3 Shibata,K., I Konno,H., Aki Komi,N., Ishi	prepare full- Genome Res. 1 20499374	2 Carninci, P., Itoh, M., Konn	High-efficien Meth. Enzymol 99279253	Eukaryota; Me Mammalia; Eut 1	HTC; CAP trap Mus musculus clone_lib:RIK clone:0610009 Mus musculus

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AUTHORS

Carninci, P. and Haywakinaki, Y.

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Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage-"adult"
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/strain⊷"C57BL/6J"
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/db_xref="GI:12832417"
/db_xref="MGD:MGI:106312"
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/db_xref="MGD:MGI:1909738"
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970	TCCGCAACACCCGGAATGAGATTGCGGAGATGAACCGC	911	Db
675	snGlyPheAspLeuSerThrArgThrLeuGluHisGluIleSerArg	659	Qy
910		851	Db
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656	erHisProLeuAsnAspGlnLeuArgAlaThrLeuGlyTyrGlnGlnGluValPheGly	637	Qy
790	GTGCTGTCCATGGACAACAGCCGC	731	ф
636	luLeuArgLeuSerGluAspLysLysGlyValLysLeuTyrAlaThrLysProLeu	617	Qy
730	CTCAAGACCCTTCACGAGACAGAGTTA	704	Db
616	isAsnLeuIleAsnArgAspGlyTyrGlnAlaGly	597	Qу
703	GCCAAGGCGGACAGTCTGCAGGATGAGATCAACTTC	668	Db
596	lyGlnIleGlyLeuGlyTrpGlySerAspThrGly	577	Qy
667	CACGAACAAGGTGGAGTTGGAG	623	Db
576	1Phe	557	40
622	TGTGTTGCTG	593	Db
556	roGluArgThrAlaLeu	537	Qy
592	GAGGAGATCAACCGACGC	575	Db
536	erIleLeuGlyArgIleSerAspAlaValSerAlaValAlaArg	517	Qy
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516	lLeuAlaIleAsnHisAsp	497	Qy
520	GAG 5	518	Db
496	IleSerProIleGluPheSerAlaSerAsnLeuIleGlnAspLysLeuAsnLeuValAla 4	477	Qy
517	ceccre s	467	Db
476	GluSerThrLeuGluProValIleGluThrValGluLeuThrAspGlyIleLeuMetAsp 4	457	Qy
166	CAGGAACAGAAGTCAGCCAAGAGCAGCCAGCTTCCCCCGAATCTTTGAGGCTCAGATT 4	410	Db
156	spGlnValSerPheGluGlnSerSerSerSerArgThrGluProAlaGlnValAsp 4	437	Qy
601	ACCAAGTGGGCGCTGCTG 4	392	Db
136	heAsnMetValAsnThrGluIleValPheProGluArgGluGlnIleGln 4	417	Qy
391	AACAGCAGAACAAGATGCTGGAG	332	Db
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                                                                                                                                                                                                                                                                                                                                                       Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@lmage.llnl.gov) for further information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1996)
Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dub
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 1022)
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4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               house mouse
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                                                                             the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of
                                                 double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into
                                                                                                                                                                                                              /db_xref="taxon:10090
/clone="IMAGE:338008"
                                                                                                                                                                                                                                                 /organism="Mus musculus"
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              oVal---TyrIleAspTyrArgAlaValGluValArgGlyGluGlyAlaAsp---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCCTTTTCTCGATAACCACAAA-----AACCCCCCTTTAACCGCACAAAAAGGGCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGCAAAGAGAACAACCCAATCCATACCCGCATACACTCTCCCCGCCCACGCATATCA
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                                                                                                                                                       gLeu---ArgGlnThrAlaLeuValAlaAlaArgAlaValGlyTyrTyrAspIleAspLe
                                                                                                                                                                                                                                                                                                                                        GAATGCAAGCCCCGCAGAACGCAGCTTAACGGTACTTGGAGGTCAGCACGGTGCTCACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nGluSerThrGluMetGlyIleAsnProAsnAspTyr----IleProGluTyrGlnGl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pThrAlaIleAsnGlnAlaLysAlaGlyAsnProProValLeuLeuThrProGluGlnIl
                                                   CTGCAGCATTGGCCAGAGCATCGGCGACCTTCTTGCCGTGACCCTTGACCTGGGCAGAGC
                                                                                  uSerIleIleArgAsnSerIleGlyGluValAspValIleIleHisAspLeuGlyGluPr
                                                                                                                       CTTGTGGGCATGCAGGTCGCTCAGAGCAGACAGGGCACCGGGCAGGTCATCGAG-GTGGC
                                                                                                                                                                                            AGCCAAGGTCACCAGCAGGCAGTGGCTCAGGAGCTTGAAGTTGACGGGATCCACACGCAG
                                                                                                                                                                                                                               uGluAspIleThrGlnGluSer--
                                                                                                                                                                                                                                                                  AGGCAAGGAATTTATCCAGAGAGGCATGCACCGCGGGGTGAAATCGGCAGGGTGGTGGCT
                                                                                                                                                                                                                                                                                                                                                                         nSerSerGlnSerGlyGluThrSer----AlaIleGlySerSerHisGln-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACGCGAGTTAAATTCGGGG----AACCCCACAGGTTTTTCCCCAAGTACCGCAGTTTGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------CTTTTTCCGATATCTCCCCCACTCTCCAAAAGGGGGATTCTGCTCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -ProGlyLeuIleLysArgLeuTyr------
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-DB--Pending_Patents_NA_New -QFWF-fastap -SUFFIX-rnpn -MINNATCH-0.1 -LOOPCL-0
-LOOPEXT-0 -UNITS-blts -START=1 -END-1 -MATRIX-blosum62 -TRANS-human40.cdi
-LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100 -THR_MIN=0 -ALIGN-40
-MODE-LOCAL -OUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-200000000
-USER-US09914168_@CGN_1_1_465_@runa_HEAPSIZE-500 -MINLEN-0 -NCPU-6 -ICPU-3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WANN_TIMEOUT=30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6 -FGAPEXT-7
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-MODEL=frame+_p2n.model -DEV=x1h
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Fgapop 6.0 , Fgapext
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/cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
/cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
/cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq2:*
/cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq3:*
/cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq3:*
/cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq2:*
/cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq2:*
/cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq2:*
/cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq2:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*
/cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
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         US-10-419-128-14784

US-10-366-633-14784

US-10-417-886-3279

US-09-913-101-1

US-09-913-101-3

US-10-419-128-14663

US-10-366-683-14663
                                                                                                                                                                                                                                                       SUMMARIES
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Sequence 14784, A
Sequence 14784, A
Sequence 3279, Ap
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equence 3767	Sequence 23985, A	equence 4226	equence 1498	equence 2938	1,	equence 1,	equence 2993	equence 39,	equence 1,	equence 24,	equence 30,		equence 44808,	equence 27975,	e 135, A	e 42248,	15, Ap	e 327	equence 4165,	e 4165,	14662,	62,	4442, A	4442, A	7	7, Appl	1, Appl	equence 1, Appl	10, App	2, Appl	ن ن	equence 6,	9, Appl	Sequence 81, Ap	equenc	ce 14966,	96

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## ALIGNMENTS

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RESULT 1
US-10-419-128-14784
(Sequence 14784, Application US/10419128
; Sequence 14784, Application US/10419128
; GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; FILE REFERENCE: 107196.136
                                                                                                                     Pred
                        Query Match:
                                             Percent Similarity:
Best Local Similarity:
                                                                                             Score:
                                                                                                                                    Alignment Scores:
                                                                                                                                                                                      US-10-419-128-14784
                                                                                                                                                                                                                               SEQ ID NO 14784
LENGTH: 1818
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/419,128 CURRENT FILING DATE: 2003-04-21 PRIOR APPLICATION NUMBER: US/09/252,991 PRIOR FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                         ORGANISM: Pseudomonas aeruginosa
                                                                                                                   No . .
8.39e-41
620.50
40.61%
24.45%
13.13%
                                                                                        Length:
Matches:
                     Indels:
                                             Conservative: Mismatches:
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**р** õ Вb Ŷ Ъ 9 ₽ ő В Ş рь ô В γ рь δ DЬ ş В Qy В δÃ В Ş DЬ QY Вb δ Вb Q В Š В á В Ş US-09-914-168-2 (1-919) x US-10-419-128-14784 (1-1818) 515 H1sAspAspGlyValAsnArgSerIleLeuGlyArgIleSerAspAlaValSerAlaVal 534 535 AlaArgAlaIleLeuProAspGluSerGluAsnGluValIleAspLeuProGluArgThr 554 805 GTCGACGCCGCCGACCCAGGCTCAGGCC-----495 475 MetAspIleSerProIleGluPheSerAlaSerAsnLeuIleGlnAspLysLeuAsnLeu 494 793 435 IleGlnAsnAspGlnValSerPheGluGlnSerSerSerSerArgThrGluProAlaGln 454 455 ValAspGluSerThrLeuGluProValIleGluThrValGluLeuThrAspGlyIleLeu 474 792 775 CAATCCAGCGGCTACTTC------415 IleAlaThrArgTyrPheAsnMetValAsnThrGluIleValPheProGluArgGluGln 434 715 CCGTTCAAGGCCGGCCAACCCTATGACTCCGAACTGATCGCCGAACTCAACCAGAACCTG 395 ThrValAsnMetGlyGluAlaTyrAsnLeuGlnAlaValArgAlaLeuSerAsnAspLeu 414 375 GlnLeuThrThrAspProAspLysLeuProValLysArgGluLeuLeuGluGlnLeuLeu 634 AGCGGCCAGCGCTACACCTTCGGCAAGGTGAGCTTC-----355 ThrGlyThrGlnTyrArgPheAspGluValValPhePheThrIleAspProLysThrAsn 374 574 ACCCAGCGCCTGAGCATCGATCCGCGCGCGCGATCGCCGACATCGACCTGGTCTACGAC 335 AspArgSerValAspValIleLeuProAspAsnThrAlaAspValSerLeuIleTyrAsp 354 315 LysLysAsnLeuIleGluAsnAlaSerAlaGluHisGlyTyrPheAspGlyArgTrpLeu 334 457 CCGTCGGGCAAG---CAACTGAAAGCGGGGGGGGAAGCTGAACCAGGGTGTCTACGAGGAC 513 295 ValAlaAspGluValProLeuLeuIleGlyAspValPheHisHisGlyLysTyrGluThr 314 397 CTGCGCCAGGTGAACATCCAGGTGCTCGGCGAGGCCGCCAGCCTGGAGAGCTTCCGCTTG 456 275 IleAspTyrArgAlaValGluValArgGlyGluGlyAlaAspAspLysAlaPheThrThr 294 337 GTGAAGGACGGCAAGCCGCCGAAGCTCAACGCTCAAGGTAGTGCCCGGCGAGCCCGTGCGC 396 247 GCGTTGCAACGTTTCCGTCGCAATGCCGAGGCGCAGGCGGAAAAGGCCGCCCAGGCGCTC 210 AlaAsnileLysAlaAlaLeuGluAspIleThrGlnGluSerAlaMetAspLeuAsnGly 229 307 246 230 199 GCCAATATCGAGGCCTACGTGGGTAGCCTCGGCGAGCGGGAC------GAGGCG -----GACGGCGCGCGCCAGGCGATC-ValAlaAlaLysAlaArgHisLeuTyrAspMetProAspAspArgValLeuAlaIleAsn 514 GGCTACTTCCAG-------336 GlyTyrTyrAspIleAspLeuSerIleIleArgAsnSerIleGlyGluValAspValIle 265 SerIleProArgLeuArgGlnThrAlaLeuVal------------------AlaAlaArgAlaVal 245 -GACGGCGACTCGATC---ATCGAGGAAGAACTGTTGCGCCGCATGGTG 714 ----GAGGGAGTGCGG ---- 855 804 792 774 394 669 633 306 246

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RESULT 2
US-10-366-683-14784
Sequence 14784, Application US/10366683
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APPLICANT: Nolling, Jork
APPLICANT: Deloughery, Craig
APPLICANT: Bush, David
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375 GlnLeuThrThrAspProAspLysLeuProValLysArgGluLeuLeuGluGlnLeuLeu 394
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                                         AGCGGCCAGCGCTACACCTTCGGCAAGGTGAGCTTC----
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ValAsp-----ValAlaThrGlyValLysGluGluGlyAsnProIleLysLeuHisPhe
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                                                                                                                  AspThrLysIleGlyAlaGlyValGlyValArgTrpAlaSerProValGlyGlnValArg
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GENERAL INFORMATION:
APPLICANT: Ruelle, Jean-Louise
APPLICANT: Thonnard, Joelle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Haemphilus Influenzae RD Outer Membrane TITLE OF INVENTION: Sequences Used as Vaccine FILE REFERENCE: BM45368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 9902880.5
PRIOR FILING DATE: 1999-02-09
PRIOR APPLICATION NUMBER: PCT/EP00/00887
PRIOR FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/913,101 CURRENT FILING DATE: 2002-12-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Haemophilus
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                                                                                                                                                                                                                              360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ValAspValI1eI1eHisAspLeu-----GlyGluProValTyrI1eAspTyrArgAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGCGATTTATTGATTGCTCATGTTACACCAGGCGAGCCAACAAAATTGCGGGGACTGAT
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GATCCGTATTTAATGAATAATTTGTCGGATTTAACCAGCGATTTTCCATCTTCAAATTGG
                                 GluAlaTyrAsnLeuGlnAlaValArgAlaLeuSerAsnAspLeuIleAlaThrArgTyr
                                                                                                                                                                                                                  ArgPheAspGluValValPhePheThrIleAspProLysThrAsnGlnLeuThrThrAsp
                                                                                                                                                                                                                                                                                                                                                                    TCACGTTTAGCATTAAAATCGTGGGTATTTTGATGGGAACTTTAAAATTTCACGTTTAGAA
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                                                                                                                                                                                   CATTATGGCAATATTACTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCG---AAAGATGGCGTTTTGGTTGAGCACCAAACTTACGATGATTACAAAACAGCGATT
                                                                                                                                   ProAspLysLeuProValLysArgGluLeuLeuGluGlnLeuLeuThrValAsnMetGly
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                                                                                   AGCCATTCACAAATTCGGGATGATTACTTAAATAATATTCTTAACATCAAATCTGGT
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Matches:
Conservative:
Mismatches:
Indels:
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783	64 IleAla	Oy 7
	22 GTGCAA	Db 12
763	45Gln	0у 7
1221	62 CCAACT	-
	39 ProMet	0у 7
1161	35	Db 11
738	19 GlnGluAlaLeuLeuAlaGlyValAlaValHisLysThrValAlaAspAsnLeuValAsn	Oy 7
1134	26 CAAGCG	1
718	99 GlnAla	Оу б
1125	69 AATGCG	سر
698	79 GlnAsn	Qy 6
1068	15 GAGAAT	1
678	59 ThrAsnGlyPheAspLeuSerThrArgThrLeuGluHisGluIleSerArgSerIleIle	Оу 6
1014	67 CCATTAAATTATTACTATGATTTTGCCGTCGGTTGGGAA	Db 9
658	39 ProLeuAsnAspGlnLeuArgAlaThrLeuGlyTyrGlnGlnGlnValPheGlyHisSer	Оу б
	07 TATCTCTCTGCACCAAAACAAACTCTAGAGGCAACTTATCGAATGCCACTGCTTAAAAAAT	Db 9
638	20 ArgLeuSerGluAspLysGlyValLysLeuTyrAlaThrLysProLeuSerHis	Оу б
906	47 CAAATAGGCTGGACAAAACCTTGGATTAATAGCCGTGGACATAGTTTGCGTTCAAATCTT	Db 8
619	0	0у 6
846	œ	Db 7
599	œ	0у 5
786	4	Db 7
579	6	
744	4	Db 7
559	4	
744	44	Db 7
539	.20 AsnArgSer[leLeuGlyArgIleSerAspAlaValSerAlaValAlaArgAlaIleLeu 5	Qy 5
744	44	Db 7
519	00 ArgHisLeuTyrAspMetProAspAspArgValLeuAlaIleAsnHisAspAspGlyVal 5	Qy 5
744	24 7TAGTTCAGCCTAATGTTAAT 7	Db 7
199	80 IleGluPheSerAlaSerAsnLeuIleGlnAspLysLeuAsnLeuValAlaAlaLysAla 4	4
723	23 7	Db 7
179	60 LeuGluProValIleGluThrValGluLeuThrAspGlyIleLeuMetAspIleSerPro 4	Оу 4
723	23 7	Db 7
159	,40 ${ t ValSerPheGluGlnSerSerSerSerArgThrGluProAlaGlnValAspGluSerThr}$ 4	_
723	11 :::	Db 7
139	20 PheAsnMetValAsnThrGluIleValPheProGluArgGluGlnIleGlnAsnAspGln 4	Dy 4

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Sequence 3, Application US/09913101

GENERAL INFORMATION:
APPLICANT: Ruelle, Jean-Louise
APPLICANT: Thonnard, Joelle
TITLE OF INVENTION: Haemphilus Influenzae RD Outer Mem
TITLE OF INVENTION: Haemphilus Influenzae RD Outer Mem
TITLE OF INVENTION: Sequences Used as Vaccine
TILE REFERENCE: BM45368
CURRENT APPLICATION NUMBER: US/09/913,101
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: 9902880.5
PRIOR FILING DATE: 1999-02-09
PRIOR APPLICATION NUMBER: PCT/EP00/00887
PRIOR APPLICATION NUMBER: PCT/EP00/00887
PRIOR FILING DATE: 2000-02-04
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US-09-913-101-3
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; ORGANISM: Haemophilus influenzae
US-09-913-101-3
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DB:
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Best Local Similarity:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1731
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1561 GATAGTGGATTAGCTGCCGATAATTACACAGCAAAAGAGCTGCGTTATGGCACAGGCGTT
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                                                                                                                    211 CGTGTGTTTGGTTATTATGAATCTTCCGTGCGTTTTGAACGAAAACAGCGTCAAGGCAAA 270
                                                                                                                                                      243 ArgAlaValGlyTyrTyrAspIleAspLeuSerIleIleArgAsnSer---IleGlyGlu
280 ValGluValArgGlyGluGlyAlaAspAspLysAlaPheThrThrValAlaAspGluVal 299
                                          271 CGCGATTTATTGATTGCTCATGTTACACCAGGCGAGCCAACAAAAATTGCGGGGACTGAT 330
                                                                               262 ValAspValIleIleHisAspLeu-----GlyGluProValTyrIleAspTyrArgAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HisAspSerLeuSerProIleSerAspLysGlyTyrLeuThrGlyGlyGlnValLeuAla 843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ArgAlaHisGlnMetThrGlyGlyIleGlnAlaGlyTyrIleTrpSerAspAsnPheAsn 803
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ValGlyThrAlaGluTyrAsnTyrGluPheMetLysAspLeuArgLeuAlaValPheGly 863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GluGluGlyAsnProIleLysLeuHisPhePheIleGly 916
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427.50
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Matches:
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Indels:
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658	39 ProLeuAsnAspGlnLeuArgAlaThrLeuGlyTyrGlnGlnGluValPheGlyHisSer 	0у 6
960	620 ArgLeuserGluasplysLysGlyVallysLeuTyrAlaThrLysProLeuSerHis	Db s
900	CAAATTGGCTGGACAAAACCTTGGATTAATAGCCGTGGACATAGTTTGCGTTCAAATCTT	
619	- ž	0у (
840	CACGGA	Db
599	GlyTrpGlySerAspThrGlyThrArgLeu	Oy 5
780	739	Db 3
579	laSer	Qy
738	738	Db .
559	540 ProAspGluSerGluAsnGluValIleAspLeuProGluArgThrAlaLeuAlaAsnArg	Qy
738	738	pb :
539	520 AsnArgSerIļeLeuGlyArgIleSerAspAlaValSerAlaValAlaArgAlaIleLeu	Qy :
738	738	Db
519	500 ArgHisLeuTyrAspMetProAspAspArgValLeuAlaIleAsnHisAspAspGlyVal	Oy :
738	AGTTCAGCCTAATGTTAAT	Ъ
499	leGlnAspLysLeuAsnLeuValAlaAlaLysAla	04 ,
717	717	Db
479	$\tt 460\ LeuGluProValIleGluThrValGluLeuThrAspGlyIleLeuMetAspIleSerPro$	Oy ,
717	717	Db .
459	${\tt 440~ValSerPheGluGlnSerSerSerSerArgThrGluProAlaGlnValAspGluSerThr}$	Qy ,
717	706 TTTAGCTCAGTA	Db 1
439	AsnMetValAsnThrGluIleValPheProGluArgGluGlnIleGlnAsnAspGln	Qy ,
705	**OV GLUALALY EASTHAUGHTHALA VALAE GALA BAUGUSEERS INSS DAULLEA LATITIKATSTYYE ::::       :::::::::::::::::::::::::::	Db dd
645	89 AGCCATTCACAAATCCGTGACGATTATCTCAATAATATTCTTAACATCAAATCTGGC	
399	80 ProAspLysLeuProValLysArgGluLeuLeuGluGlnLeuLeuThrValAsnMetGly	
588	568 CATTATGGCAATATTACTTTT	Db :
379	360 ArgPheAspGluValPhePheThrIleAspProLysThrAsnGlnLeuThrThrAsp	Qy :
567		Db
359	IleLeuProAspAsnThrAlaAspValSerLeuIleTyrAspThrGlyThrGlnTyr	Qy
507	CACGCTTGGCATTAAATCGTGGGTATTTTGATGGGAACTTTAAAATTTCACGTTTAGAA	
339	rpLeuAspArqSerValAsp	Qy
319 447	300 ProLeuLeuIleGlaspValPheHisHisGlyLysTyrGluThrLysLysAspLeuIle	Db 04
390	TITE TO THE TITE TO THE TITE TO THE TITE TO THE TERM T	

TO PSEUDOMONAS	419-128-14663 419-128-14663, Application US/10419128 ence 14663, Application US/10419128 RAL INFORMATION: LICANT: Marc J. Rubenfield et al. LE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING LE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS E REFERENCE: 107196.136 E REFERENCE: 107196.136 E REFERENCE: 107196.136 E REFERENCE: 2003-04-21 OR APPLICATION NUMBER: US/09/252,991 OR APPLICATION NUMBER: US/09/252,991 OR FILING DATE: 1999-02-18 OR FILING DATE: 1999-02-18 OR APPLICATION NUMBER: US 60/074,788 OR APPLICATION NUMBER: US 60/074,788 OR APPLICATION NUMBER: US 60/094,190	US-10 Seguing
	::::::	e d
	904 GluGluGlyAsnProIleLysLeuHisPhePheIleGly 916	Qy
1674	1615 GGTGTGCGTTGGGCATCGCCAGTGGGTGCGATTAAATTTGATATTGCCACACCCATTCGT	DЪ
903	ΙY	Qy
1614		Db
883	864 AspIleGlyAsnAlaTyrAspLysGlyPheThrAsnAspThrLysIleGlyAlaGlyVal	Qy
863 1554	844 ValGlyThrAlaGIuTyrAsnTyrGluPheMetLysAspLeuArgLeuAlaValPheGly :::        ::: :::     1495 ACCACTTCTTTAGAAAATCAATATCAAGTTTATCCAAATTGGTGGGCGGCAACTTTTGCA	Qy Db
1494	1435 TATAAAAAATTGCGCCTAAAAATAGAAATTGGAAAATTGGTTGG	DЪ
843	824 HisAspSerLeuSerProIleSerAspLysGlyTyrLeuThrGlyGlyGlnVaÎLeuAla	Qy
1434	1375 AAAATTCCGCCTACACTGCGTTTCTTTGCTGGTGGCGATCGTAGTGTGCGCGCGTTACGGC	Db
823	804 HisValProTyrArgLeuArgPhePheAlaGlyGlyAspGlnSerIleArgGlyTyrAla	Qy
1374	1321CATCGTATCGTTGCTCGTGCTGAAATCGGGTATTTACATACA	Db
803	784 ArgAlaHisGlnMetThrGlyGlyIleGlnAlaGlyTyrIleTrpSerAspAsnPheAsn	Qy
1320	1276 AAAGTGCAAGCATCTAGCGCGTGGGTTCGTACTTATGCAGAAAAT	Db
783	764 IleAlaArgAlaGlyIleSerGlyValTyrSerPheGlyAspAsnAlaTyrGlySerAsn	Qy
1275		-
763	745GlnArgTyrSerLeuGluValGlySerSerGlyLeuValSerAspAlaAsnMetAla	Qy
1215	 	-
744	739 ProMetArgGlyTyrArg	Qy
1155	1129	DЬ
738	AlaAspAsnLeuV	Qy
1128	1120 CAAGCGGAT	Дb
718	699 GlnAlaProProGluThrTrpGlnAspLeuProValAspPheValAsnGlyLysProSer	Qy
1119		
698	679 GlnAsnGlyGlyTrpAsnArgThrTyrSerLeuArgTyrArgLeuAspLysLeuLysThr	Qy
1062		Дb
678	GlyPheAspLeuSerThrArgThrLeuGluHisGluIle	Qy
1008	961 CCATTAAATTATTACTATGATTTTGCCGTCGGTTGGGAAGGGGAAAAA	Db

PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 14663 LENGTH: 4497

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; TYPE: DNA; ORGANISM: Pseudomonas US-10-419-128-14663
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Percent Similarity:
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CURRENT APPLICATION NUMBER: US/10/366,683
CURRENT FILING DATE: 2003-02-13
PRIOR APPLICATION NUMBER: 09/252,991
PRIOR FILING DATE: 1999-02-18
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 14663
LENGTH: 4497
EXECT.
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APPLICANT: Nolling, Jork
APPLICANT: Deloughery, Craig
APPLICANT: Deloughery, Craig
APPLICANT: Bush, David
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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                                 SerGlyLeuValSerAspAlaAsnMetAlaIleAlaArgAlaGlyIleSerGlyValTyr 773
                                                                       GACAACAAGGTCGACCCCAGCCATGGCTACCGCCTGCAGTTCAACGTCAAGGGGGGCGAAG
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US-10-419-128-14966/c

Sequence 14966, Application US/10419128

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MAIC J. Rubenfield et al.
APPLICANT: MAIC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING:
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/10/419,128
CURRENT APPLICATION NUMBER: US/03-04-21
PRIOR APPLICATION NUMBER: US/09/252,991
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
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DB:
                                                                                                                                                         US-09-914-168-2 (1-919) x US-10-419-128-14966 (1-726)
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                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 14966
LENGTH: 726
TYPE: DNA
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Best Local Similarity:
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                                                                                                                                                                                                                                             SEQ ID NO 14966
LENGTH: 726
TYPE: DNA
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APPLICANT: Nolling, Jork
APPLICANT: Deloughery, Craig
APPLICANT: Deschery, Craig
APPLICANT: Bush, David
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS
FILE REFERENCE: PATH03-04
CURRENT APPLICATION NUMBER: US/10/366,683
CURRENT FILING DATE: 2003-02-13
                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 09/252,991
PRIOR FILING DATE: 1999-02-18
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                           ORGANISM: Pseudomonas
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Sequence 21979, Application US/10144771

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craiq
TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
FILE REFERENCE: CL001321
CURRENT APPLICATION NUMBER: US/10/144,771
CURRENT FILING DATE: 2002-05-15
NUMBER OF SEQ ID NOS: 47235
SEQ ID NO 21979
LENCTH: 1416
TYPE: DNA
ORGANISM: HUMAN
US-10-144-771-21979
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GlnSerLysLysValProLeuTyrValPheValAlaSerAspLysProArgAspGlyGln
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                                                                            GTGCGCTGGGAATCGCCGGTCGGGCCAATCAAACTCGATTTTGCCGTACCGGTCGCGGAT
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Percent Similarity:
Best Local Similarity:
Query Match:
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SEQ ID NO 81
LENGTH: 1365
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TITLE OF INVENTION: GENES OF AN OTITIS MEDIA ISOLATE OF H. INFLUENZAE
FILE REFERENCE: 28335/38815
CURRENT APPLICATION NUMBER: US/60/453,134
CURRENT FILING DATE: 2003-03-06
NUMBER OF SEQ ID NOS: 588
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ORGANISM: H. influenzae
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                                          GluValGlySerSerGlyLeuValSerAspAlaAsnMetAlaIleAlaArgAlaGlyIle
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GENERAL INFORMATION:
APPLICANT: Thonnard, Joelle
TITLE OF INVENTION: BASB207 Polypeptides and Polynucleotides
TITLE OF INVENTION: BASB207 Polypeable Haemophilus Influenzae
FILE REFERENCE: BM45424
CURRENT APPLICATION NUMBER: US/10/399,416
CURRENT FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: PCT/EPOL/11983
PRIOR APPLICATION NUMBER: GB 0025488.8
PRIOR APPLICATION NUMBER: GB 0025488.8
PRIOR APPLICATION NUMBER: GB 0025488.8
PRIOR APPLICATION NUMBER: GB 0025488.8
PRIOR FILING DATE: 2000-10-17
NUMBER OF SEO ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
SEO ID NO 9
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Best Local Similarity:
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                                             CCTTGGATTAATAGCCGTGGACATAGTTTGCGTTCAAATCTTTATCTCTCTGCACCAAAA
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                                                                                                                            US-10-148-534-6
Sequence 6, Application US/10148534
GENERAL INFORNATION:
APPLICANT: CHIRON SPA
APPLICANT: STATENS INSTITUTT FOR FOLKEHELSE
TITLE OF INVENTION: 85KDa NEISSERIAL ANTIGEN
FILE REFERENCE: P023527WO
CURRENT APPLICATION NUMBER: US/10/148,534
CURRENT FILING DATE: 2002-10-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              645 ArgAlaThrLeuGlyTyrGlnGlnGluValPheGlyHisSerThrAsnGlyRheAspLeu
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PRIOR APPLICATION NUMBER: GB-9928197.4
PRIOR FILING DATE: 1999-11-29
PRIOR FRITON NUMBER: GB-0005698.6
PRIOR FILING DATE: 2000-03-09
NUMBER OF SEQ ID NOS: 106
SOFTWARE: SeqWin99, version 1.02
SEQ ID NO 6
SEQ ID NO 6
LENGTH: 2379
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GATTTCCGTATCCTCGATACCGACATCCAAACCAACGAAGACAAAACCAGGCAGACCATC
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                                                                CAGAAATTCGCCCAAGACATGGAAAAAGTAACCGACTTCTACCAGAACAACGGCTACTTC
                                                                                              GlyLysTyrGluThrLysLysAsnLeuIleGluAsnAlaSerAlaGluHisGlyTyrPhe
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690	HisGlulleSerArgSerIleIleGlnAsnGlyGlyTrpAsnArgThrTyrSerLeuArg	671	Qу
1562	:::::	1516	Db
1515	GATATTTACGGAAAAGCCTTCGACCCGCGCAAAGCATCGACCAG	1462	ДĎ
0	lnGlnGluValPheGlyHisSer	65	Qy
650	TyrAlaThrLysProLeuSerHisProLeuAsnAspGlnLeuArgAlaThrLeuGlyTyr:::::::::::::::::::::::::::::::::::	631	ду
1461		1402	да
630	AspGlyTyrGlnAlaGLyAlaGluLeuArgLeuSerGluAspLysLysGlyValLysLeu	611	Db
1401		1348	Qy
610 1347	pGlySerAspThrGlyThrA             GGTTCAGGATACCGGC	591 1294	Оу
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481	ThraspGlyIleLeuMetAspIleSerProIleGlu	470	Qy
1059		1000	dd
469	ThrGluProAlaGlnValAspGluSerThrLeuGluProValIleGluThrValGluLeu	450	Qy
999		961	Db
449	ProGluArgGluGlnIleGlnAsnAspGlnValSerPheGluGlnSerSerSerSerArg :::	430	Qy
960		919	dd
918	GTTTTGGGT	910	Db
429	${\tt AspLeuIleAlaThrArgTyrPheAsnMetValAsnThrGluIleValPhe}$	410	ОУ
409	LeuGluGlnLeuLeuThrValAsnMetGlyGluAlaTyrAsnLeuGlnAlaValArgAla	390	ду
909		850	ф
389	AspProLysThrAsnGlnLeuThrThrAspProAspLysLeuProValLysArgGluLeu :::               :::	370	Qy
849		817	Db
369	SerLeuIleTyrAspThrGlyThrGlnTyrArgPheAspGluValValPhePheThrIle :::	350	Qy
816		766	Db

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Sequence 5, Application US/10320800
GENERAL INFORMATION:
APPLICANT: ROBINSON, ANDREW
APPLICANT: GORRINGE, ANDREW
APPLICANT: HUDSON, MICHAEL
APPLICANT: REDDIN, KAREN
TITLE OF INVENTION: MULTICOMPONENT MENINGOCOCCAL VAC
FILE REFERENCE: 1581.0790001
CURRENT APPLICATION NUMBER: US/10/320,800
CURRENT ETLING DATE: 2002-12-17
PRIOR APPLICATION NUMBER: PCT/GB99/03626
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; LOCATION: (1)..(239
; OTHER INFORMATION:
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NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn version 3.3
SEQ ID NO 5
LENGTH: 2391
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              AsnalaSerAlaGluHisGlyTyrPheAspGlyArgTrpLeuAspArgSerValAspVal 340
                                                                                                                                                                                                                                                                                                                                                                GlyGluProValTyrIleAspTyrArgAlaValGluValArgGlyGluGlyAlaAspAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                            ATCGACATCACGATTGACGAGGGCAAATCCGCCAAAATCACCGACATCGAATTTGAA---
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                                                                                                CTGACACGAAGCAACCAATTCAACGAGCAGAAATTTGCCCCAAGATATGGAAAAAGTAACC
                                                                                                                                                                                                                                                                  LysAlaPheThrThrValAlaAspGluValProLeuLeuIleGlyAspVal------
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Conservative:
Mismatches:
Indels:
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169

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681 1536	662 PheAspLeuSerThrArgThrLeuGluHisGluIleSerArgSerIleIleGlnAsnGly	Qy Db
661 1488	642 AspGlnLeuArgAlaThrLeuGlyTyrGlnGlnGluValPheGlyHisSerThrAsnGly :::        :::    :::    1435 ACGGCAGACGGGGTCAGCCTGGGCTACGATGTTTACGGAAAAGCCTTCGACCCG	Qу
641 1434	622 SerGluAspLysLysGlyValLysLeuTyrAlaThrLysProLeuSerHisProLeuAsn	Оy
621 1380	602 LysPheGluHisAsnLeuIleAsnArgAspGlyTyrGlnAlaGlyAlaGluLeuArgLeu	Оy
601 1320	84 AspGlyGlnIleGlyLeuGlyTrpGlySerAspThrGlyThrArgLeuValThr	Оy
1269	69	Db
83	564 AspValTyrGlnSerLysLysValProLeuTyrValPheValAlaSerAspLysProArg	Qy
563 1269	luValIleAspLeuProGluArgThrAlaLeuAlaAsnArgLysThrProAla  GTCGATTTGAACATGAGTCTGACCGAACGTTCCACC	дь Vo
543 1233	524 LeuGlyArgIleSerAspAlaValSerAlaValAlaArgAlaIleLeuProAspGluSer	Db Oy
1197		Db
523	snHisAspAspGlyValAsnArgSerIle	οy
508 1146	493 AsnLeuValAlaAlaLysAlaArgHisLeuTyrAspMetProAspAsp	Db
1089	33 CGGAAAATCTACGTCAACGAAATACACATCACCGGCAACAACAACAACACCGGCGACGAA	DЬ
492		Qγ
479 1032	leLeuMetAspIleSerPro :::::         TCGTCCTGCACATCGAACCGGGC	Оу
972	TCAGCGTA	Db
460	erPheGluGlnSerSerSerSerArgThrGluProAlaGlnValAspGluSerThrLeu	Qy
939	OGLUATGGLUGITILEGINASNASPGINVAL :::	B 5
918	83 TGGTACGAACGCCAGCAGATGACCGCCGTTTTGGGT	Db
420	1 AlaTyrAsnLeuGlnAlaValArgAlaLeuSerAsnAspLeuIleAlaThrArgTyrPhe	γ
400 882	tGLyGlu    ::: CGGCAAA	p 49
834	99 TGGGGCAAAGTCTCCATCGAAGGCGACACCAACGAA	Db
380	61 PheAspGluValValPhePheThrIleAspProLysThrAsnGlnLeuThrThrAspPro	Qy
798	ACCAAGCAGACCATCAAAATCACCGTCCACGAAGGCGGACGTTTCCGT	Db
	41 IleLeuProAspAsnThrAlaAspValSerLeuIleTyrAspThrGlyThrGlnTyrArg	Qγ
738	679 GACTTCTACCAAAATAACGGCTACTTCGATTTCCGTATCCTCGATACCGACATCCAAACC	Db

	-10-148-534-2 Sequence 2, Application US/10148534 SENERAL INFORMATION: APPLICANT: CHIRON SPA APPLICANT: STATENS INSTITUTT FOR FOLKEHELSE TITLE OF INVENTION: 85kDa NEISSERIAL ANTIGEN EILE REFERENCE: P02357WO	US-10-148-5 Sequence GENERAL I APPLICAN APPLICAN TITLE OF	
	TCCAACGCTTCCAATTCCAACTCGGCACGACG	2356 SULT 15	Db RE
		908	Qy
2355	CCTTTAGGCCCGATGAAATTCAGCTACGCCTACCCGCTGAAGAAAAACCGGAAGACGAA	2296	Дb
907		890	Qy
2295	AAATCCACCTTTACCAACGAATTGCGCTATTCCGCCGGCGCGCGC	2236	Дb
689	LysGlyPheThrAsnAspThrLys	871	Qy
2235	AACAGCAGTTCCGCGACCGGCGGCAGGGTTCAAAACATTTACGGCGCCGGCAATACCCAT	2176	Дb
870		870	Qy
2175		2116	Db
870		857	Qy
2115	AAAGCCAACGTCTCCGCCGAGCTGCTCCTTCCCGATGCCCGGCGCGAAAGACGCG	2056	Db
856	ThrAlaGluTyrAsnTyrGluPheM	846	Qy
2055	CCGAAAGTCTATGACGAATACGGCGAAAAAATCAGCTACGGCGCAACAAA	2005	DЬ
845	ProlleSerAsp	829	Qy
2004	GAAAACTTCTACGGCGGCGGGCTGGGTTCGGTGCGCGGATACGAAAGCGGCAC	1945	Db
828	LeuAr	809	Qy
1944	GAAGTCGGCATTGCGGGGGGGCTACGGCAGAACCAAAGAAATCCCCCTTCTTT	1894	Дb
808	pSer	791	γΩ
1893	ACCCACAACCAAACCTGGTTCTTCCCCCTGAGCAAAACCTTCACGCTGATGCTCGGCGGC	1834	Db
790	AlaHisGlnMetThrGly	785	Qy
1833	CCI	1798	Дb
784	AlaArgAlaGlyIleSerGlyValTyrSerPheGlyAspAsnAlaTyrGlySerAsnArg	765	Qy
1797	CTGACGGGCGTGAACGCCGAAATC	1774	Db
764	GlnArgTyrSerLeuGluValGlySerSerGlyLeuValSerAspAlaAsnMetAlaIle	745	Qy
1773	ACCGTCGGCTGGGGGCGCAACAAAACCGACAGCGCGTTATGGCCGACGCGCGCCT	1717	οb
744		731	Qy
1716	AAGAAATACGGCAAAACCGACGGCACAGACGGCAGCTTCAAAGGCTGGCT	1657	Db
730	AsnGlyLysProSerGlnG	714	Qγ
1656	GCAGAACACCTGACCGTCAACACCTACAACAAAGCGCCCAAACACTATGCCGACTTTATC	1597	рь
713	rpGlnAspLeuPro	697	Qy
1596	GCAGGCATCCGCATGAGCGTGCCTGTTACCGAATACGACCGCGTGAATTTCGGTTTTGGTG	1537	Дb
696	GlyTrpAsnArgThrTyrSerLeuArgTyrArgLeuAspLysLeu	682	Qy

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CURRENT APPLICATION NUMBER: US/10/148,534
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: GB-9928197.4
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: GB-0005698.6
PRIOR FILING DATE: 2000-03-09
NUMBER OF SEO ID NOS: 106
SOFTWARE: SeqWin99, Version 1.02
SEO ID NO 2
SEO ID NO 2
LENGTH: 2394
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; ORGANISM: Neisseria meningitidis
US-10-148-534-2
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                                                                                                                                                                                                         AlaArgLeuPheAsnAspGlyValAsnLysValPro-----ArgLeuLysAlaLys 186
                                                                                                                                                 LysalaPheThrThrValAlaAspGluValProLeuLeuIleGlyAspVal------
                                                                                                                                                                                                                                                                                      IleAspLeuSerIleIleArgAsnSerIleGlyGluValAspValIleIleHisAspLeu 269
                                                                                                                                                                                                                                                                                                                         GGCAAACTCAATATCCAAATCACGCCCAAAGTAACCAAACTCGCCCGCAACCGCGTCGAC
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          AsnAlaSerAlaGluHisGlyTyrPheAspGlyArgTrpLeuAspArgSerValAspVal 340
                                                                                                                 -----CAAATGTCCCTGACCGAAGGCGGCATTTGGACATGG
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                                              CTGACACGAAGCAACCAATTCAACGAGCAGAAATTTGCCCCAAGATATGGAAAAAAGTAACC 678
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681	PheAspLeuSerThrArgThrLeuGluHisGluIleSerArgSerIleIleGlnAsnGly	662	Qy
1488	ACGGCAGACGGGGTCAGCCTGGGCTAC	1435	DЪ
661	AspGlnLeuArgAlaThrLeuGlyTyrGlnGlnGlnValPheGlyHisSerThgAs	642	Qy
641 1434	SerGluAspLysLysGlyValLysLeuTyrAlaThrLysProLeuSerHisProLeuAsn	622 1381	Qy Db
621 1380	LysPheGluHisAsnLeuIleAsnArgAspGlyTyrGlnAlaGlyAlaGluLeuArgLeu :::	602 1321	Oy Db
601 1320	AspGlyGlnIleGlyLeuGlyTrpGlySerAspThrGlyThrArgLeuValThr	584 1270	Oy .
1269	4	1269	Db
583	${\tt AspValTyrGlnSerLysLysValProLeuTyrValPheValAlaSerAspLysProArg}$	564	Qу
1269	GluAsnGluValIleAspLeuProGluArgThrAlaLeuAlaAsnArgLysThrProAla :::	544 1234	Db Qy
N	ĠĊĊĠĠĊĄĊĠĊĊĊĠĂĊĄĄĄ	1198	Db
543	rgIleSerAspAlaValSerAlaValAlaArgAlaIleLeuProAspGluSe	524	Qy
1197	CGAGCTTTTGGGCTACTTCGACAATGT	1147	Дb
523	isAspAspGlyValAsnArgSerIle ::	509	Qy
508 1146	ASDLEUVALAIAAIALYSAIAATGHÍSLEUTYTASPMETPTOASPASP	493 1090	Qy Db
1089	ACATCACCGGCAACAACAAAACC	1033	Db
492	LeuIleGlnAspLysLeu :::   :::	480	Qy
1032	AGCCGCTGCCGAACGCTGAAACCAAAACCGTCGATTTCGTCCTGCACATCGAACCGGGC	973	Db
479	ProValIleGluThrValGluLeuThrAspGlyIleLeuMetAspIleSerPro	461	Qy
460 972	SerPheGluGlnSerSerSerArgThrGluProAlaGlnValAspGluSerThrLeu	<b>441</b> 940	Qy Db
939	TGGGC	919	Db
440	GluGlnIleGlnAsnAspGlnVal	421	Qy
918	CAGATGACCGCCGTTTTGGGT	883	Db
420	nAlaValArgAlaLeuSerAsnAspLeuIleAlaThrArgTyrPhe	401	Qy
882	AAGCCCGGCAAA	835	Db
400	٠،	381	Qy
834	1 1 1 1 1 1 1 1 1	799	Db
380	lPhePheThrIleAspProLysThrAsnGlnLeuThrThrAspPro	361	Qy
798	:::	739	Db
360	SerLeuIleTyrAspThrGlyThrGlnTyrArg	341	Qy
738	::: : :: :: :: :: :: :: :: :: :: :: ::	679	DЬ

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Sequence 10, Application US/10148534
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
APPLICANT: STATEMS INSTITUTT FOR FOLKEHELSE
TITLE OF INVENTION: 85kDa NEISSERIAL ANTIGEN
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                                                                                                    LysAlaPheThrThrValAlaAspGluValProLeuLleGlyAspVal------
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                                                       CAGATGTCGCTGACCGAAGGCGGCATTTGGACATGG
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681	${\tt PheAspLeuSerThrArgThrLeuGluHisGluIleSerArgSerIleIleGlnAsnGly}$	662	Qy
1488	CCTGGGCTACGATGTTTACGGAAA		Db
661	ThrLeuGlyTyrGlnGlnGluValPheGlyHisSerThrAs	642	Оу
1434	TCACGAAGCAAAACCACGCTCAACGGCTCGCTGTCGTTTACCGACCCGTACTTC	1381	Db
641	erGluAspLysLysGlyValLysLeuTyrAlaThrLysProLeuSerHisPr	622	94
1380	TCCGCAGGCGTTTCCCAAGACAACCTGTTCGGTACGGCCAAGTCGGCCGCCCTGCGCCCC	1321	Db
621	snLeuIleAsnArgAspGlyTyrGlnAlaGlyAlaGluLeuArg	602	Qy
1320	CGCTCGACTTGAGCGCGGGCTGGGTACAGGATACCGGCCTGC	1270	Дb
601	lyGlnIleGlyLeuGlyTrpGlySerAspThrGlyThrArgLeuValT	584	Qy
1269		1269	Db
583	${ t ValTyrGlnSerLysLysValProLeuTyrValPheValAlaSerAspLysProA}$	564	9
1269	ATTTGAAC	1234	Ф
563	AsnGluValIleAspLeuProGluArgThrAlaLeuAlaAsnArgLysThrProA	544	Qy
1233	TTTGATGCCGTCCCGCTTGC	1198	Db
543	eSerAspAlaValSerAlaValAlaArgAlaIleLeuProAspGluSe	524	Qy
1197	ACGCTO	1147	DЪ
523	ArgValLeuAlaIleAsnHisAspAspGlyValAsnArgSerI	509	Оу
1146	CTCCAAGC	1090	Db
508	AlaLysAlaArgHisLeuTyrAspMetProAspAsp	493	Qy
1089		1033	рь
492	···IleGluPheSerAlaSerAsnLeuIleGlnAspLysLe	480	Qy
1032	GAAACCAAAACCGTCGATTTCGTCCTGCACATCGAACCGGG	973	рb
479	luProValIleGluThrValGluLeuThrAspGlyIleLeuMetAspIleSerPr		Qy
972	AGCGAAATCAGCGT	940	Db
460	erPheGluGlnSerSerSerSerArgThrGluProAlaGlnValAspGluSerThr	441	οy
939		919	рь
440	snThrGluIleValPheProGluArgGluGlnIleGlnAsnAspGlr 	421	Оy
918	GTACGAACGCCAGCAGATGACCGCCGTTTTGGGT	883	Db
420	TyrAsnLeuGlnAlaValArgAlaLeuSerAsnAs	401	Оу
882	AAGCCCGGC	835	Ф
400	\rgGluLeuLeuGluGlnLeuLeuThrValAsnMe	381	Qy
834	TGGGGCAAAGTCTCCATCGAAGGCGACCCAACGAA	799	рь
380	heAspGluValValPhePheThrIleAspProLysThrAsnGlnLeuThrThr	361	Qy
798	CCACGAAGGCGGACGTTTCC	739	DЬ
360	uProAspAsnThrAlaAspValSerLeuIleTyrAspThrGlyThrGlnTyr	341	Qy
738	GACTTCTACCAGAACAACGGCTACTTCGATTTCCGCATCCTCGATACCGACATCCAAACC	79	DЬ
340	erAlaGluHisGlyTyrPheAspGlyArgTrpLeuAspArgSer	321	Qy

METHODS AND	ESULT 17  S-09-689-055A-1  S-09-689-055A-1  Sequence 1, Application US/09689065A  GENERAL INFORMATION:   APPLICANT: Pfizer Products, Inc.   APPLICANT: Pfizer Products, Inc.   TITLE OF INVENTION: LAWSONIA INTRACELLULARIS PROTEINS AND RELATED	RE US
	y 908 ProlleLysLeuHisPhePhelleGlyThTrToPhe 919 :::     :::[         b 2356 ATCCAACGTTCCAATTCCAACTCGGCACGTTC 2391	Db Qy
AA 2355	2296 CCTTTAGGCCCGATGAAATTCAGCTACGCCTACCCGCTGAAGAAAAAACCGGAAGAAG	рь
n 907	890 ProvalGlyGlnValArgValAspValAlaThrGlyValLysGluGluGlyA	Qy
cc 2295	2236 AAATCCACCTTTACCAACGAATTGCGCTATTCCGCCGGCGGCGCGCTTACCTGGCTCT	Db
er 889	871LysGlyPheThrAsnAspThrLysIleGlyAlaGlyValGlyValArgTrpAlaS	Qy
AT 2235	2176 AACAGCAGTTCCGCGACCGGCGGCAGGGTTCAAAACATTTACGGCGCCGGCAATACCC	ф
870	870	Qy
AC 2175	2116 GTCCGCCTGAGCCTGTTTGCCGACGCAGGCAGCGTGTGGGACGCAAAACCTACGACG	da
870	857 LeuArgLeuAlaValPheGlyAspIleGlyAsnAlaTyrAsp	Qy
CC 2115	b 2056 AAAGCCAACGTCTCCGCCGGAGCTGCTTCCCGATGCCCGGCGCGAAAGACGCGCGCAC	Db
sp 856	846 ThrAlaGluTyrAsnTyrGluPheMet	Qy
AA 2055	2005 CCGAAAGTGTATGACGAATACGGCGAAAAAATCAGCTACG	Db
845	829 ProlleSerAspLysGlyTyrLe	Qy
GT 2004	1945 GAAAACTTCTACGGCGGCGGCGCCTGGGTTCGGTGCGCGCATACGAAAGCGGCACGCTCG	Дb
er 828	809 LeuargPhePheAlaGlyGlyAspGlnSerIleArgGlyTyrAlaHisAspSerLeuS	Qy
TT 1944	b 1894 GAAGTCGGCATTGCGGGCGGCTACGGCAGAACCAAAGAAATCCCCTTCTT	Дb
rg 808	791GlyIleGlnAlaGlyTyrIleTrpSerAspAsnPheAsnHisValPr	Qy
3C 1893	b 1834 ACCCACAACCAAACCTGGTTCTTCCCCTTAAGCAAAACCTTCACGCTGATGCTCGGCGGC	Db
790	785 AlaHisGlnMetT	Qy
C 1833	1798	Db
:g 784	765 AlaArgAlaGlyIleSerGlyValTyrSerPheGlyAspAsnAlaTyrGlySerA	Qy
rc 1797	1774	Db
e 764	y 745 GlnArgTyrSerLeuGluValGlySerSerGlyLeuValSerAspAlaAsnMetAlaIl	Qy
- 1773	1717 A	Db
·9 744	731 ThrValAlaAspAsnLeuValAsnProMetArgGlyTyrAr	Qy
9T 1716	1657 AAGAAATACGGCAA	Db
's 730	714 AsnGlyLysProSerGlnGluAlaLeuLeuAlaGlyValAlaValHisLy	Qy
C 1656	1597 GCAGAACACCTGACCGTCAACACCTACAACAAAGCGCCCAAACACTATGCCGACTTTAT	Дb
1 713	697 LysThrGlnAlaProProGluThrTrpGlnAspLeuProValAspPheVa	Qy
15	1537 GCAGGCATCCGCATGAGCGTGCCTGTTACCGAATACGACCGCGTGAATTTCGGTTTG	B 5
969 ne	682 GlyTrpAsnArgThrTyrSei	0
  C 1536		Db

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NUMBER OF SEQ ID NOS: 112
SOPTWARE: PatentIn version 3.2
SEQ ID NO 1
LENGTH: 6617
TYPE: DNA
ORGANISM: Lawsonia intracellularis
US-09-689-065A-1
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Best Local Similarity:
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FILE REFERENCE: 3153.00187/PCI10589A
CURRENT APPLICATION NUMBER: US.099/689,065A
CURRENT FILING DATE: 2000-10-12
PRIOR APPLICATION NUMBER: US Prov. 60/160,922
PRIOR FILING DATE: 1999-10-22
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
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4271 GATCATGCCAAAATTAATGCAGAAATCAAAAAAATATGGGAATTAGGA-----TATTTT 4324
                                                                     4211 AAAGTTCTTGATCCTGATGTAATCCTTACACGACTCACTATTAATAAGGGAGATCATACT 4270
                                                                                                                                                                                                                                                                                              4043 ATTGATAGTAGGCTTATTGATAGTACAGGTGTAGCATCTGCACGTCCATTATACATAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3824 TCAAATGATGAAGAGTTACAAACAGAACTACCAATGCTTCTTGCAACTGCATTAAAGAAT 3883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3764 AATGCTGCTTCAAAAGACGATCCTTCTATTGTGGTTCTCCCATTTCAAATTAATGGCTCA 3823
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                                                                                                                                                                                                                                                                                                                               189 GlnSerSerGlnSerGlyGluThrSerAlaIleGlySerSer------HisGlnLys 205
                                    266 IleHis----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70 LeuAsnAlaGlyLeuAsnAlaLys---ProGlnSerGlnAlaLeuAspValValAsn 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SerGluValValValProProThrLeuGluProGluLysProGlyLeuIleLysArgLeu 168
                                                                                            GlyTyrTyrAspIleAspLeuSerIleIleArgAsnSerIleGlyGluValAspValIle
                                                                                                                                                                                                                     AAACCAAAATTTAATGAGCTAAATATTGCTGTAACAGAACTTGCTGAACGTATAAGT---
                                                                                                                                                                                                                                                                                                                                                                       TACGGCAGTTTCAATCAAACAGGTGAAAAT---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ThrGluMetGlyIleAsnProAsnAspTyrIleProGluTyrGlnGlyGluGlnProAsn 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MetSerValIleGluGluThrThrProLeuSerLeuGluGluLeuPheAlaGlnGluSer 128
                                                                                                                                                                     AspLeuAsnGlySerIleProArgLeuArgGlnThrAlaLeuValAlaAlaArgAlaVal 245
                                                                                                                                                                                                                                                          ThrGluProTyrAlaAsnIleLysAlaAlaLeuGluAspIleThrGlnGluSerAlaMet 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                GCTGACTATGTAGTA-----
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                                                                                                                                            -----AATGGCCTTATAAAGAAA----AACACTATTGCTGATGTACGTATTCATGGGCTT
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                              -----AspLeuGlyGluProValTyr 274
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5299	5240 GGAGATCTTTTAATGGTCAACATCTCCGACGCTCTAATGAATG	Вb
566	566	Qy
N	80 GTTGAAGGAATTACTCGTACTAGAGATAATGTTATCCTCCGTGAATTACGCCTTGCTGAT	
566	AspValTyr	Ov
556 5179	547ValileAspLeuProGluArgThrAlaLeu	Qу
546 5119	lAlaargAlaIleLeuProAspGluSerGluAsnGlu	Qy Db
529 5062	eSerAsp        TTCAGAT	Qу Db
5008	<pre>spLysLeuAsnLeuValAlaAlaLysAlaArgHisLeuTyrAspMetProAspAspArg :::::          </pre>	Дb
489 4948	ThraspGlyIleLeuMetAspIleSerProIleGluPheSerAlaSerAsnLeuIleGln:::	
469 4888	VallleGluThrValGluLeu 	Qу
457 4828	438 AspGlnValSerPheGluGlnSerSerSerSerArgThrGluProAlaGlnValAspGlu	Дb
437 4777	nAsn : ACGT	Db .
431 4717	412 AsnAspLeuIleAlaThrArgTyrPheAsnMetValAsnThrGluIleValPheProGlu :::     ::     4667 CTTGAAACAATAAAAGCTAAAACTTTAAAAAAAGAGTTAGCATTAACAGAA	Db .
411 4666	392 GlnLeuLeuThrValAsnMetGlyGluAlaTyrAsnLeuGlnAlaValArgAlaLeuSer 	Оу
391 4606	372 LysThrAsnGlnLeuThrThrAspProAspLysLeuProValLysArgGluLeuLeuGlu	Ωy
371 4582	352 IleTyrAspThrGlyThrGlnTyrArgPheAspGluValValPhePheThrIleAspPro :::	Qy Db
351 4528	334 LeuAspArgSérValAspValIleLeuProAspAsnThrAlaAspValSerLeu 	Db Oy
333 4477	314 ThrLysLysAsnLeuIleGluAsnAlaSerAlaGluHisGlyTyrPheAspGlyArgTrp:::	Qy Db
313 4435	294 ThrValAlaAspGluValProLeuLeuIleGlyAspValPheHisHisGlyLysTyrGlu	Оу
293 4375	275 IleaspTyrArgAlaValGluValArgGlyGluGlyAlaAspAspLysAlaPheThr	р Qy

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RESULT 18
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FILE REFERENCE: 3153.00187/FC10589A
CURRENT APPLICATION NUMBER: US/09/689,065B
CURRENT FILING DATE: 2000-10-12
PRIOR APPLICATION NUMBER: US Prov. 60/160,922
PRIOR APPLICATION NUMBER: US Prov. 60/163,858
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 112
SOFTWARE: Patentin version 3.2
SEQ ID NO 1
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APPLICANT: Pfizer Products, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Lawsonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 6617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6284 ATGGGAGATTTGCGA 6298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3764 AATGCTGCTTCAAAAGACGATCCTTCTATTGTGGTTCTCCCATTTCAAATTAATGGCTCA 3823
                                                                                                                                                                              4007
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AsnGlnAlaLysAlaGlyAsnProProValLeuLeuThrProGluGlnIleGlnAlaArg
                                                                                                                                                                                                                                                                                                                                                                                     TTTCGTGTCATCCCTAATAAATCTGCATTAAATCTT-----CTATATAAAACAAAATATC 3943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCAAATGATGAAGAGTTACAAACAGAACTACCAATGCTTCTTGCAACTGCATTAAAGAAT 3883
                                                                                                                                          GlnSerSerGlnSerGlyGluThrSerAlaIleGlySerSer------HisGlnLys
                                                                                                                                                                                                            TyrAlaArgLeuPheAsnAspGlyValAsnLysValProArgLeuLysAlaLysPheTyr 188
                                                                                                                                                                                                                                                                               SerGluValValProProThrLeuGluProGluLysProGlyLeuIleLysArgLeu 168
                                                                                                                                                                                                                                                                                                                                                  {\tt ThrGluMetGlyIleAsnProAsnAspTyrIleProGluTyrGlnGlyGluGlnProAsn}
                                                                                                                                                                                                                                                                                                                                                                                                         MetSerValIleGluGluThrThrProLeuSerLeuGluGluLeuPheAlaGlnGluSer 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PheAspAspGlnSerProIleSerArgIleGlyGluGlnSerProProLeuGlyLeuAsp 108
 AspLeuAsnGlySerIleProArgLeuArgGlnThrAlaLeuValAlaAlaArgAlaVal
                                  AAACCAAAATTTAATGAGCTAAATATTGCTGTAACAGAACTTGCTGAACGTATAAGT---
                                                                                                       ATTGATAGTAGGCTTATTGATAGTACAGGTGTAGCATCTGCACGTCCATTATACATAGAA
                                                                                                                                                                             TACGGCAGTTTCAATCAAACAGGTGAAAAT----
                                                                                                                                                                                                                                                  GCTGACTATGTAGTA-----
                                                                                                                                                                                                                                                                                                                     TCCCAACTTAATATTTCTACTGCAAAAAAGGTA---
                                                                     {\tt ThrGluProTyrAlaAsnIleLysAlaAlaLeuGluAspIleThrGlnGluSerAlaMet}
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Mismatches:
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ρĎ	4325	AGTGATGTCTCTGCAAGTATTGAAGAAAGCGGGGAAGGACGATTACTTGTA 437	U
ОУ	294	ThrValAlaAspGluValProLeuLeuIleGlyAspValPheHisHisGlyLysTyrGlu 313	
DЬ	4376	  GCTCAAAAGCTGTA	G
Qγ	314	ThrLysLysAsnLeuIleGluAsnAlaSerAlaGluHisGlyTyrPheAspGlyArgTrp 333	
Ъ	4436	:	7
Qy	334	spArgSerValAspValIleLeuProAspAsnThrAlaAspValSerI	
Ф	4478	TCAGTTATTAGTGATAGACTATTGTCCCAAGATATTCAAAAAATT	8
Qy	352	leTyrAs	
В	4529	TATAGAAAAGAAGGCTACTATCTCGCTGAAGT	2
QΥ	372	hrAsnGlnLeuThrThrAspProAspLysLeuProValLysArgGl	
В	4583	AAAGAAAATACTTCTTCTGCAACA 460	6
γQ	392	laValArgAlaLeuSe	
В	4607	ATGTCC	6
Qy	412	spLeuIleAlaThrArgTyrPheAsnMetValAsnThrGluIleValPhePr	
ф	4667	AATAAAAGCTAAA	7
Qy	32	ArgGluGlnIleGlnAsn 437	
Db	4718	ATTTTTTATCATGGTTTACTGGAACAGGTGTATTACGT	7
Qy	38	ValSerPheGluGlnSerSerSerSerArgThrGlu	
Вb	4778	GACTCTATAGCAATCTCTGCCTATGCCATGAATCATGGCTATGTAGATATT 482	œ
Qy	458	ValIleGluThrValGluLe	
Ф	4829	AGTAACATTCAAT	œ
Qy	470	spGlyIleLeuMetAspIleSerProIleGluPheSerAlaSerA:	
Db	4889	- 년	8
Qy	490	snLeuValAlaAlaLysAlaArgHisLeuTyrAspMetProAspAspA	
Db	4949	TGAACAACTCCTTAAAAGTAACAAAAATTGATGATCATAAAAACTATGAG	80
Qy	510	alleAsnHisAspAspGlyValAsnArgSerIleLe	
Db	5009	GATGATGTAAAAGCATTAACAGATTT	δ
γо	530	nArgAlaIleLeuProAspG	
DЪ	Ō	TGGTTATGCATTTGCTGAAGTAGATCTTGAAACAACCAAAAATGAAGAAGATGC	9
Qγ		VallleAspLeuProGluArgThr	
망	5120	CAATTGATGTTACTTTCCTTATTGATAAAAAAAAGTCTTTCTT	φ

Qy	Qy Db	Qy Db	Db	Db Db	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	DЪ	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	DЪ	Qy	Db	Qy	Дb	Qy
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ThrGlyGlyGlnValLeuAlaValGlyThrAlaGluTyrAsnTyrGluPheMetLysAsp 8	SerlleargGlyTyrAlaHisAspSerLeuSerProIleSerAspLysGlyTyrLeu 836 	TrpSerAspAsnPheAsnHisValProTyrArgLeuArgPhePheAlaGlyGlyAspGln 817 ::: ::::::	TCAAGAAGTAAAAACCATATAATACATTGGCGTACACGTGCAGGTGCAGCT 598		SerAspAlaAsnMetAlaIleAlaArgAlaGlyIleSerGlyValTyrSerPheGlyAsp 777	AGACCATCTAAAGGGCATATTGCAAAACTAATTGTTGAATATGGAGGTGGTGGTGGTCTTGGT 5878	AsnProMetArgGlyTyrArgGlnArgTyrSerLeuGluValGlySerSerGlyLeuVal 757	ATTICTAGTGTAGTGGTGGTTTTTACTTTTGATTCTACAGACAGTCGTGAG 5818	alAl	CTATATGATATTCCATCTACAGCACCACGCTCTTATCTTGACTATCAAGGGAAAAAT 576	<b>~1</b>	GAGAATATTCATCTTTGTTGGCTATCGAATTGATCAATATCGT	euLys 6	TTCCGTAAAAAAACTTATGGAGATACCATACGTCTATTTCACCCTATA 5		TTTGGCTTTAGTAATAACATTTATACGCTACGAGATGAATGGGATGAC 5	GlnGlnGluValPheGlyHisSerThrAsnGlyPheAspLeu 664	TCTTTACCAATCCTCGTGTTTATGATACAGAC 55	TyrAlaThrLysProLeuSerHisProLeuAsnAspGlnLeuArgAlaThrLeuGlyTyr 650	GGTTATATTTTAAGTATTGAAGGTTTTATTTCTAGTAAGTCATCTTCTCTTGATCTT	GlyAlaGluLeuArgLeuSerGluAspLysLysGlyValLysLeu 6	TCAACACATTCTAAATTTGGTGTTTCAGGAAGTATCTCAGAAAGAA	AspThrGlyThrArgLeuValThrLysPheGluHisAsnLeuIleAsnArg 610	CTTGTAAAAGTTCAAGAAGCTCGAACAGGTGCAATCACAGGTGGTGTTGGTTAC 5	AlaSerAspLysProArgAspGlyGlnIleGlyLeuGlyTrpGlySer 5	TATTTTAACCAAGTAGATACAGATACACTGCCTACAGGGAAAGATGATGAAGTTGATCTA 535	GlnSerLysLysValProLeu 573	GGAGATCTTTTTAATGGTCAACATCTCCGACGCTCTAATGAATG	5	GTTGAAGGAAATACTCGTACTAGAGATAATGTTATCCTCCGTGAATTACGCCTTGCTGAT 523	AlaAsnArgLysThrProAlaAspValTyr 566
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da da	0y 103 ProProLeuGlyLeuAspMetSerValIleGluGluThrThrProLeuSerLeuGluGlu 122	_
Qy	196	-
당 :	Qy 83 AlaLeuAspValValAsnPheAspAspGlnSerProIleSerArgIleGlyGluGlnSer 102	0
Qy	Db 136 AAAGAAATGAAAGTCCAGTTTCTTATGTCGGGCTTTCTTACATGTCTGACATGCTC 195	_
Db .	Qy 64 GluGlnTleGlnAlaArgLeuAsnAlaAlaGlyLeuAsnAlaLysProGlnSerGln 82	0
Qy	Db 76 AAAAATGAAGTTCAAAGAAATGAAGCTCAAAAAAGAAACCCCCCAATCCAATCAAACGCCT 135	_
Db	Qy 44 AlaHisAspThrAlaIleAsnGlnAlaLysAlaGlyAsnProProValLeuLeuThrPro 63	0
Qy Qy	QY 24 MetThrSerGlnAlaLeuAlaGlnGlnAsnAsnProAlaAsnIleIleAsnHisValPro 43 ::::	п О
Qy	US-09-914-168-2 (1-919) x US-09-988-067B-7 (1-3012)	c
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Qy	; APPLICANT: Kleanthous, Harold ; APPLICANT: Tomb, Jean-Francois	
Db 3	INFORMATION: NT: Haas, Rainer	
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105	TGGTGAAGCCAGACTTG	Db
438	heAsnMetValAsnThrGluIleValPheProGluArgGluGlnIleGlnAsnAs	Qy
418 102	402 TyrasnLeuGlnalaValargalaLeuSerasnaspLeuIlealaThrarg :::   ::::: :::     ::: 961 TTTAATATTGAGCATTTAAGAGCGGATGCGCAAATTTTAAAAACCGAAATCGCCGATAAG	Qy Db
<u> </u>	AACCTTAGAAAAAGCGCTTAAAGTGAAAAGGAAAGATGTC	Db
0	euProValLysArgGluLeuLeuGluGlnLeuLeuThrValAsnMetGlyGluAla	Qy
906	AATAGAGATTGACAACCCG	Db
381	luValValPhePheThrIleAspProLysThrAsnGlnLeuThrThrAspProAsp	Qy
876	TAAGCTTCATTATAAAGTCAAAGAGGGGATCCAATACAGGATT	Db
6	nThrAlaAspValSerLeuIleTyrAspThrGlyThrGlnTyrArgPhe	Qy
816	ACTTAGACGCTCATATTTCTTCGCCTTTTTTGAAAACGGAT	DЬ
344	spArgSerValAspValIleLeuProAsp	Qy
756	TGCGTTTAGATCAACTAGAATACGATTCTATGCGTATCCAAGAT	Db
ū	1	Оy
969	AATCTTTGAGTGCGAACAAGCAACGAGATTTCATGGGCTGGATGTGGGGC	Db
2	IleGluAsnAlaSerAlaGluHisGly	Qy
636	ATCAAACAATCCATTTATGAGGGAAGCGCGAAATTAAAACGC	Db
316	isHisGlyLysTyrGluThrLysLys 	Qy
576	CACAGAAAAGGTCAGTGAGGGTGCATTATTGATCGTGTTTC	Db
297	0 ValGluValArgG	Qy
516	08 GGG1	dd
279	lyGlu	Qy
507	481 ACCGCTTTAGAGGGGCAGGGCTATTAT5	Db
259	laAlaArgAlaValGlyTyrTyrAspIleAspLeuSerIleIleArgAsnSerIle 2	Qy
081	GCATGCTAAAAACGGCTTTAAAA 4	Db
239	<pre>stAspLeuAsnGlySerIleProArgLeuArgGlnThrAlaLeu 2</pre>	Qy
141	GAAAAGGAAAAAGACGGCTTAAAATCCCAAATGGGGATCAAAAAGGGCGACACCTTT 4	Db
20	rSerHisGlnLySThrGluProTyrAlaAsnIleLysAlaAlaLeuGluAspIleThr 2	Оy
81	22 TTAGAGTTTCATTTTGATGAAAAAGCCAGGATTGCCGGGGTAGAAATCAAGGGTTATGGG 3	Db
00	3 LeuLysAlaLysPheTyrGlnSerSerGlnSerGlyGluThrSerAlaIleGly 2	Qy
21	80 GGGTATTTTAAAGACGTTTATGCCACTTTTGAAGGCGGCATA	Db
82	63 GlyLeuIleLysArgLeuTyrAlaArgLeuPheAsnAspGlyValAsnLysValProArg 1	οy
79	79 2	_
62	143 GlnGlyGluGlnProAsnSerGluValValValProProThrLeuGluProGluLysPro 1	Qy
79	268 TIGTTCAATCAA 2	DЪ

751 .941	41 ArgGlyTyrArgGlnArgTyrSerLeuGluVal 7	Oy 7 Db 18
740 .881	34	Oy 7 Db 18
733 [82]	16 L 62 T	Oy 7 Db 17
715 L761	98 ThrGl	Oy 6 Db 17
597 1701	<pre>i83TrpAsnArgThrTyrSerLeuArgTyrArgLeuAspLysLeuLys 6</pre>	Оу 6 Db 16
582 L641	70GluHi ::::: 82 GCGGATTA	Qy 6 Db 15
569 L581	51 GlnGlnG]	Qy 6 Db 15
550 L539	636	Qy 6 Db 15
535 1512	525LysLysGlyValLysLeuTyrAlaThrLysPro	Qy 6 Db 14
624 1452	05 HisasnLeuIleAsnArgAspGlyTyrGlnAlaGlyAlaGluLeuArgLeuSerGluAsp 	Оу 6 Db 13
604 1392	87 IleGlyLeuGlyTrpGlySerAspThrGlyThrArgLeuValThrLysPheGlu :::            ::       45 TTGCAATTTGGGTTAGGCTATGGCTCTTATGGAGGGCTTATGCTTAAT	Oy 5 Db 13
586 1344	67 Glns	Qy 5 Db 13
566 1311	47 VallleAspLeuProGluArgThrAlaLeuAlaAsnArgLysThr ::::::       00 CTCATGGATTTA	Qу 5 Db 13
546 1299	527 IleSerAspAlaValSerAlaValAlaArgAlaIleLeuProAspGluSerGluAsnGlu 5 	Qy 5 Db 12
526 1257	07 AspAspArgValLeuAlaIleAsnHisAspAspGlyValAsnArgSerIleLeuGlyArg	Qy 5 Db 12
506 1224	89GlnAspLysLeuAsnLeuValAlaAlaLysAlaArgHisLeuTyrAspMetPro   ::	Qу <b>4</b> Db 11
488 1188	7IleSerPtoIleGluPheSerAlaSerAsnLeuIle	Qy 47 Db 112
476 1128	59 ThrLeuGluProValIleGluThrValGluLeuThrAspGlyIleLeuMetAsp	Qy 4 Db 10

	RESULT 20  JS-10-335-977-157  Sequence 157, Application US/10335977  Sequence 157, Application US/10335977  Sequence 157, Application US/10335977  Sequence 157, Application US/10335977  APPLICANT LOUGLAS SMITH et al TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES  RELATING TO HELICOBACTER PYLORI FOR  NUMBER OF SEQUENCES: 10031  CORRESSOR LAHIVE & COCKFIELD  STREET: 28 State Street  CITY: BOSTON  STATE: MASSACHUSETTS  COUNTRY: USA  ZIP: 02109-1875  COMPUTER READABLE FORM:  MEDIUM TYPE: CDJROM IS09660  COMPUTER: IBM PC Compatible OPERATING SYSTEM: Windows NT 4.0  SOFTWARE: UNIX  CURRENT APPLICATION DATA: APPLICATION NUMBER: US/10/335,977  FILLING DATE: 17-DEC-2002  PRIOR APPLICATION NUMBER: 08/93,002  PRIOR APPLICATION NUMBER: 08/93,002  FILLING DATE: 17-DEC-1997  ATTORNEY/AGENT INFORMATION:  NAME: Mandragouras, Amy E.	SULT 20 10-335-97; Sequence 1: GENERAL APPITITI APPITITI COMI COMI COMI PRIC	USE
	TrpAlaSerProValGly 892          :::    TGGATTTCGCCCATGGGG 2544	887 2527	Qy Db
2526	GTTATAGGGGCTGGGTTTGAAAGAGCGACTTGGAGGGCTTCCACAGGCTTGCAGATTGAA	2467	Дb
886	AlaTyrAspLysGlyPheThrAsnAspThrLysIleGlyAlaGlyValGlyValArg	868	Qy
2466	ACTAGAGGGAGTTTTTTCTATAACGCTCCTGTTACGACAGCGAATTTTAAAAGATTATGGC	2407	ДĎ
867	Asn	867	Оу
4	TTC	2347	DЬ
966	AspLeuArgLeuAlaValPheGlyAspIleGly	856	ОУ
w	TGGCTTGGAGGCGATGGGATTTTTACCGCTTCTACTGAATTGAGCTATGGGGTGCTAAAG	2287	Дb
855	$LeuThr \texttt{GlyGlyGlnValLeuAlaValGlyThrAlaGluTyrAsnTyrGluPhe\texttt{MetLys}$	836	ОУ
N	GTAACCACGGTGAGAGGCTTTAGGAACGGATCGGGTTACTCCTAAAGATGAGTTTGGCTTG	2227	da L
י נ	AspG]pSerT]eArgG]vTvrA]aHisAspSerT.euSerProT]eSerAspIvsG]vTvr	00	0
815 2226	<pre>ILETTPSSCTASpAsnPheAsnHisValProTyrArgLeuArgPhebheAlaGlyGly         : : :                          </pre>	797 2167	dg Vy
2166	GTT	2107	ф
796	IleGlnAlaGlyTyr	792	Qy
2106	AACGGGTTAGGCGGGAATGTCCGTAACACCAAAGTTTATGGTAAATTCGCCGCTTACCAC	2047	Db
791		778	Оу
2046	TCCTATGCGACGATGTCTGGCTTGCCAAGCTCTGGCACGCTCAATTCTTGG	1996	da
777	MetAlaIleAlaArgAlaGlyTleSerGlyValTyrSerPheGlyAsp	762	Оу
1995	AGCTATGACAACACCGATGATTATTACTTCCCTAGAAATGGGGTTATCTTTAGT	1942	Db
761	GlySerSerGlyLeuValSerAspAlaAsn	752	Qy

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NAME/KEY: misc_feature;
LOCATION: (B) LOCATION 1...2778;
SEQUENCE DESCRIPTION: SEQ ID NO: 157:
US-10-335-977-157
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Query Match:
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REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
TELEFAX: (617)247-74400
TELEFAX: (617)242-4214
INFORMATION FOR SEQ ID NO: 157:
SEQUENCE CHARACTERISTICS:
LENGTH: 2778 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                            319
                                                                                                                                                                                                                                                                                                                                                                           145 GluGlnProAsnSerGluValValValProProThrLeuGluProGluLysProGlyLeu 164
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     242 AlaArgAlaValGlyTyrTyrAspIleAspLeuSerIleIleArgAsnSerIleGlyGlu 261
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                                              541 CAAAAATTAGAG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87 ValAsnPheAspAspGlnSerProIleSerArgIleGly------GluGlnSerProPro 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 GlnAlaArgLeuAsnAlaAlaGlyLeuAsnAlaLysProGlnSerGlnAlaLeuAspVal 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: circular MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
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ORGANISM: Helicobacter pylori
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                                                                                                                                                     HisGlnLysThrGluProTyrAlaAsnIleLysAlaAlaLeuGluAspIleThrGlnGlu 222
                                                                                                                                                                                                                                                                                                    IleLysArgLeuTyrAlaArgLeuPheAsnAspGlyValAsnLysValProArgLeuLys 184
                                                                                                                                                                                                                                                                                                                                          GATATGGTGGATTCTAAAAAAAATAGACACCGCTGTTTTAGCTTTGTTCAACCAAGGGTAT 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------CTCAATCCAATCAAACGCCTAAAGAAATGAAAGTCAAGTCCATTT 253
                                                                           SerAlaMetAspLeuAsnGlySerIleProArgLeuArgGlnThrAlaLeu---ValAla 241
                                                                                                                    AAGGAAAAAGGCCCTTAAAATCCCCAAATGGGGATCAAAAAGGGCCGACACCTTTGATGAG
                                                                                                                                                                                           TTTCATTTTGATGAAAAAGCCAGGATTGCCGGGGTAGAAATCAAGGGTTATGGGACTGAA 480
                                                                                                                                                                                                                            AlaLysPheTyrGlnSerSerGlnSerGly-----GluThrSerAlaIleGlySerSer 202
                                                                                                                                                                                                                                                                     TTTAAAGACGTTTATGCC---ACTTTTGAAAACGGCATT-----TTAGAG 420
                                                                                                                                                                                                                                                                                                                                                                                                                    GCTAATGAAATTGCAAAGATTCGCGTG-----
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                                              -----CATGCTAAAACGGCTTTAAAAACGGCT 579
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576	A la Asn Arg Lys Thr Pro A la Asp Val Tyr Gln Ser Lys Lys Val Pro Leu Tyr Val Phenomen Control of the Control	557	Qy
1404	GTCAATAGCTCATTGATGGATTTG	1381	Db
556	AlaIleLeuProAspGluSerGluAsnGluValIleAspLeuProGluArgThrAlaLeu	537	Qy
1380	TAGGGTTTTTCTCTAAAGTCAAGATTGAAGAAAA	1327	DЬ
536	AspGlyValAsnArgSerIleLeuGlyArgIleSerAspAlaValSerAlaValAlaArg	517	Qy
1326	AGGGAATTGTTACTAGGGCCTAAAGATAAATACAACTTGACCAAACTGAGAAATTCCGAA	1267	Db
516	ArgHisLeuTyrAspMetProAspAspArgValLeuAlaIleAsnHisAsp	500	Qy
1266	GTCATCATTTCAGGGAACCAGCGCACGAGCGATAGGATCATTAGG	1222	Db
499	IleGluPheSerAlaSerAsnLeuIleGlnAspLysLeuAsnLeuValAlaAlaLysAla	480	Qy
1221	PATC	1168	Db
479	lyīl	460	Qy
1167	GACGAAAAAAACGGG	1153	дb
459		441	Qy
1152	GCGTTTGCGGTGGTGAAGCCAGACTTGGATAAA	1120	Db
440	oGluArgGluGlnIleGlnAsnAspGl	421	Qy
1119	ATTGAGCATTTAAGAGCGGATGCGCAAATTTTAAAAACCGAAATCGCCGATAAGGGCTAT	1060	Дb
420	LeuGlnAlaValArgAlaLeuSerAsnAspLeuIleAlaThrArgTyrPhe	404	Qy
1059	ACCTTAGAAAAGCGCTTAAAGTTAAAAGGAAAGATGTCTTTAAT	1006	Db
403	roValLysArgGluLeuLeuGluGlnLeuLeuThrValAsnMetGlyGluAlaTyrAsn	384	Оу
1005		976	Db
383	LeAspProLysThrAsnGlnLeuThrThrAspProAspLysLeu	364	Оу
975	AGGATTTCAGAT	916	Db
363	laAspValSerLeuIleTyrAspThrGlyThrGlnTyrArgPheAspGlu	346	Qy
915	ი.	856	Db
345	erValAspValIleLeuProAspAsn	333	Оy
855	: : : GACGGGAAATTGCGCTTAGATCAATTAGAATACGATTCTTTGCGTATCCAAGATGTGTAT	96	Db
332	spGlyArg	330	Qy
795	ATTGAATCTTTGAGCGCGAACAAGCAGCGCGATTTCATGGGCTEGATGTGGGGCTTGAAT	736	Db
329	sGlyTyrPhe	319	Оу
735	cerere	676	Db
318	(leGlyAspValPheHisHisGlyLysTyrGluThrLysLysAsnLeu	299	Qy
675	ATAGGGGG	616 (	Db
298	lyGluGlyAlaAspAspLysAlaPheThrThrValAlaAspGlu	282	Qy
615		607 (	DЬ
281	spValIleIleHisAspLeuGlyGluProValTyrIleAspTyrArgAlaValGlu	2	Qy
506		580 :	Db

В

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 641 AsnAspGlnLeuArgAlaThrLeuGlyTyrGlnGlnGlnValPheGlyHisSerThrAsn 660 :::|||
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CTCAATCACACCTAAAGATGAGTTTGGCTTGTGGCTTGGAGGCGATGGGATTTTTACCGC 2408
                                      pSerLeuSerProIleSerAspLysGlyTyrLeuThrGlyGlyGlnValLeuAlaValGl 845
                                                                                                                                         lProTyrArgLeuArgPhePheAlaGlyGlyAspGlnSerIleArgGlyTyrAlaHisAs
                                                                                                                                                                                                                                                                                                       CCCTAGAAATGGGGTTATCTTTAGT-----TCCTATGCGACAATGTCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----TyrSerLeuGluValGly-----
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                                                                                                                                                                                                       GATCGCTCGTTTTAAAACGCAAGGGGGCTATATCTTTAGGTATAACACCGATGATTACTT
                                                                                                                                                                                                                                 yValTyrSerPheGlyAsp·····--AsnAlaTyrGlySerAsnArgAlaHisGl 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         yValAlaValHisLys.....ThrValAlaAspAsnLeuValAs 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGCTACTATTCCTCTGTTAATGAAGTG-GCCTCTCCAAGGCAATGTTCCACACCCGCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGCTTAGGGTATAACTTGAATGTTACCAAACTCCTTGGTTTCAGCAGCCCCCTTATACAAC 1824
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                                                                                                       GCCCTTAAACTCCACTTTCTACATGGGGGGCGTAACCACGGTGAGAGGCTTTAGGAACGG
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SNALASERALAGluHiSGlyTyrPheAspGlyArgTrpLeuAspArgSerValAspValI 341    :::       :::       :::       :::       :::	euIleGlyAspValPheHisHisGlyLysTyrGluThrLysLysAsnLeuIleGluA 321 :::   ::: :::    ::: ACGTCGGCGAGCCATCGACGACCAGGCCCTGGTCCAGGCCACCCGCTCCCTGTTCAAGA 283	alArgGlyGluGlyAlaAspAspLysAlaPheThrThrValAlaAspGluValProLeuL 302 ::    ::    TCCGGGTCAATGGCCTGCAGCGCGTGTCCGCCGGTAGCGTGTTCGCCGCCCTGCCGCTGA 223	lAsp-ValIleIleHisAspLeuGlyGluProValTyrIleAspTyrArgAlaValGluV 282     :::    :::	aArgAlaValGlyTyrTyrAspIleAspLeuSerIleIleArgAsnSerIleGlyGluVa 262	SerAlaMetAspLeuAsnGlySerIlePro-ArgLeuArgGlnThrAlaLeuValalaAl 242      :::	-168-2 (1-919) x US-10-419-128-4442 (1-2466)	Alignment Scores: 4.3e-05 Length: 2466  Pred. No.: 186.00 Matches: 175  Score: 33.74% Conservative: 132  Best Local Similarity: 19.23% Mismatches: 276  Query Match: 3.93% Indels: 330  DB: Gaps: 42	Oy 845 yThraladulTyrasTyrGluPheMetLysAspLeuArgLeuAlaPheGl 863 Db 2409 TTCTACTGAATTGAGCTATGGGGTGTAAAAGCGGCTAAAATGCGTTTACGTGTTTT 2468 Oy 863 yAspIleGly

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US-10-366-683-4442
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LENGTH: 2466
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/366,683
CURRENT FILING DATE: 2003-02-13
PRIOR APPLICATION NUMBER: 09/252,991
PRIOR FILING DATE: 1999-02-18
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Nolling, Jork
APPLICANT: Deloughery, Craig
APPLICANT: Bush, David
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PATH03-04
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                                                                                                             snAlaSerAlaGluHisGlyTyrPheAspGlyArgTrpLeuAspArgSerValAspValI 341
                                                                                                                                                                                                     euIleGlyAsp---ValPheHisHisGlyLysTyrGluThrLysLysAsnLeuIleGluA 321
                                                                                                                                                                                                                                                                                                                                          TGATCGCCGAGGTTCAC--------GCCGAGTCCTTCACTGTTTCCGATA
                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGAAAAAAAGGACTCCATGAA----ACGCTTTCTGCTACCCGCGCTGCTGTCAGCGCTGA 121
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Qy 335 AspArgSerValAspVall1LeLeuProAspAsnThrAlaAspValSerLeuILeTyrAsp 354	Qy 295 ValAlaAspGluValProLeuLeuIleGlyAspValPheHisHisGlyLysTyrGluThr 314		Qy 266 IleHisAsp	Qy 246 GlyTyrTyrAspIleAspLeuSerIleIleArgAsnSerIleGlyGluValAspValIle 265	230 SerIleProArgLeuArgGlnThrAlaLeuVal	US-09-914-168-2 (1-919) x US-10-419-128-14662 (1-516)	Alignment Scores:  A. 95e-05  Score:  174.50  Matches:  Percent Similarity:  Best Local Similarity:  Query Match:  3.69%  A. 95e-05  Matches:  4.9  Conservative:  38  Mismatches:  62  Indels:  39  Gaps:  6	RESULT 23  US-10-419-128-14662  REQUENCE 14662, Application US/10419128  REQUENCE 14662, Application US/10419128  REMERAL INFORMATION:  APPLICANT: MARC J. RUBENFIELD AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  FILE REFERENCE: 107196.136  CURRENT FILING DATE: 2003-04-21  PRIOR APPLICATION NUMBER: US/09/252,991  PRIOR APPLICATION NUMBER: US/09/252,991  PRIOR APPLICATION NUMBER: US/094.788  PRIOR FILING DATE: 1998-02-18  PRIOR APPLICATION NUMBER: US 60/074,788  PRIOR APPLICATION NUMBER: US 60/094,190  PRIOR APPLICATION NUMBER: US 60/094,190  PRIOR APPLICATION NUMBER: US 60/094,190  PRIOR SEQ ID NOS: 33142  SEQ ID NO 14662  LENGTH: 516  TYPE: DNA  ORGANISM: Pseudomonas aeruginosa  US-10-419-128-14662	Oy 899 laThrGlyValLySGluGluGlyAsn 907        :::   :::	Oy 880GlyAlaGlyValArgTrpAlaSerProValGlyGlnValArgValAspValA 899	Qy 871 R79

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; ORGANISM: Pseudomonas aeruginosa
US-10-366-683-14662
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LENGTH: 516
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CURRENT FILING DATE: 2003-02-13
PRIOR APPLICATION NUMBER: 09/252,991
PRIOR EILING DATE: 1999-02-18
NUMBER OF SEQ ID NOS: 33142
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APPLICANT: Deloughery, Craig
APPLICANT: Bush, David
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS
FILE REFERENCE: PATH03-04
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355 ThrGlyThrGlnTyrArgPheAspGluValValPhePheThrIleAspProLysThrAsn
                                                                        335 AspArgSerValAspValIleLeuProAspAsnThrAlaAspValSerLeuIleTyrAsp
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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SEQ ID NO 4165
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CURRENT FILING DATE: 2003-04-21
PRIOR APPLICATION NUMBER: US/09/252,991
PRIOR EILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
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US-10-366-683-4165/c
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APPLICANT: Rubenfield, Marc J.
APPLICANT: Nolling, Jork
APPLICANT: Nolling, Jork
APPLICANT: Deloughery, Craig
APPLICANT: Bush, David
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PATHO3-04
CURRENT APPLICATION NUMBER: US/10/366,683
CURRENT FILING DATE: 2003-02-13
PRIOR APPLICATION NUMBER: 09/252,991
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                                                                                                                                                                                                                                                                                                -----GlyAlaGlyValGlyValArgTrpAlaSerProValGlyGlnVa
                                                                                                                                                                                                                                                                                                                                    TAGCACCTTCGATACCGACTGCCCGACCAAGACCACCACCAACTGCGACGGCATCAAGAC
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US-09-914-168-2 (1-919) x US-10-366-683-4165 (1-1530)
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yAspAsnAlaTyrGlySerAsnArgAlaHisGlnMetThrGlyGlyIleGlnAlaGlyTy 796
                                                                                                                                                                                                                                       uValSerAspAlaAsnMetAlaIleAlaArgAlaGlyIleSerGlyValTyrSerPheGl 776
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APPLICANT: Wang, Liangsu
                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
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                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A
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FILING DATE: 2000-12-22
APPLICATION NUMBER: 60/267,636
FILING DATE: 2001-02-09
APPLICATION NUMBER: 60/269,308
FILING DATE: 2001-02-16
                                                              APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
                                                                                                                                                        APPLICATION NUMBER: 60/230,335 FILING DATE: 2000-09-06
                                                                                                     APPLICATION NUMBER: 60/242,578 FILING DATE: 2000-10-23
                                                                                                                              APPLICATION NUMBER: 60/230,347 FILING DATE: 2000-09-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAGCTTCAGCCTGGCGACGCCGATCAAGAAGCCGGACAAC
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Ohlsen, Kari
Zyskind, Judith
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 32708
LENGTH: 2163
                                                                                                                                                                             394 LeuThrValAsnMetGlyGluAlaTyrAsnLeuGlnAlaValArgAlaLeuSerAsnAsp
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GlnIleGlnAsnAspGln-
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---ATCCACGGTGATATTTTAGGGAATAATCATGTGGATACCAAAATCAATTTTGCTTAT
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                                              TTTAAAGGCACCAGTGTTGATAACATCATTAATAAAGATATTGTATTAATTGCTTCAGAC
                                                                                      LeuIleAlaThrArgTyrPheAsnMetValAsnThrGluIleValPheProGluArgGlu 433
                                                                                                                                                                                                                          AAT----ACTGATGAAACTATCTTACATGTTACCGGCGAT-
                                                                                                                                                                                                                                                                    AsnGlnLeuThrThrAspProAspLysLeuProValLysArgGluLeuLeuGluGlnLeu
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1812	3 ACTTACCAATATCAATGGCTCAAT	17	da
w	20 GluAlaLeuLeuAlaGlyValAlaValHisLysThrValAlaAspAsnLeuValAsnPro	7	Qy
1752	9 ATTAACGCTGGCACCTATTTGGATTTTGATTTTATCC	1	рь
719	00 AlaProProGluThrTrpGlnAspLeuProValAspPheValAsnGlyLysProSerGln	7	νο
1698	9 GGATGGCAAGGAAATACCA	163	д .
699	<pre>2 GlyTrpAsnArgThrTyrSerLeuArgTyrArgLeuAspLysLeuLysTh</pre>		νο
1638	B5 TTAAATATTGGTTATTACACTGTCGATAGTGAGAGGGATATCGGTGGTAATACG	158	DЪ
681	2 PheAspLeuSerThrArgThrLeuGluHisGluIleSerArgSerIleIleGlr	, 66	δ
1584	8 T1	152	망
661	2 AspGlnLeuArgAlaThrLeuGlyTyrGlnGlnGluValPheGlyHisSerThrAsnGly	64	Qy
1527	TACGCTAAAGCCGATGCTAAACAACGTAATGCAAGCAAAGAAATTAGCCAT	1477	В
641	oLeuAsn	63	Qy
1476	ATCGGTACTGATTATGAAATAAATCAAGATGCGCTAATTGGCGTTTCTTTAGCATATAAC	1417	рb
630	AlaGlyAlaGluLeuArgLeuSerGluAspLysLysGlyValLysLeu	615	Q <sub>y</sub>
1416	7 GGTACGCAAAGTCAACAAGGTGGAATTAACGGCTACAATACTTATCGCACTGGTATTCAA	135	рь
614	0 ValThrLysPheGluHisAsnLeuIleAsnArgAspGlyTyrGln	60	9
1356	9 GAAAGAGAAATAGGTTGGAATAGCTGGGCAAATATTCTGTACGGTTAT	130	Db
599	2 ProArgAspGlyGlnIleGlyLeuGlyTrpGlySerAspThrGlyThrArgLeu	58	Qy
1308	2 CGCTATGATGAA	128	Db
581	2 ProAlaAspValTyrGlnSerLysLysValProLeuTyrValPheValAlaSerAspLys	56	ογ
1281	9 GATATGCGCAACAATATT	124	DЬ
561	2 GluSerGluAsnGluValIleAspLeuProGluArgThrAlaLeuAlaAsnArgLysThr	54	٧ <u>٩</u>
1248	TGACGGTAGTGATATTCAAGCAGGATTAATCATGGTTGAA	119	망
541	ArgIleSerAspAlaValSerAlaValAlaArgAlaIleLeuProAsp	52	Qy
1194	TAATATTGCTGCACTATCAAATGAT	116	DЬ
521	pArgValLeuAlaIleAsnHisAspAspGlyValAsnAr	50:	Q
1164	TAATAAT	110	Вb
501	nLeuIleGlnAspLysLeuAsnLeuValAlaAlaLysAlaArgHis	48:	Qy
1104	ATTTAAT 1	107	B
181	ValIleGluThrValGluL	463	Qy
1071	AATTTTATTAGCGCTGCTGAACGTGGCAATGTCACAGAGAATGGATTAGCAGCAGCTAAA 1	1012	Db
162	SerSerArgThrGluProAlaGlnValAspGluSerThrLeuGluPro 4	447	Qy
011	GGTGGTGTCAGTGGTAATCAATTAATTGCGCGTTATGGTATTAGCTACGAAGGGGGGGAT 1	952	DЬ
146	valSerPheGluGlnSerSer 4	440	Qy
)51	ATTTCACCTTTATTAGAAAAAACAGATTCATGGTTAGAAACGACCACCAAATATTAGC 9	892	망
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191	TCGGCAATTAAAGATGAAGCGGGCATTACAGTGACTGATGCAAATGCCATAGCGCCAGAT 8	832	Db

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US-10-010-160-15
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GENERAL INFORMATION:
APPLICANN: Rosey, Everett L.
APPLICANN: Strugnell, Richard A.
APPLICANT: Good, Robert T,
APPLICANT: King, Kendall W.
                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version SEQ ID NO 15 \,
                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: AU PR1381
PRIOR FILING DATE: 2000-11-10
PRIOR APPLICATION NUMBER: US 60/249,596
PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NOVEL THERAPEUTIC COMPOSITIONS FOR TITLE OF INVENTION: TREATING INFECTION BY LAWSONIA SPP. FILE REFERENCE: DAVIIIO.001ANS CURRENT APPLICATION NUMBER: US/10/010,160 CURRENT FILING DATE: 2001-11-09 CURRENT FILING DATE: 2001-11-09
                                                                                                                                                                                                                                                                                                       LENGTH: 1812
TYPE: DNA
ORGANISM: Lawsonia
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LOCATION: (1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              815 GlyAspGlnSerIleArgGlyTyrAlaHisAspSerLeuSerProIleSerAspLysGly 834
SerAspAlaAsnMetAlaIleAlaArgAlaGlyIleSerGlyValTyrSerPheGlyAsp 777
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AATACCGTTGGTGGTGACATCATTAGTGCTGAATTAGGTGCA---AACCTTGATATTACC 2073
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Conservative:
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Ali	RESULT US-10 Seque GENEE GENEE APPI APPI APPI APPI APPI APPI APPI AP	DЬ	Qy	Db	Qy	Db .	0	B 5	5 5	β δ <sub>0</sub>	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	DЪ	Qy	Db	Qy
ignment	SULT 29 -10-369-493 Sequence 42: GENERAL INFO APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: TITLE OF 11 TITLE OF 11 TITLE OF 11 TITLE OF 11 TITLE OF 11 TITLE OF 11 TITLE OF 11 TITLE OF 11 TITLE OF 11 TITLE OF 12 TITLE OF 12 TITLE OF 12 TITLE OF 12 TITLE OF 12 TITLE OF 12 TITLE OF 13	1757	905	1697	885	w	869		051	831	1464	811	1405	791	1404	771	1371	751	1311	743	1251	735	1191	719
Scores:	SULT 29 -10-369-493-42248/c -10-369-493-42248, Application US/10369493  Sequence 42248, Application US/10369493  GENERAL INFORMATION: APPLICANT: Hinkle, Gregory J. APPLICANT: Slater, Steven C. APPLICANT: Soldman, Barry S. APPLICANT: Chen, Xianfeng TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)8  CURRENT FILING DATE: 2003-02-28  DRIOR APPLICATION NUMBER: US 60/360,039  PRIOR APPLICATION NUMBER: US 60/360,039  PRIOR FILING DATE: 2002-02-21  NUMBER OF SEC ID NOS: 47374  SEC ID NO 42248  LENGTH: 1890 TYPE: DNA ORGANISM: Halobacterium sp. NRC-1	CTTTATATTAGT	luGlyAsnProIleLysLeuHisPhePheIleGlyThrProPhe 919	TACGATATTATACAAGTTTTGCCCCCATACGTTTAGATATAGCAACTCCACTTCAAGATA 1756	largTrpAlaSerProValGlyGlnValArgValAspValAlaThrGlyValLysGl	TGACTTTAAAAAAATCAATA-TATTGGGGGGTAGGCCTGGGGC 1	vråsplvsGlvPheThrAsnåspThrLvsI]eGlvA]aGlvValGlvV 885	ACGATTAAAAATAACAGAATCCATTGGCATTGTGCCAATTTAATTGGATGGGGGGAATATTT 1637	AWAINIADAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	nValLeuAlaValGlyThrAlaGluTyr-AsnT     :::       CTTTTCTTTTTTTTTTTTTTTTTTTTTTTT	TTATGCTGGGGGTGGTAGGTGTAAGAGGGTATGACTATCAATCA	ePheAlaGlyGlyAspGlnSerIleArgGlyTyrAlaHisAspSerLeuSerProIleSe 831	-ATAGCAATAGGTTCCCTCCTAGGGAAAGATATAGAAAACTATCCTGCAATACTAAGGTT 1463	eTrpSerAspAsnPheAsnHisValProTyrArgL	1404	yValTyrSerPheGlyAspAsnAlaTyrGlySerAsnArgAlaHisGlnMetThrGlyGl 791	TCTTAAAACAGGGAAACTTATCTTGGCTAACAAA 1404	lGlySerSerGlyLeuValSerAspAlaAsnMetAlaIleAlaArgAlaGlyIleSerGl 771	ATATAAAAAAAAGATTTTGACTTTACGTAGTCGGTTTGATTTTAGCTTTTACATAGACGT 1370	TyrArgGlnArgTyrSerLeuGluVa 751	TCCTCTTAATCCTATCCAAGGAACAAAAGCTACCTTAAATGTTACTCCTTATATTGGTAA 1310	nLeuValAsnProMetArgGly742	TTACTCTTTTTGGCATCCCCTTATCAATAACAAGGGATAGTTCTAAAGA 12	nGluAlaLeuLeuAlaGlyValAlaValHisLySThrValAlaAspAs 735

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745 1093	ValAlaValHisLysThrValAlaAspAsnLeuValAsnProMetArgGlyTyrArgGln	726 1061	Db Qy
1060	GACTTTGATTTTTTTTTTTTGGTTGG	ū	Db
725	GlnAspLeuProValAspPheValAsnGlyLysProSerGlnGluAlaLeuLeuAlaGly	706	Qy
1036	TCAATGAAATTTAAAAGTAATGGCATTAAAACAAAT	1001	DЪ
705	ThrTyrSerLeuArgTyrArgLeuAspLysLeuLysThrGlnAlaProProGluThrTrp	686	Qy
1000	TTTGCTCTAGAATATACCCGTAATTTATATATTCAA	965	B
685	ArgThrLeuGluHisGluIleSerArgSerIleIleGlnAsnGlyGlyTrpAsnArg	667	ρ
666 964	ThrLeuGlyTyrGlnGlnGluValPheGlyHisSerThrAsnGlyPheAspLeuSerThr:::	647 926	P 64
N	CGTACGACTTATGGAAGTAATGTTACTTTAGGTTTCCCTGTAAATGAAAATACCTCCTAT	o o	рь
646	GlyValLysLeuTyrAlaThrLysProLeuSerHisProLeuAsnAspGlnLeuArgAla	627	Qy
865	GGAAATGTTTTCTTTGAAAACTACGATAACTCTAAAAGTGATACATCCTCTAACTATAAG	8,06	Db
626	AlaGluLeuArgLeuSerGluAspLysLys	617	Qy
805		746	Db
616	ThrargLeuValThrLysPheGluHisAsnLeuIleAsnArgAspGlyTyrGlnAlaGly	597	Qy
4	AATGATTATGGT	734	Db
596	ThrGly	577	Qγ
733		722	Ъ
576	AlaAsnArgLysThrProAlaAspValTyrGlnSerLysLysValProLeuTyrValPhe	557	Qy
721	AAACAAGATAATTTCTTAGGAACAGGGGCTGCAGTAAGTA	680	Db
556	$\tt AlaIleLeuProAspGluSerGluAsnGluValIleAspLeuProGluArgThrAlaLeu$	537	Оy
679	GGTATTGGTTACGGTACAGAGAGTGGTATTAGTTATCAAGCAAG	632	DЬ
536	AspGlyValAsnArgSerIleLeuGlyArgIleSerAspAlaValSerAlaValAlaArg	517	Qy
631	TATAAAGTCAAAGAACGTAACACGGGTAGTATCAACTTT	593	Db
516	AlaLysAlaArgHisLeuTyrAspMetProAspAspArgValLeuAlaIleAsnHisAsp	497	Qy
592	ATCAATGGTAGCAATGATGAAGTGGATGTCGTA	560	Db
496	lleSerProIleGluPheSerAlaSerAsnLeuIleGlnAspLysLeuAsnLeuValAla	477	Qy
559		559	DЪ
476	${\tt GluSerThrLeuGluProValIleGluThrValGluLeuThrAspGlyIleLeuMetAsp}$	457	Qy
559	TTAGATCGTACAGGTTTCTTCGAAACAGTCGAAAACCGAATNGATCCT	512	DЬ
456	AsnAspGlnValSerPheGluGlnSerSerSerSerArgThrGluProAlaGlnValAsp	437	δ
511	:::   :::: AAAAATTCGC	494	Db
436	ThrArgTyrPheAsnMetValAsnThrGluIleValPheProGluArgGluGlnIleGln	417	γQ
493	CAAGAAGGAACTTGGTATAATTCACAATTAGTT	461	DЬ
416	AsnMetGlyGluAlaTyrAsnLeuGlnAlaValArgAlaLeuSerAsnAspLeuIleAla	397	Qy
460	TCTGCTGATAGCACTTTACGTCAGGAAATGCGCCAA	425	Db

							RES US-	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	DЬ	Qy	Db	Qy	Db	Qy	дь	Qy	Db	Qy
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APPLICA FILING PLICATI LING DA PLICATI LING DA	T: Forsyth, R. T: Xu, H. INVENTION: Identif	ANT: Yamamoto, Robert	Zyskind, Wall, Da	: Ohlsen, F	: Malone, Cheryl	NT: Wang, Liangsu	-122A-27975 -27975, Application US/10282122A	CAGTTCCAATTTAGTATTGGAGGTTCTTTC 1756	LysLeuHisPhePheIleGlyThrProPhe 919	GGCCATTGGTATTCTCTTATGCCAAACCAATTAAAAAATATGAAAATGATGATGTCGAA 1726	GlyGlnValArgValAspValAlaThrGlyValLysGluGluGlyAsnProIle 909	GGCAAATCAAGCCGTATTCGCGCCTCTACAGGTGTCGGATTCCAATGGCAATCTCCTATT 1666	GlyPheThrAsnAspThrLysIleGlyAlaGlyValGlyValArgTrpAlaSerProVal 891	AGTGGAAATCGGATAAGAGTGGGTTAGATAACAATGTATTAAAAAGCTTACCCGATTAT 1606	AspLys 871	AGAGCCAAAATACGGTCCGAACTTCCCCTATTTGTTGATGCGGCAAGTGTTTGGAATACT 1546	LeuargLeualaValPheGlyAspIleGlyAsnAlaTyr 869	::: ATGCAATCACAACTGCGAGTGCAGAACTTATT	GlyGlnValLeuAlaValGlyThrAlaGluTyrAsnTyrGluPheMetLysAsp 856	   AGTAATAGTAATAGTAATGGTACTTTTAATAAGATAAGTTCTGATGTGATTGGT 1426	IleSerAspLysGlyTyrLeuThrGly 838	CGTGGTTTTGCTTATGGTAGTATTGGACCTAACGCAATTTATGCCGCTCAAAATGGTAAT 1372	ArgGlyTyrAlaHisAspSerLeuSerPro 829	TTTGGAAACAAGCGTTTACCGTTCTATCAAACTTATACAGCGGGTGGCATCGGTTCATTA 1312	AspAsnPheAsnHisValProTyrArgLeuArgPhePheAlaGlyGlyAspGlnSerIle 819	TCTGGGTTGTATCTGCAAAAGCATCTGCAGGATA	SerAsnArgAlaHisGlnMetThrGlyGlyIleGlnAlaGlyTyrIleTrpSer 799	TACTACAAACTAAGTGCAGATGTACAGGGTTTCTACCCATTA 1195	MetalaIleAlaArgAlaGlyIleSerGlyValTyrSerPheGlyAspAsnAlaTyrGly 781	ACTANAGGGGTTANAGCANGTCTTGGTGGACGNGTTACTATTCCNGGTTCTGATANCANA 1153	:uGluValGlySerSerGlyLeuVal

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Percent Similarity:
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; ORGANISM: Mycoplasma pneumoniae
US-10-282-122A-27975
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PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-06
PRIOR PELLOATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR PELLOATION NUMBER: 60/242,578
PRIOR PELLOATION NUMBER: 60/242,578
PRIOR PELLOATION NUMBER: 60/253,625
PRIOR PELLOATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PELLOATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PELLOATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
PRIOR PELLOATION NUMBER: 60/269,308
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NUMBER OF SEQ ID NOS: 78614
SOPTWARE: Patentin version 3.1
SEQ ID NO 27975
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                                                                                                                                                                                                                                                                  116 ThrProLeuSerLeuGluLeuPheAlaGlnGluSerThrGluMetGlyIleAsnPro 135
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                                                              AATGAGTTTGTCACAACTACTAGTAGAGAAACAACTACTTTTGCATCAACTCCAGTTTTT 1512
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AlaArgLeuPheAsnAspGlyValAsnLysValProArgLeuLysAlaLysPheTyrGln 189
                                                                                      GluValValProProThrLeuGluProGluLysProGlyLeuIleLysArgLeuTyr 169
                                                                                                                                                                                    AsnAspTyrIleProGluTyrGlnGlyGlu-----
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HALITIERSHITISRSPENS POST VALESHITE SUCCESSION STORMS STOR	milyonnyco	SLeuAsnLeuValAlaAlaLysAlaArgHisLeuTyrAspMetProAspAspArgValLe 511	pGlyIleLeuMetAspIleSerProIleGluPheSerALaSerAsnLeULIGGINSPLY	NAGTTTCGAGTCTGAACCAGAACCTAATTTTGAAACA	GluLeuThrAs 4	23	uGlnIleGlnAsnAspGlnValSerPheGluGlnSerSerSerSerArgThrGluProAl 453		다. 1	uLeuThrValAssnMetGlyGluAlaTyrAsnLeuGlnAlaValArgAlaLeuSerAsnAs 413	ATCTGATCCTAGCTTTGAACCAGAAGTAGAAATTCAACCTGAACCAGAA	93		ArgPheAspGluValValPhePheThrIleAspProLysThrAsnGln		eTyrAsp	- 20	335	GATTGGGAGGCGTTAATTGGTAACAGTGAATACGGTTACTTTGATGCAGAGCAAAAC 1986	ProLeuIleGlyAspValPheHisHisGlyLysTyrGluThrLysLysAsn 317	GCAGTCGAACCAGCTATTGAAACCGAGTCAAAAGCAACTTCTGAAGCCCAAGCTGAACTG 1929	ArgGlyGluGlyAlaAspAspLysAlaPheThrThrValAlaAspGluVal 299	AACATTAGCTGCAGAGACCGTTGAAGAAGCGCAAGTTGAACAAGAGTCAAC	AspLeuGlyGluProValTyrIleAspTyrArgAlaValGluVal 282	GAAGTATTAGCAGTTGTTGAAGAAGCACCACTTGCTGTAGAACCAATTGTTGAAACTTCA 1809	IleAspLeuSerIleIleArgAsnSerIleGlyGluValAspValIleIleH1# 267	CAGTTGTTACTGAAACTGTTACAGTTACTGAGAAAGCAGTAGAA	SerIleProArgLeuArgGlnThrAlaLeuValAlaAlaArgAlaValGlyTyrTyrAsp 249		AlaAlaLeuGluAspIle	TTGTTGAAACGGTTGAACTT	SerSerGlnSerGlyGluThrSerAlaIleGlySerSerHisGlnLysThrGl	GAATCAACTGTTGTAAGTGCAACATCAAATGAACCTAATGTT;

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Percent Similarity:
Best Local Similarity:
Query Match:
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NAME/KEY: unsure
LOCATION: (1)..(2183)
OTHER INFORMATION: unsure at all n
US-10-369-493-44808
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GENERAL INFORMATION:
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LENGTH: 2183
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APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION STATES CONSTRUCTED TO THE CONSTRUCT OF SEQ ID NOS: 47374
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     562
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                                                                                   ProLeuGlyLeuAspMetSerValIleGluGluThrThrProLeuSerLeuGluGluLeu 123
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                             PheAlaGlnGluSerThrGluMetGlyIleAsnProAsnAspTyrIleProGluTyrGln 143
                                                                                                                                  CTAAAAAAATACACAATC---GATCTAACTGAACGTGCCGAACAGGGCAAATTAGATCCC
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                                                                   GTGATTGGGCGCGAT---
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483 1512	Qy 464 IleGluThrValGluLeuThrAspGlyIleLeuMetAspIleSerProIleGluPheSer 4 ::::	
1455	Db 1402 GAGCTGACTGGCACTCAGAACATTAAAGCAGAATTAGAGAATACGCGCCTTGAA:	
463	roVal	
445 1401	Qy 427 IleValPheProGluArgGluGlnIleGlnAsnAspGlnValSerPheGluGlnSer .:::	
1341		
426		
406 1284	Qy 387 ArgGluLeuLeuGluGlnLeuLeuThrValAsnMetGlyGluAlaTyrAsnLeuGlnAla .	
1248		
386	368 ThrileAspProLysThrAsnGlnLeuThrThrAspProAspLysLeuProValLys	
367	AspvalSerLeulleTyrAspThrGlyThrGlnTyrArgPheAspGluValValPhePhe	
1173		
347	Qy 328 TyrPheAspGlyArgTrpLeuAspArgSerValAspValIleLeuProAspAsnThrAla :	_
1137	1081 CACCATGTACAAATTACTGATCCAGCAATTGTTGCTGCTGCGACTTTGTCTCATCGC	
327	Ov 308 HisHisGlvLvsTvrGluThrLvsLvsAsnLeuTleGluAsnAlaSerAlaGluHisGlv	
307	293 ThrThrValAlaAspGluValProLeuLeuIleGlyAspValPhe	
1020	Db 964 TACATTGAAAAAAGATGCTGCTTTGGAACGTCGTTTCCAGAAAGTGTATGTGGCGGAG	
292		
963	Db 910 GCTCGGGGTGAACTACACTGTGTTGGTGCGACGACACTGGATGAATATCGTCAG	
279		
909	Db 853 GGAGCAGGTAAGGCTGATGGCCGCAATGGATGCCGGTAACATGCTTAAACCCGCCTTG (	
259		
852		
239	nGlySerIleProArgLeuArgGlnThrAlaLeu	
801	Db 742 GGTGCGAAATACCGTGGTGAATTTGAAGAACGTTTGAAAGGTGTTTTGAACGATCTCGCC (	
220		
741	Db 688 GAGGGCTGAAAAACAAACGCGTTCTGTCCCTTGATATGGGAGCGCTAGTGGCG	-
200		
687	Db 637 ACCGCCATAGTTGAAGGTCTGGCGCGCAGCGTATTATTAATGCTGAAGTTCCA (	
181	lyValAsnLysValPro	
636		
161	luProGluLys	

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US-10-282-122A-33378
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APPLICANT: Wang, Liangsu
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APPLICANT:
                                                                                                  APPLICANT:
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TITLE OF INVENTION: Identification of Essential FILE REFERENCE: ELITAR.034A CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20 PRIOR APPLICATION NUMBER: 60/191,078
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                                                                                                                  Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Malone, Cheryl
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Carr, Grant
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Best Local Similarity:
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; TYPE: DNA
; ORGANISM: Pseudomonas
US-10-282-122A-33378
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 33378
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PRILING DATE: 2000-11-27

DR FILING DATE: 2000-11-27

DR APPLICATION NUMBER: 60/257,931

DR FILING DATE: 2000-12-22

DR FILING DATE: 2001-02-09

PR FILING DATE: 2001-02-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 2000-09
APPLICATION NUMBER:
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FILING DATE: 2000-05-23
APPLICATION NUMBER: 60/:
FILING DATE: 2000-05-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/230,347
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                                                                                                                GlyGluGlnProAsnSerGluValValValProProThrLeuGluProGluLysProGly 163
                                                                                                                                                                                                                                                                          ProLeuGlyLeuAspMetSerValIleGluGluThrThrProLeuSerLeuGluGluLeu 123
                                                                                                                                                                                                                                                                                                                     GTCGAT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AlaLeuAlaGlnGlnAsnAsnProAlaAsnIleIleAsnHisValProAlaHisAspThr
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                                  LeufleLysArgLeuTyrAlaArgLeuPheAsnAspGlyValAsnLysValProArgLeu 183
                                                                                                                                                                                                                                       AGCGTG---CTGGACGTGGCGGGCGTAAAAGAA----
                                                                                                                                                                                            PheAlaGlnGluSerThrGluMetGlyIleAsnProAsnAspTyrIleProGluTyrGln
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  TACCTCGCTCTGATGGGCGACAAGGTCGATAACATCCCCGGCGTG
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Matches:
Conservative:
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Ъ	571	6TTGGCGAAAAAACCGCTGTCGC 6
Οy	204	hrGluProTyrAlaAsnIleLysAlaAlaLeuGluAspIleThrGlnGluSer 2        ;:::::::
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₽ 5	224 661	AlaMetAspLeuAsnGlySerIleProArgLeuArgGlnThrAlaLeuValAlaAlaAlaArg 243 :::    :::
ν	244	yTyrTyrAspIleAspLeuSerIleIleArgAsnSerIleGlyGlu :::
8	715	GATGGCCTTCCTCTTACGAGTTGGCGACCATCAAGA)
₽ 5	264 760	roValTyrIleAspTyrArgAlaValG    :::     :::
Ωy	284	luGlyAlaAspAspLysAlaPheThrThrValAlaAspGluValProLeuL
B	796	TGATGGAACTGTACGCCGAGCTGGAATTCAAGAGCT
ργ	303	IleGlyAspValPheHisHisGlyLysTyrGluThrLysLysAsnLeuIleGluAsnAla 322
Ф	856	TCGAAGACCTGCAACGCGATGCCAAAACGCGCAGGCCAGGAGCTGGTGGTCG
} \{\doldar{\d	323	SerAla
νQ	332	LeuAspArgSer 3
B	976	. : : AAAAGCTTCAGGCGGCACCGCTTTTCGCCTTCGTTACC
Дy	338	
9	1033	SCCCAGCGTGCGCAACTGGTGGGCCTGTCTTTCGCCATO
Ωγ	34	SerLeuIleTyrAspThrGlyThrGlnTyrArgPheAspGluVal 364
δ β	1093 365	%TCCCGCTGACCCACTCCTATATGGGCGTGCCGCAGCAACTGGATCGCGAC PheThr I leAspProLysThrAsnGlnLeuThrThrAspProAspLysLeu
	1153	GTCCTCAAGACGCTCAAGCCGCTACTGGAAGACCCGAACAAGATCAAG 1200
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Dy	398	MetGlyGluAlaTyrAsnLeuGlnAlaValArgAlaLeuSer 411
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₽	1321	ACCGCGACAGCCTGGTGGCCAAG
Y Q	425	ArgGluGlnIleGlnAsnAspGln 43
5		- TAUTICANCTIC CANADACTANADA TACCAMACTANCCII CANCCII CANCCAMA
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8 5	1501	CCTGGCCGCGATTCCGACCTTGCAGCCGGTGCTCAACGAG 15

Oy 67 GlnalaargLeuAsnalaAlaGlyLeuAsnalaLysProGlnSerGlnAlaLeu 84	**O9-914-168-2 (1-919) x US-10-263-929-30 (1-4802)  **8 AlaASNArgSerPheMetProValAlaLeuAlaAlaTyrLeuProLeuMetThrSerGln	10-263-929-30 gnment Scores: d. No.: re: cent Similarity: t Local Similarity: ry Match:	TITLE OF INVENTION: Alzheimer's Disease Linked Genes FILE REFERENCE: LSD-07417 CURRENT APPLICATION NUMBER: US/10/263,929 CURRENT FILING DATE: 2002-10-03 NUMBER OF SEQ ID NOS: 213 SOCTWARE: Patentin version 3.2 SEQ ID NO 30 LENGTH: 4802 TYPE: DNA ROGANISM: Drosophila melanogaster	:TGGTGGAAGTCGGGG	Db 2524 CAGGGCACGCGGCGAC
Qy 373 ThrAsnGlnLeuThrThrAspProAspLysLeuProValLysArgGluLeuLeuGluGln 392 2941 AAGCACGAAGCCATCAAGGACCCACAACGCTTG	Qy 315 LysLysAsnLeuIleGluAsnAlaSerAlaGluHisGlyTyrPheAspGlyArgTrpLeu 334  Db 2841	2680TCGCTAGACGACCTACGCTCCTATCTGGCCGAGGACGGATCCTGTGTGTG	215 AlaLeuGluAspIleThrGlnGluSerAlaMetAspLeuAsnGlySerIleProArgLeu	Qy 161 LysProGlyLeuIleLysArgLeuTyrAlaArgLeuPheAsnAsp 175   :::	Db 2140 AACACGCCCCAATCTCGACCCAAAGGC

730 4056	711 AspPheValAsnGlyLysProSerGlnGluAlaLeuLeuAlaGlyValAlaValHisLys	Оу
710 4002	691 TyrArgLeuAspLysLeuLysThrGlnAlaProProGluThrTrpGlnAspLeuProVal	Qу Дъ
690 3975	671 HisGluIleSerArgSerIleIleGlnAsnGlyGlyTrpAsnArgThrTyrSerLeuArg	Оy
670 3924	651 GlnGlnGluValPheGlyHisSerThrAsnGlyPheAspLeuSerThrArgThrLeuGlu:::	Qу
650 3888	634LysProLeuSerHisProLeuAsnAspGlnLeuArgAlaThrLeuGlyTyr	Оy
633 3828	616 GlyAlaGluLeuArgLeuSerGluAspLysLysGlyValLysLeuTyrAlaThr :::::: 3787 AAGCCCAAAGTG	Оy
615 3786	596 GlyThrArgLeuValThrLysPheGluHisAsnLeuIleAsnArgAspGlyTyrGlnAla	Оу
595 3726	580AspLysProArgAspGlyGlnIleGlyLeuGlyTrpGlySerAspThr	Оу
579 3666	562 ProAlaAspValTyrGlnSerLysLysValProLeuTyrValPheValAlaSer	Ф
561 3606		Фр
558 3546	VallleAspLeuProGluArgThrAlaLeuAlaAsn	рb
541 3492	522 SerIleLeuGlyArgIleSerAspAlaValSerAlaValAlaArgAlaIleLeuProAsp   ::: :::::::::::::::::::::::::::::::	Ф
521 3432	502 LeuTyrAspMetProAspAspArgValLeuAlaIleAsnHisAspAspGlyValAsnArg ::::::	Оу
501 3372	<pre>alaAlaLysAlaArgHis       AAGCTGGTGGCAACTCCGATTTCTCC</pre>	Фр
484 3312	PheSerAla :::    GATACCGCC	Db Qy
471 3252	458 SerThrLeuGluProVallleGluThrValGluLeuThrAsp	Qу
457 3192	438 AspGlnValSerPheGluClnSerSerSerSerArgThrGluProAlaGlnValAspGlu	Фр
437 3132	430ProGluArgGluGlnIleGlnAsn 430	Qу

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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US-10-267-502-24
; Sequence 24, Application US/10267502
; GENERAL INFORMATION:
APPLICANT: Kim, Jaeseob
; APPLICANT: Galant, Ron
; TITLE OF INVENTION: Obesity Linked Genes
; FILE REFERENCE: LSD-07416
; FILE REFERENCE: LSD-07416
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                                                                                                                                                                                                                                                                                                                            ; LENGTH: 4802
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-10-267-502-24
                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.2 SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/267,502
CURRENT FILING DATE: 2003-01-27
NUMBER OF SEQ ID NOS: 439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4057 TTGGTGGAGTTTAACATGGTCAAAGGCAACGAGGGTTTTCGAGAAAGTATCATTCCCCAT 4116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----TCCAAGCACTTCTCCGAGTCTCTTAAGCAGAGAAATGCTGGCTTAAAAAGAGGAC 4260
ThrAlaIleAsnGlnAlaLysAlaGlyAsnProProValLeuLeuThrProGluGlnIle 66
                                 TACAAGATAAGTACCAGCAACAATCCTGCTCCAATG-----AAGGTAAAGGCGCTGGGC 1980
                                                ---AlaLeuAlaGlnGlnAsnAsnProAlaAsnIleIleAsnHisValProAlaHisAsp 46
                                                                                                 CTGCTGGGCAAAGATCTACTCTCGAAAAAAGTTAGCACCCACAGCTACCTGGAGCACATG 4452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LeuThrGlyGlyGlnValLeuAlaValGlyThrAlaGluTyrAsnTyr---GluPheMet 854
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                                                                                                                                                                                                 0.119
148.50
33.50%
18.94%
3.14%
                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----CACGATGAACTGGTGGACCTGGAAAAG 4332
                                                                                                                                                                                                               Mismatches: Indels:
                                                                                                                                                                                              4802
190
146
376
291
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SerProlleSerArgIleGlyGlu	GAAATGATTTATCCCGACGACGAAAACAAAGA	2841 335 2842	Оy
SerProlleSerArgIleGlyGlu	GAAATGGATGTGGCTGGCCTGAACCTCGATGAGATTGTCCACTTT  LysLysAsnLeuIleGluAsnAlaSerAlaGluHisGlyTyrPhe	284	ν,
SerProlleSerArgIleGlyGlu	GAAATGGATGTGGCTGGCCTGAACCTCGATGAGATTGTCCACTTT  LysLysAsnLeuIleGluAsnAlaSerAlaGluHisGlyTyrPhe	284	
SerProlleSerArgIleGlyGlu			В
SerProlleSerArgIleGlyGlu	GAAATGGATGTGGCCTGGACCTCGATGAGATTGTCCACTT	315	9
SerProlleSerArgIleGlyGlu	ValAlaAspGluValProLeuLeuIleGlvAspValPheHisHi	295	B Qy
SerProlleSerargIleGlyGlu		2731	Ъ
SerProlleSerArgIleGlyGlu	IleAspTyrArgAlaValGluValArgGlyGluGlyAlaAspAsp	275	δ
SerProlleSerargIleGlyGlu	lleargAsnSerlleGlyGluValAspValIleIleHlsAspLe     ::: :::::  TCGCTAGACGACCTACGCTCCTATCTGGCCGAGGA	2680	8 6
SerProlleSerArgIleGlyGlu	CATCCAACAGGCATTGTGCTGCGACGCGTGGGTTACTATAC	263	дb
SerProlleSerArgIleGlyGlu	ArgGlnThrAlaLeuValAlaAlaArgAlaValGlyTyrTyrAs	235	δ
SerProlleSerArgIleGlyGlu	GCCATTGAGGCAGCTGCTGCAGAGGCAGCAGCAGCAGCAC	2590	Вb
SerProlleSerArgIleGluGlu	AlaLeuCluAspIleThrGlnGluSerAlaMetAspLeuAsnGly	215	ð
NSETPTOILESETATGILEGLYGLU	ThrSerAlalleGlySerSerHisGlnLysThrGluProTyrAl :::           ::::::       AGTGTGCTTTCGAACAGATCTAATGAGGCAGAGGACTCTGCAGG	2530	B 64
AAATCCCTCTAGCTCTACTTGAGATTCAGATCATGCCTCTAGCCGCGCGCG	CAATCCAGCACCATTGCACGTCGCGAAACCTTCACTTCG	247	용 :
AAATCCCTCTAGCTGAATTGAGATCATAGCATTGAGAATCCATTGAGAATTCAAAATCCATTGAGAATTCAAAATCCATTGAGAATTCAAAATCCATTGAGAATTCAAAATCCATTAGCAGAATTAGAAATCCAAAATCCAAAATCCAAAATCCAAAATCCAAAATCCAAAATCCAAAATCCAAAATCCAAAATCCAAAATCAAAAAA	GlvValAsnLvsValProArgLeuLvsAlaLvsPheTvrGlnSer	17	Ş
nSerProlleSerArgIleGlyGlu 100 ::	LysProGlyLeuIleLysArgLeuTyrAlaArgLeu:::     :::     CGACCATCCTCCACCGTTCGCCTCTCGGTGTCAACCATCCCAGAG	, 161 , 2416	d Q
nSerProlleSerArgileGlyGlu 100 :::	GGATCGCCCATAACAGCACCCTCAACGAGCTTGTGCCACG	2356	Дb
nSerProlleSerArgIleGlyGlu 100 :::	GlyGluGlnProAsnSerGluValValValPro	144	Š
SerProlleSerArgIleGlyGlu 100 :::	CTGCATCCTAACAACCTTGAGAAGGTACGCCAGCACAACATTCAG	229	Вb
SerProlleSerArgIleGlyGlu 100 :::	<pre>IleAsnProAsnAspTyrIleProGluTyr</pre>	, 133	δ
SerProlleSerArgIleGlyGlu 100 :::	:::	223	8
SerProlleSerArgIleGlyGlu 100 :::	GlnGluSerThrGluMetGlv	, 126	ó
ASPMetSerVallieGluGluThrThrPro 117	AACAAAGAACGCGAGTCGTTTAGCGGAGCCATTCCAAGTGAGCCG	N	Дb
SerProlleSerArgileGlyGlu 100 :::                         AATCCCTCTAGCTCTATTGGCAGTGCTCCC 213 ASPMetSerVallleGluGluThrThrPro 117	LeuSerLeuGluGluLeuPheAla	/ 118	Ş
SerProlleSerArglleGlyGlu 100 :::	AACACGCCCAATCTCGACCCAAAGGC	21	8
SerProlleSerArgileGlyGlu 100	lnSerProProLeuGlyLeuAspMetSerValIle	, 101	Ş
SerProlleSerArdleGlvGlu 100		208	8
C. C. I. C.	AspValValAspPheAspAspGlnSerProTleSerArc		ò
AlaLysProGlnSe :: CTGAAGCCCAGTGC	GlnAlaArgLeuAsnAlaAlaGlyLeuAsnAlaLysProGlnSer	, 67 5 2026	β 6
	::: :::   ::: AGCACACTTAATAGAAAATCGCTGTTTC	1981	Вb

670 3924	GlnGlnGluValPheGlyHisSerThrAsnGlyPheAspLeuSerThrArgThrLeuGlu ::: TACAAAGGACGCAGCTTTAAGCTCAGTTTTGGTCCA	651 3889	Оу	
650 3888	LysProLeuSerHisProLeuAsnAspGlnLeuArgAlaThrLeuGlyTyr:::::::::::::::::::::::::::::::::::	634 3829	Qу рь	
633 3828	GlyAlaGluLeuArgLeuSerGluAspLysLysGlyValLysLeuTyrAlaThr ::::: AAGCCCAAAGTG	616 3787	Оу	
615 3786	GlyThrArgLeuValThrLysPheGluHisAsnLeuIleAsnArgAspGlyTyrGlnAla 	596 3727	Qy Db	
595 3726	AspLysProArgAspGlyGlnIleGlyLeuGlyTrpGlySerAspThr	580 3667	Qy Db	
579 3666	ProAlaAspValTyrGlnSerLysLysValProLeuTyrValPheValAlaSer	562 3607	Qy Db	
3606	ArglysThr	559 3547	Qy Db	
558 3546	GluSerGluAsnGluVallleAspLeuProGluArgThrAlaLeuAlaAsn	542 3493	ОУ	
541 3492	SerileLeuGlyArgileSerAspAlaValSerAlaValAlaArgAlaileLeuProAsp 	522 3433	Qy Db	
521 3432		502 3373	Qy Db	
501 3372	SerasnLeuIleGlnAspLysLeuAsnLeuValAlaAlaLysAlaArgHis	485 3313	ОУ	
484 3312	GACCCAAAAGCCTTGGTCGCAGGTGTTGCCAGCGGATTCAGGCCAATGGATGATACCGCC	472 3253	Qу Дъ	
471 3252	SeThrLeuGluProValIleGluThrValGluLeuThrAsp	458 3193	Qy Db	
457 3192	റ – >	438 3133	Qy Db	
437 3132		430 3073	Qy Db	
429 3072	AspLeuIleAlaThrArgTyrPheAsnMetValAsnThrGluIleValPhe	413 3022	Qy Db	
412 3021	LeuLeuThrValAsnMetGlyGluAlaTyrAsnLeuGlnAlaValArgAlaLeuSerAsn :::	393 2974	Qy Db	
392 2973	ThrAsnGlnLeuThrThrAspProAspLysLeuProValLysArgGluLeuLeuGluGln::::::               :::	373 2941	Qy Db	
2940	CTAAACCGTGACGCCCAGGTCACTTTGGACCAAGTATGGCCGTTGGACAAGACC	2887	מם	

Alignment Scores: 0.288 Length: 6609 Pred. No.: 146.00 Matches: 185 Percent Similarity: 34.148 Conservative: 138 Best Local Similarity: 19.568 Mismatches: 365	; SOFTWARE: PatentIn version 3.1 ; SEQ ID NO 1 ; LENGTH: 6609 ; TYPE: DNA ; ORGANISM: Staphylococcus epidermidis US-10-172-502-1	FILE REPERENCE: POTAGUSOLIBAS  FILE REPERENCE: POTAGUSOLIBAS  CURRENT APPLICATION NUMBER: US/10/172,502  CURRENT FILING DATE: 2002-06-17  PRIOR APPLICATION NUMBER: US 60/298,098  PRIOR FILING DATE: 2001-06-15  NUMBER OF SEO ID NOS: 29		Qy       855 LysAspLeu 857                               Db       4453 TTGGATTTA 4461	Qy 836 LeuThrGlyGlyGlnValLeuAlaValGlyThrAlaGluTyrAsnTyrGluPheMet 854:	Qy 833 LysGlyTyr	Oy 813 AlaGlyGlyAspGlnSerIleArgGlyTyrAlaHisAspSerLeuSerProIleSerAsp 832	Qy 796 TyrIleTrpSerAspAsnPheAsnHisValProTyrArgLeuArgPhePhe 812	Qy 776 GlyAspAsnAlaTyrGlySerAsnArgAlaHisGlnMetThrGlyGlyIleGlnAlaGly 795	Qy 759AspAlaAsnMetAlaIleAlaArgAlaGlyIleSerGlyValTyrSerPhe 775	Qy 749 LeuGluValGlySerSerGlyLeuValSer	Qy 731 ThrValalaAspAsnLeuValAsnProMetArgGlyTyrArgGlnArgTyrSer 748	Qy 711 AspPheValAsnGlyLysProSerGlnGluAlaLeuLeuAlaGlyValAlaValHisLys 730	Qy 691 TyrArgLeuAspLysLeuLysThrGlnAlaProProGluThrTrpGlnAspLeuProVal 710	Db 3925CAAAACTCATTGGTACTGCCAAGCACCTATAATAACATGCAAAAACCTAAAAA 3975	671 HisGluTleSerArgSerTleTleGlnAsnGlvGlvTrnAsnArgThrTvrSerTenArg
Ob 4912 CTTAAACAAGGTCAACAAGATTAGACAATACGACACAAGATGCA 4956  Oy 327 GlyTyrPheAspGlyArgTrpLeuAspArgSerValAspValIleLeupfro 343	291AlaPheThrThrValAlaAspG              4852 GATACACCACATGCTACGACAGATGAATTAGATG 307 PheHisHisGlyLysTyrGluThrLysLysAsnL	Db 4774	Qy 237 ThrAlaLeuValAlaAlaArgAlaValGlyTyrTyrAspIleAspLeuSerIleIleArg 256 :::      Db 4747 AATGGTATTGCTACGTTAAAAGGCGTA	Qy 217 GluAspIleThrGlnGluSeralaMetAspLeuAsnGlySerIleDroArgLeuArgGln 236	Qy 197 SerAlaIleGlySerSerHisGlnLysThrGluProTyrAlaAsnIleLysAlaAlaLeu 216 :::	Qy 177 ValAsnLysValProArgLeuLysAlaLysPheTyrGlnSerGlnSerGlyGluThr 196	Qy 157 LeuGluProGluLySProGlyLeuIleLySArgLeuTyrAlaArgLeuPheAsnAspGly 176 :::    :::	Qy 137 ASpTyrIleProGluTyrGlnGlyGluGlnProAsnSerGluValValValValProProThr 156	Qy 119SerLeuGluGluLeuPheAlaGlnGluSerThrGluMetGlyIleAsnProAsn 136 ::: :::       :::         Db 4429 TTAGATAAAATCAATGATTAGTTGCTAAAAGCTATGACAAATATCACGAAT 4479	Qy 104 ProLeuGlyLeuAspMetSerValIleGluGluThrThrProLeu	Qy 87 ValAsnPheAspAspGlnSerProIleSerArgIleGlyGluGlnSerPro 103 :::         ::::::::         :::::::::	Qy 67 GlnAlaArgLeuAsnAlaAlaGlyLeuAsnAlaLysProGlnSerGlnAlaLeuAspVal 86 :::::::::	Qy 47 ThrAlaIleAsnGlnAlaLysAlaGlyAsnProProValLeuLeuThrProGluGlnIle 66        :::       Db 4234 GCAGCTATTGACCAAGCT	Qy 27 GlnAlaLeuAlaGlnGlnAsnAsnProAlaAsnTleIleAsnHisValProAlaHisAsp 46	Gaps: 168-2 (1-919) x US-10-172-502-1 (1-6609)	Query Match: 3.09% Indels: 258

696	677 IleIleGlnAsnGlyGlyTrpAsnArgThrTyrSerLeuArgTyrArgLeuAspLysLeu	, 8
5880	21 CAGTTACAAAACATTTATGACACTGCTATTGGACAAATTGATCAAGATCGTAGCAATGC	Db
676	657 HisSerThrAsnGlyPheAspLeuSerThrArgThrLeuGluHisGluIle	. 9
œ	AAGCGAATGTTCAAGCAACAGTAGAAGAAAGAATAGTATTTTAG	Db
656	uArgAlaThrLeu(	οy
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5619	5581 GCAATAGTACAAGTTGAAAAAGAGTTAATTAAAGCTAAAA	рь
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5580	::: ::     AGCGACAGATGAAGAACAAAATGC	Вþ
563	luValIleAspLeuProGluArgThrAlaLeuAlaAsnArgLysT	Q V
5520	AAACCAGCGACAACAGTTAAAGCAACAGCATTACAA	Db
543	eSerAspAlaValSerAlaValAlaArgAlaIleLeuProAspGluSe	9
5460	5407GATAAGACTGCGCAAGTTAATCAAAATAGTATCGATGCTCAAAATATTATTTCA	В
525	ValLeuAlaIleAsnHisAspAspGlyValAsnArgSerIleLeuG	Qy
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16	397 AsnMetGlyGluAlaTyrAsnLeuGlnAlaValArgAlaLeuSerAsnAspLeuIleA	, Q
5142	92 GATACAACGCAAGATGAACGAAATGTTGCTATTGCTGCGTTAAATAAA	b B
396	377 ThrThrAspProAspLysLeuProValLysArgGluLeuLeuGluGlnLeuLeuThrVal	Qy
5091	5044ATTGATGAAAGTAATAATAATCAACTCGATGCAATACGAAATACGCTA	Db
376	hrIleAspProLysThrAsnGlnLe	Оу
5043		В
356	344AspAsnThrAlaAspValSerLeuIleTyrAspThrGly	γo

CSE CSE	Ωy	Db	Qy	DP QA	Db	Qy	Дb	ΟУ	Db 43	ο <sub>ν</sub>	Db Qy	Db	Qy	Db	Qy	Db	γQ	Db	Qy	Db	Qy	ДD
RESULT 37 Sequence 39 GENERAL INF APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT FILI PRIOR APPL PRIOR FILI PRIOR FILI PRIOR FILI PRIOR FILI SOFTMARE: SOFTMARE: SOFTMARE: SOFTMARE: SOFTMARE: SOFTMARE: NOGANISM: FEATURE: NAME/KEY:	900 6448	6388	881	6328	6268	854	6211	834	6151	814	79 <b>4</b> 6112	6070	774	6019	754	598	737	5950	717	5896	697	5881
37 30-800-39 100-800-39 100-800-39 101-800-39 102-800-39 103-800-39 103-800-39 103-800-39 103-800-39 103-800-39 103-800-39 103-800 103-800-39 103-800	ThrGlyValLysGluGlu 905     :::   :::    ACGCCTATTAAAAAAAAA 6465	TTACCTGCTGAAGTGATAAAAGCGTCACCAAAAGTGGGGCAACCTGCTCCAAAAGTTTGT 6	erProV	ThrAsnAspThrLysIleGly 8		MetLysAspLeuArgLeuAlaValPheGlyAspIleGlyAsnAlaTyrAspLysGlyPhe 8	CTAAA	GlyTyrLeuThrGlyGlyGlnValLeuAlaValGlyThrAlaGluTyrAsnTyrGluPhe 8	GGCGATATAGAAGCAGTAATTACTGAAAAAAGAAAATAGCTTACTGCGCATTGATAACATT 6	5	AlaGlyTyrileTrpSerAspAsnPheAsnHisValProTyrArgLeuArgPhePheAla 8 :::         :::         :	TTACAAATGGATGAAGAATTAAAAAACAGCACGCACTAATGCT	AsnArgAlaHi	GTAAGTGATCGTAATAAGGCTGATGCATTAAAAGCTATAACTGCATTAAAA 6	SerGlyValTyr	ACGTGTTACACATTTAGTGCAAAATTATCGAAAA	ValAsnProMetArqGlyTyrArqGlnArqTyrSerLeuGluValGlySer 7		oSerGln	၈ –	Lys	::::::::::::::::::::::::::::::::::::::
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CACCAAC 15	lSerAlaMetAspLeuAsnGlySerIleProAs     :::    :::           GGTGCACTGGATAATTCAGGCAGTATTATTGC	- AlaLeuGluAspileThrGlnGluSerAlaMetAspLeus- 	1569	Оу
CACCAAC 15	CAT	AACGGCAACAGGTACGGGTACTGC	09	Оy
209	AATGCATCTTTCCATTCATCC	rSerHisGlnLysThrGluProTyr     :::    AAGCAATCAAACCGGCAATAGTTAC	201 1449	Оy
erAlaIleGlySe 201 ::::       CGTCAAATGGTTC 144	SerGlyGluThrSerAlaIleG     ::::  TTACAAGATACCGCACCAACCGCGTCAAATG	AATGGATAACCGTGGCCGCATGGGTTTAC	193 1389	Оу
erSerGln 192 :::    ATGCACAAGGCAA 138	LysAlaLysPheTyrGlnSerSerGln	nLysValProArgLeu	178 1329	Оу
snAspGlyValAs 178     :::   CCGACACACTTAA 132	ysArgLeuTyrAlaArgLeuPheAsnAsp :: AAGCCGCTCGTTTGGCTATTGATACCGAC	uProGluLysProGlyLeuIleLys :            ::: aaaTGaaaCATCAGGCACCATTGAA	158 1269	Qу
ProProThrLeuGl 158 :::   :: ACAATTCGGGCAGCCTGAA 126	GluValValValPi    :::::::: AGGCGAAATATTGATTCACAATTO	AAACACTGGCACATTATTGTCCTCA	150 1209	Qу
er: 149 	.spTyrIleProGluTyrGlnGlyGluGlnProAsnSer:        	eAsnProAsnAspTyrIleProGlu : ::: TGAAAACAGCGGTACGGCGGTATCC	133 1149	Оy
hrGluMetGlyIl 133    :: AGTCAGGGCGT 114	luLeuPheAlaGlnGluSerT	uGluThrThrProLeuSerLeuGluG ;       ::::::: GCGGAACACAAA-GTCAATATCCGC-	1114	Qу
LeuAspMetSerValIleGl 113 ::: ::: † :: CGAAAGATACGGATAATACA 111	Gly	ProlleSerArgIleGlyGluGlnSer-ProProLeu :::	94 1057	Оy
eAspAspGlnSer 93	<pre>\$lnAlaLeuAspValValAsnPhe         : : :       sTGGCGATTGATGCA</pre>	GlyLeuAsnAlaLysProGlnSerGlnAlaLeuAspVa 	74 · 1012 ·	Оy
InalaargLeuAsnalaala 73 ;         GCATTCGTAATCAAGGG 101	ProValLeuLeuThrProGluGlnIleGlnAlaArg		955	Qу
aGlyAsnPro 57     AGGAGGTATGTAT 954	AspThrAlaIleAsnGlnAlaLysAlaGlyAsnPro	IleAsnHisValProAlaHisAspT    :::    GGCACACATATCCCTTTATTT	39 901 •	Оy
nProAlaAsnIle 38          TACAGCCAACAAC 900	lnalaLeualaGlnGlnAsnAsr      CTGCTGCCAATACGTCAAACAA	TyrLeuProLeuMetThrSer :::    ::::: :: CATTCGCCTATTCTCAATAAT	9	Db Db
	Length: 7542 Matches: 187 Conservative: 150 Mismatches: 336 Indels: 297 Gaps: 48	Scores: 0.376 145.50 imilarity: 34.818 l Similarity: 19.328 ch: 3.088 9	gnment d. No.: re: cent Si t Local t Local ry Matc	Align Pred. Score Perce Best Query DB:

2498	CAGCGGTAA	Дb
585	GlnSerLysLysValProLeuTyrValPheValAlaSerAspLysProArgAspGl	Qy
565 2486	549 pLeuProGluArgThrAlaLeuAlaAsnArgLysThrProAlaAspVa	Qу
549 2426	532 rAlaValAlaArgAlaIleLeuProAspGluSerGluAsnGluValIleAs	Qу
532 2366	512 aIleAsnHisAspAspGlyValAsnArgSerIleLeuGlyArgIleSerAspAĺaValSe 	ДУ
512 2318	LeuAl	Qу
492 2267	480 eGluPheSerAlaSerAsnLeuIleGlnAspLysLe :::: ::	Оy
480 2207	eLeuMetAspIleSerProIl   ::: :: ::   CGGATTAAAGCAAATAACCT	Qу
460 2160	440 1SerPheGluGlnSerSerSerSerArgThrGluProAlaGlnValAspGluSerThrLe :	Оу
440 2126	420 eAsnMetValAsnThrGluIleValPheProGluArgGluGlnIleGlnAsnAspGlnVa	Qy Db
420 2066	402 rAsnLeuGlnAlavalArgAlaLeuSerAsnAspLeuIleAlaThrArgTyrPh .::::	Qy Db
402 2009	hrValAsnMetGlyGluAlaTy    :::      CGATACAATCAGGCCGTGATGT	Qy Db
382 1986	362 pGluValValPhePheThrIleAspProLysThrAsnGlnLeuThrThrAspProAspLy	Qy Db
362 1962	346 rAlaAspValSerLeuIleTyrAspThrGlyThrGlnTyrArgPheAs:	Qy Db
346 1907	327 yTyrPheAspGlyArgTrpLeuAspArgSerValAspVallleLeuProAspAsnTh:	Qу
327 1847	313 uThrLysLysAsnLeu	Оу
313 1796	IleGlyAspValPheHisHisGlyLysTyrGl	Db .
294 1736	leaspTyrArgAlaValGluValArgGlyGluGlyAlaAspAspLysAlaPheThrTh	Qy Db
274 1695	SluProValTy	Qy Db

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                                                                                                                                      US-10-282-122A-29937
                                                                                                 Sequence 29937, Application US/10282122A GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Maione, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3033
                                                                                                                                                                                                3287 TC---AATAAAGGCTATCTT
                                                                                                                                                                                                                                                                           3269 TATACATT
                                                                                                                                                                                                                                                                                                                                                                                                                           3152 CGCATCGCAAAGCATTAAGCCATCATGCGCCCAGCCAAGGCACTGAGTTGCCGCAAAGCA
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
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PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR PELICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
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APPLICANT:
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TYPE: DNA
1114
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FILING DATE: 2000-09-06
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GCGGAACACAAA-GTCAATATCCGC
                                     uGluThrThrProLeuSerLeuGluGluLeuPheAlaGlnGluSerThrGluMetGlyIl 133
                                                                            CGTTTAGTCAATAGTGGCACGATGGCTGCCGCCAATG----CGAAAGATACGGATAATACA 1113
                                                                                                                  ProIleSerArgIleGlyGluGlnSer-ProProLeuGlyLeuAspMetSerValIleGl 113
                                                                                                                                                            CAGTTGTTTGCTTCCGGTAATGTGGCGATTGATGCA--
                                                                                                                                                                                                 GlyLeuAsnAlaLysProGlnSerGlnAlaLeuAspValValAsnPheAspAspGlnSer
                                                                                                                                                                                                                                         GCCAACAAAATCACCTTGATCAGTACGGCCGAGCAAGCAGGCATTCGT---AATCAAGGG 101
                                                                                                                                                                                                                                                                                                                      GGCACACATATCCCTTTATTT-----GCGATTGATACAGGCAAATTAGGAGGTATGTAT
                                                                                                                                                                                                                                                                                                                                                           IleAsnHisValProAlaHisAspThrAlaIleAsnGlnAlaLysAlaGlyAsnPro---
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Matches:
Conservative:
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2066	AAATCGTTATCCAACAACGGCACACTTO	2010	DЬ
420	LeuGlnAlaVa	402	οy
2009	ACGATACAATCAGGCCGTGATGT	1987	Db
402	lLysArgGluLeuLeuGluGlnLeuLeuThrValAsnMe	382	Qy
1986		1963	В
382	leAsp	362	Qγ
1962	ACCAATCAACAACTGATTATTCACGATGGTCAGCAATCT	1908	Db
362	spValSerLeulleTyrAspThrGly7	346	δδ
1907		1848	Db
346	pValIleLeuPrc	327	Qy
1847	ATTGAAACCGAT	1797	В
327	AsnLeuIleGluAsnAlaSerAlaGlu	313	Qγ
1796	TATCAGTGATGCGGTCCACATTCAAGCCGGCAGCCTGAATAATCAAAATGGCAACATCAC	1737	Ъ
313	AlaAspGluValProLeuLeuIleGlyAspValPheHis	294	Qy
1736	AATGCAAAAGGTTCGGCGTTTGACAATCAAATGGAACAAT	1696	Db
294	1GlyAlaAspAspLysAlaPheTh	274	δÃ
1695	AATAATGCAGGACAAATAGACATTCATCAGTTA	1663	망
274	alIleIleHisAspLeuGlyGluPr	254	ş
1662	TGGTCAAACAGATGTTAGTGCGCAACAAGGTTTA	1629	В
254	lnThrAlaLeuValAlaAlaArgAlaVa	234	δÃ
1628	GATGGGACAATTCGCACTCATGGTGCACTGGATAATTCAGGCAGTATTATTGC	1569	ф
234	aLeuGluAspIleThrGlnGluSerAlaMetAspLeuAsnGl	215	Qy
1568	GTACGGGTACTGCAACCGTTTCTATATCAAACATAACTGCGCCTACCTT	1509	В
214	AlaAsnIleLys	210	Qy
1508	ATGCATCTTTCCATTCATCCACTACCACACAA	1449	DЪ
209	SerHisGlnLysThrGl	201	Qy
1448	TGGATAACCGTGGCCGCATGGGTTTACAAGATACCGCACCAACCGCGTCAAATG	8	В .
201	SerGlvGluThrSerAlaIleGl	193	VO
1388		1329	Ф
192	LysValProArgLeuLysAlaLysPheTyrGlnSerSerGln	178	γQ
1328		1269	Db
178	;ProGlyLeuIleLysArgLeuTyrAlaArgLeuPheAsnAspGlyValAs	158	Оу
N		0	gg '
158	ProProThrLeuGl	150	VQ VQ
1208	GCGGTATCGCAACAAGGCACTCAAATTCACAGTCGATTCA	1149	Ъ
149	eAsnProAsnAspTyrIleProGluTyrGlnGlyGluGlnProAsnSer	133	Qy

spAsnLeuValAsnProMetArgGlyTyrArgGlnArgTyrSerLeuGluValGlySerS 754	734	Qy
ATTTAATACCGATAGCCAAATCATTGCTGGTGGCAATCTCATTGTACAAACAGAAAAAAA 2972	2913	дb
ProSerGlnGluAlaLeuLeuAlaGlyValAlaValHisLySThrValAlaA 734	717	ОУ
CCAAACTGCGCCAGCCAAAATCATTTCAGGTAATGATTTAACCATTGATGGTAAAGAAGT 2912	2853	Db
AlaPro-ProGluThrTrpGlnAspLeuProValAspPheValAsnGlyLys- 716	700	Qy
T	2808	ДD
pAsnArgThrTyrSerLeuArgTyrArgLeuAspLysLeuLysThrGln 699	683	ργ
TGTCTATAACGATGAATCAGACCACTTACGCACCCCTGATGGAGCGGCGCGCATGAAAATTG 2807	2748	Db
rIleIleGlnAsnGlyGlyTr 683	676	Qy
	2700	Db
yHisSerThrAsnGlyPheAspLeuSerThrArgThrLeuGluHisGluIleSerArgSe 676	656	Qy
TTTGAAAACGCAGTTGGTAGAAACAGGGCGCGCGCATATTGTTGATTACGAAGCATTTGG 2699	2640	Db
nLeuArgAlaThrLeuGlyTyrGlnGlnGluValPheG1 656	643	Qy
AGAAAAGCTGCACAATACCAATGAGCA 2639	2613	Дb
spLysLysGlyValLysLeuTyrAlaThrLysProLeuSerHisProLeuAsnA	623	Qy
GATACACAATGCCGGCGCAACCATTGAAGCTGCAGGCAAAATGCGTTTAGGTGT 2612	2559	Дb
sAsnLeuIleAsnArgAspGlyTyrGlnAlaGlyAlaGluLeuArgLeuSerGl 623	605	Qy
CGATATGGCGGTTGGCGGCGCATTAGATACCAATGGCCAAGCCACAGGCAAAGCCCAAAG 2558	2499	дb
yGlnIleGlyLeuGlyTrpGlySerAspThrGlyThrArgLeuValThrLysPheGluHi 605	585	Qy
TTACAGCGGTAA 2498	2487	Db
lTyrGlnSerLysLysValProLeuTyrValPheValAlaSerAspLysProArgAspGl 585	. 565	Qy
ATCGGACAATTA	2427	Дb
pLeuProGluArgThrAlaLeuAlaAsnArgLysThrProAlaAspVa 565	549	Qy
CGCTATTGCGGCTACCCGCTTAGACAATCAAGATGAAAACGGTACAGGTGCCGCCATTGC 2426	2367	Db
rAlaValAlaArgAlaIleLeuProAspGluSerGluAsnGluValIleAs 549	532	Qy
CGGGCAAATGAATAATATCGGTACAGGTCGGATTTATGGCGACAATAT 2366	2319	Db
aIleAsnHisAspAspGlyValAsnArgSerIleLeuGlyArgIleSerAspAlaValSe 532	512	Qy
CAATTTAACCAATAGAGGCTTGATTGACGGACAACAAACCAAAATCCAAGC 2318	2268	Db
uAsnLeuValAlaAlaLysAlaArgHisLeuTyrAspMetProAspAspArqValLeuAl 512	492	Qy
TGATAATGCAGCACAAGGCAACATTCAATCCGGCGGTACGACAGACA	2208	Db
eGluPheSerAlaSerAsnLeuIleGlnAspLysLe 492	480	Qy
	2161	Db
rc	460	Qy
GTCGCTCAGTACACGAGGCAGCCTGAAAAATTCA 2160	2127	Db
lserPheGluGlnSerSerSerSerArgThrGluProAlaGlnValAspGluSerThrLe 460	440	Qy
	2067	Db
eAsnMetValAsnThrGluIleValPheProGluArgGluGlnIleGlnAsnAsnGlnVa 440	420	0 <b>v</b>

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Percent Similarity:
Best Local Similarity:
                                                                                       Alignment Scores: Pred. No.:
                                                                                                                                      ; ORGANISM: Neisseria
US-10-018-470-1
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US-10-018-470-1/c
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                       Query Match:
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CURRENT FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/113,068
PRIOR FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: PCT/US99/25373
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: GB-0004695.3
PRIOR APPLICATION NUMBER: GB-0004695.3
PRIOR APPLICATION NUMBER: PCT/US/05928
PRIOR FILING DATE: 2000-03-08
                                                                                                                                                                                                     SOFTWARE:
SEQ ID NO 1
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Grandi, Guido
TITLE OF INVENTION: Neisseria Genomic Research
FILE REFERENCE: CHIR-0319
                                                                                                                                                                   LENGTH: 22
TYPE: DNA
                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 107
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Scarlato, Vincenzo
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-GAGATTCAGAACCGCATGGGC 179868
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764 179010	GlnArgTyrSerLeuGluValGlySerSerGlyLeuValSerAspAlaAsnMetAlaIle :::::: 	745 179033	g 99
744 179	ThrvalAlaAspAsnLeuValAsnProMetArgGlyTyrArg	731 179090	д О
730 1790	AsnGlyLysProSerGlnGluAlaLeuLeuAlaGlyValAlaValHisLys	714 179150	ОУ
713 1791	LysThrGlnAlaProProGluThrTrpGlnAspLeuProValAspPheVal	697 179210	Db dd
696 1792	GlyTrpAsnArgThrTyrSerLeuArgTyrArgLeuAspLysLeu 	682 179270	d Q
681 1792	PheAspLeuSerThrArgThrLeuGluHisGluIleSerArgSerIleIleGlnAsnGly	662 179318	QУ
661 1793	AspGlnLeuArgAlaThrLeuGlyTyrGlnGlnGluValPheGlyHisSerThrAsnGly:::   ::    ::: ::: ::: ::: ::: ::: :::	642 179372	₽ Q
641 1793	SETGluAspLysLysGlyValLysLeuTyrAlaThrLysProLeuSerHisProLeuAsn	622 179426	Оy
621 1794	LysPheGluHisAsnLeuIleAsnArgAspGlyTyrGlnAlaGlyAlaGluLeuArgLeu :::	602 179486	DP GA
601 1794	AspGlyGlnIleGlyLeuGlyTrpGlySerAspThrGlyThrArgLeuValThr	584 179537	DP GA
7		w ·	망
563 1795	GluAsnGluValIleAspLeuProGluArgThrAlaLeuAlaAsnArgLysThrProAl:::      :::     :::     :::     :::	544 179573 564	o B o
543 1795	LeuGlyArgIleSerAspAlaValSerAlaValAlaArgAlaIleLeuProAspGluSer	524 179609	Оу Дъ
523 1796		509 179660	Оy
508 1796	AsnLeuValAlaAlaLysAlaArgHisLeuTyrAspMetProAspAsp	493 179717	B 6
492 1797		480 179774	Qу
479 1797	GluProValIleGluThrValGluLeuThrAspGlyIleLeuMetAspIleSerPro :::   :::     :::	461 179834	Дb
460 1798	SerPheGluGlnSerSerSerSerArgThrGluProAlaGlnValAspGluSerThrLeu	441 179867	DP P

Sequence 1. Application US/10018470A  GENERAL INFORMATION:  APPLICANT: Hickey, Erin  APPLICANT: Hickey, Erin  APPLICANT: Peterson, Jeremy  APPLICANT: Tettelin, Herve  APPLICANT: Wenter, J. Craig  APPLICANT: Wenter, J. Craig  APPLICANT: Masignani, Vega  APPLICANT: Mora, Masignani, Vega  APPLICANT: Galeotti, Cesira  APPLICANT: Mora, Mariosa  APPLICANT: Scarlato, Vincenzo  APPLICANT: Rappuoli, Maria  APPLICANT: Rappuoli, Rino  APPLICANT: Rappuoli, Rino  APPLICANT: Pizza, Mariagratia  APPLICANT: NUMBER: US/10/018,470A  CURRENT APPLICATION NUMBER: US/10/018,470A  CURRENT FILING DATE: 1999-04-30  PRIOR APPLICATION NUMBER: PCT/US99/25373  PRIOR APPLICATION NUMBER: GB-0004695.3  PRIOR APPLICATION NUMBER: GB-0004695.3  PRIOR APPLICATION NUMBER: PCT/US99/25378	Qy 908 ProlleLysLeuHisPhePhelleGlyThrProPhe 919 Db 178451 ATCCAACGCCTTCCAATTCCAACTCCGCACGTTC 178416	Qy 890 ProvalGlyGlnValArgValAspValAlaThrGlyValLySGluGluGlyAsn 907	Qy 871LysGlyPheThrAsnAspThrLysIleGlyAlaGlyValGlyValArgTrpAlaSer 889            ::::	Db 178631 AACAGCAGTTCCGCGACCGGCGGCAGGGTTCAAAACATTTACGGCGCCGGCAATACCCAT 17857	Qy 870 870	Qy 857 LeuArgLeuAlaValPheGlyAspIleGlyAsnAlaTyrAsp	Qy 846 ThralaGluTyrAsnTyrGluPheMetLysAsp 856	Qy 829 ProlleSerAspLysGlyTyrLeuThrGlyGlyGlnValLeuAlaValGly 845	Qy 809 LeuArgPhePheAlaGlyGlyAspGlnSerIleArgGlyTyrAlaHisAspSerLeuSer 828	Qy 791GlyIleGlnAlaGlyTyrIleTrpSerAspAsnPheAsnHisValProTyrArg 808	Qy 785 AlaHisGlnMetThrGly790	Db 179009 GCCCTGCCTGGCAAACTGCAATACTACTCCGCC 17897

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PRIOR FILING DATE: 2000-03-08
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 2272325
TYPE: DNA
ORGANISM: Neisseria meningitidi
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Best Local Similarity:
Query Match:
                                                                   Db 180128 GACTTCTACCAAAATAACGGCTACTTCGATTTCCGTATCCTCGATACCGACATCCAAACC 180069
                                                                                                                                                                  Db 180188 CTGACACGAAGCCAATTCAACGAGCAGAAATTTGCCCCAAGATATGGAAAAAGTAACC 180129
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                                                                                                                                                                                                                                                                                                                                                                 180260 GGCAACCAAGTCTATTCCGACCGCAAACTGATGCGG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180377 GGCAAACTCAATATCCAAATCACGCCCAAAGTAACCAAACTCGCCCGCAACCGCGTCGAC 180318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180437 TTTAATCAGGCGACACTCAATCAGGCAGTCGCCGGCCTGAAAGAAGAATACCTCGGGCGC 180378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180548 GTTATCGAACGCCCCACCATCGGCTCGCTCAACATCACCGGCGCAAAAATGCTGCAAAAAC 180489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180701 ACCGAGCCGAGTACCGTATTCAACTACCTGCCCGTCAAAGTCGGCGACACCTACAAC··· 180645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 AsnAsp------TyrIleProGluTyrGlnGlyGluGlnProAsnSer 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 ThrProLeuSerLeuGluGluLeuPheAlaGlnGluSerThrGluMetGlyIleAsnPro 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             225 MetAsp------LeuAsnGlySerIleProArgLeuArgGln------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150 GluValValProProThrLeuGluProGluLysProGlyLeuIleLysArgLeuTyr 169
341 IleLeuProAspAsnThrAlaAspValSerLeuIleTyrAspThrGlyThrGlnTyrArg
                                                                                                 321 AsnAlaSerAlaGluHisGlyTyrPheAspGlyArgTrpLeuAspArgSerValAspVal 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           187 PheTyrGlnSerSerGlnSerGlyGluThrSerAlaIleGlySerSerHisGlnLysThr 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          170 AlaArgLeuPheAsnAspGlyValAsnLysValPro-----ArgLeuLysAlaLys 186
                                                                                                                                                                                                                                                                                                               290 LysAlaPheThrThrValAlaAspGluValProLeuLeuIleGlyAspVal------
                                                                                                                                                                                                                                                                                                                                                                                          270 GlyGluProValTyrIleAspTyrArgAlaValGluValArgGlyGluGlyAlaAspAsp 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           250 IleAspLeuSerIleIleArgAsnSerIleGlyGluValAspValIleIleHisAspLeu 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              207 GluProTyrAlaAsnTleLysAlaAlaLeuGluAsp-----IleThrGlnGluSerAla 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----ThrAlaLeuValAlaAlaArgAlaValGlyTyrTyrAsp 249
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Indels:
Gaps:
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121
342
278
                    360
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696 179211	GlyTrpAsnArgThrTyrSerLeuArgTyrArgLeuAspLysLeu	179270	Db dd
179271	  GCAAAGCATCGACCAGCATCAA	179318	Db
681		662	Qy
661	AspGlnLeuArgAlaThrLeuGlyTyrGlnGlnGluValPheGlyHisSerThrAsnGly::::    ::: ::: ::: ::: ::: ::: ::: :::	642	Qy
179319		179372	Db
641	SerGluAspLysGlyValLysLeuTyrAlaThrLysProLeuSerHisProLeuAsn	622	Qy
179373		179426	Db
621	LysPheGluHisAsnLeuIleAsnArgAspGlyTyrGlnAlaGlyAlaGluLeuArgLeu :::	602	Qy
179427		179486	dd
601	AspGlyClnIleGlyLeuGlyTrpGlySerAspThrGlyThrArgLeuValThr	584	Qy
179487		179537	Db
179538		179538	ρþ
583	${\tt AspValTyrGlnSerLysLysValProLeuTyrValPheValAlaSerAspLysProArg}$	564	Qy
563	GluAsnGluValIIeAspLeuProGluArgThrAlaLeuAlaAsnArgLysThrProAla :::       :::	544	Qy
179538		179573	Db
543	LeuGlyArgIleSerAspAlaValSerAlaValAlaArgAlaIleLeuProAspGluSer	524	0y
179574		179609	0y
523	ArgvalLeuAlaIleAsnHisAspAspGlyValAsnArgSerIle	509	Db
179610		179660	Db
508	AsnLeuValalaAlaLysAlaArgHisLeuTyrAspMetProAspAsp	493	Qy
179661		179717	Qy
492		480	Db
179718		179774	Db
479	GluProValIleGluThrValGluLeuThrAspGlyIleLeuMetAspIleSerPro :::   :::	461	Qy
179775		179834	Db
460		441	Qy
179835		179867	Db
440	AsnMetValAsnThrGluIleValPheProGluArgGluGlnIleGlnAsnAspGlnVal:::	421	Db
179868		179888	Oy
420	gTyrPhe	401	Qy
179889		179924	Db
400	AspLysLeuProValLysArgGluLeuLeuGluGlnLeuLeuThrValAsnMetGlyGlu	381	Qy
179925		179972	da
380	PheaspGluValValPhePheThrIleAspProLysThrAsnGlnLeuThrThrAspPro::: ::	361	dd
179973		180008	VQ
180009	AACGAAGACAAAACCAAGCAGACCATCAAAATCACCGTCCACGAAGGCGGACGTTTCCGT	180068	дд

Оy Db	дь 94	g dd d	g	Qy	Db !	٥	3 5	8 8	QY	Db	Qy	ρb	9	Дb	δõ	Db	Qy	DЪ	ρ	Db	Qy	Дb	Qy	DЬ	Qy
908 178451	11	71 71 71		870	<b>⊢</b>	857	178751		829	178862	809	178913	791	178973	785	179009	765	179033	745	179090	731	179150	714	179210	697
ProIleLysLeuHisPhePheIleGlyThrProPhe 919 :::     ::           ATCCAACGCTTCCAATTCCAACTCGGCACGACGTTC 178416	ProvalGlyGlnValArgValAspValAlaThrGlyValLysGluGluGlyAsn 907    :::    :::::	LysGlyPheThrAsnAspThrLysIleGlyAlaGlyValGlyValArgTrpAlaSer 889  LysGlyPheThrAsnAspThrLysIleGlyAlaGlyValGlyValArgTrpAlaSer 889	17	870	GTCCGCCTGAGCCTGTTTGCCGACGCAGGCAGCGTGTGGGACGGCAAAACCTACGACGAC 178632	17	ThrataGluTyrAsnTyrGluPheMetLysasp 856	CCGAAAGTCTATGACGAATACGGCGAAAAAATCAGCTACGGCGCAACAAA 178752	ProIleSerAspLysGlyTyrLeuThrGlyGlyGlnValLeuAlaValGly 845	17	808	GAAGTCGGCATTGCGGGCGGCTACGGCAGAACCAAAGAAATCCCCTTCTTT 178863		TCTTCCCCCTGAGCAAAACCTTCACGCTGATGCTCGGCGGC	70	GCCCTGCCTGCCAACTGCAATACTACTCCGCC 178974	AlaArgAlaGlyIleSerGlyValTyrSerPheGlyAspAsnAlaTyrGlySerAsnArg 784	ъ.	D		Ω	AAGAAATACGGCAAAACCGACGGCACAGACGGCAGCTTCAAAGGCTGGCT		GCAGAACACCTGACCGTCAACACCTACAACAAAGCGCCCCAAACACTATGCCGACTTTATC 179151	LysThrGlnAlaProProGluThrTrpGlnAspLeuProValAspPheVal 713

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